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this sequence represents the polyprotein of the BeV proteivpe isolate BFVI. When compared with all known viral sequences, small but stantient terilinear behalouses are cheered with the non-structural proteins of the Hamburius family, and with the pestivitieses. The demains shown in the features table are however, rentained by assignand. The polyprotein, and epitopes of it are bestoric in discount induction intrologies, in a subject analyst BFV. The presence of Abs against BFV can be detected using an
                                                                                                                              Polypoptide(s) comprished from eated hepatitis C virus sequences for detection, presention and treatment of hepatitis C intection
                                                                                                                                                                                           Train to Fig 1: Huppy English.
                                                        white DY. Butter W.
                                                                                             WELL 1993 - 345334/4.
                  ARTON STH. ( SIM.)
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Sporty Match. 0.50; Score 50; DR-14; Louoth 3011; Rost Local Stain mity 34,50; Fred. No. 4,46.00; Matches 10; Conservative 9; Mismatches 10; Indels 0; Gaps

Sequences and AA: Immunicates 17.

47 THE VELFAIRMITRELERNMENHAMPPMSTEE 1849 (do 1745 ciaptophowikhottwakhmwhiisqiq 1774

Berrand angles ed Necesiter et grott Aziztettő Do times 207 sec

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Reagents for isolating, amplifying and detecting HCV polynucleotide(s) - used to monitor spread of blood-borne non-a, non-b hepatitis virus infection and screen blood samples for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kuo G, Weiner AJ, Urdea MS, Irvine BD;
                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure: Fig 1: 67pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tabel: (GLY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tabele (VAn)
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                                                                                                                                                                                                                                                     /label- (ASN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= (GLY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tabel (CYS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= (SER)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Tabel TYR
                                                                                                                                                                                                                  /label- ILE
                                                                                                                                                                                                                                                                                           /label- SER
                                                                                                                                                                                                                                                                                                                                                                Alabel LEU
                                                                        /label- ARG
                                                                                                           /label- THR
                                                                                                                                             /label= THR
                                                                                                                                                                                  /label: VAL
                                                                                                                                                                                                                                                                                                                             label= THR
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N-PSDB; AAQ21744.
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Hepatitis C virus 1.
                                                                                                                              Misc-difference 176
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                                                                                                                                                                Misc-difference 334
                                                                                           Misc-difference 11
                                                       Misc-difference 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton M.
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The sequence is derived from a composite HCV cDNA from HCVI, a prototypic HCV. The DNA sequence is based upon sequence information derived from a no. of HCV cDNA clones, which were isolated form a no. of HCV cDNA clones, including the "c" library present in lambda qt11 (ATCC No.40394), and from human serum. The HCV cDNA clones isolated by methods described in We9014436.

The clones from which the sequence was derived arc 5'clone32, b114a, 18q, aq30a, CA20a, CA20a, CA216a, pil4a, CA167b, CA156e, CA84b, 33c, 40b, 37b, 35, 36, 81, 25, 13i, 12f, 14i, 11b, 7t, 7e, 8h, 33c, 40b, 37b, 35, 36, 81, 23, 37b, 25c, 14c, 81, 33f, 33q, 39c, 35f, 19q, 26g, 16a, 6k and p131jh.
                                                                                                                                                                                                                                                                                                                                    Gaps
acid indicated in the features, the parentheses indicated that the heterogeneity was detected at or near to the 5^{\circ} or 3^{\circ} end of the HCV in the clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis; liver disease; HCVI; monoclonal antibody; epitope; immobilised reagent; immunoassay; diagnosis; detection; treatment; infection.
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                   0.5%; Score 59; DB 13; Length 3011; 34.5%; Pred No 4 40+03;
                                                                                                                                                                                                                                                                                                                                     Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- NS3
/inote- "putative protease domain"
1651..2100
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/label- E2/NS1
/note= "possible envelope"
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/note= "unknown function"
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/note= "unknown function"
                                                                                                                                                                                                                                                                                                                                                                    1821 VLLPAIKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                                                                                                                                                       Repatitis C virus (RCV) Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR31621 standard; protein; 3011 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/note= "polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= C domain
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                                                                                                                                                                                                                                                                                                                                         10; Conservative
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                                                                                                                                                                                                                                                                                                                        Rest Local Similarity
                                                                                                                                                                                                                                                        Sequence 3011 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9300365-A.
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                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR31621;
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                                                                                                                                                                                                                                                                                                                                       Matches
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91115-0722489.

24-JHN 1991-

Heterogeneities in cloned DNAs of HCV1 are indicated  $b_T$  the amino

AAY 14571

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HCV1; serum; qt111.
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                                                                                                                                                                                                                                                                                                                  16-MAR-1990;
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                                                                                                                                                                                                                                                                                    20-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                            Houghton M,
                                                                                                                                                                                                                                                                                                    18-MAY-1989;
                                                                                                                                                                                                          13-SEP-2000.
                                         15-JAN-2001
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            AAB18541;
The insertion procedus two mew isolates of deparities C virus (BPV), JI and JP. inser two isolates compeles indicated and confidences when that are fishing the uncertainty the much of described and sequences may be used to detect near, non-H BPV (NAMEH) polymorleotides by hydriths attention for distincts of NAMEH intections. They may also be used to serve these distincts or named to be one of the isolates and the polymorleotides for this intection. The isolates are naturally occurring within as a the polypeptides may be used as a zaccine for the initial static to periods to protect against injection with many in the processure sequence represents the amino acid sequence of HCV-1 oRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Silve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Heparthis " Witts isolates, assemble of diamesis of hepartitis
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                                                                                                                                                                                              Heger Pits ( with as HeV) als J^{2}: HeV-Es and A. non-B HeV; NANBHE HeV interference varieties.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Scure Se; DR 20; Length 2955;
44.5%; Pred. No. 4.4e+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on M. Tryine Mb. Kolbert JA:
Weiner AJ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ξ
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1745 yinpayitowaklettwakhowotisaiq 1773
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                                                                         AAY14375 standard; Protein; 2955 AA
                                                                                                                                                                                                                                                                       Loration/Malifiers
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                                                                                                                                                                 Amino acid sequence of BCV 1 oRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                            SOFF STOLES.
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8808 408045.
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                                                                                                                                    ANVIOLETTE (THE COLTE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WP1: 1999 480844/41.
                                                                                                                                                                                                                                                                                         Mish difference 441
                                                                                                                                                                                                                                                                                                                    MISC difference 4:1
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15 SEP 1999
                                                                                                                                                                                                                                                                                                                                                                  EPUSULA A.
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                                                                                                      AAY 14471
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M.1.\* \*\*...

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comprises a hepatitis C View (HCV) artisense polynocleotide. The HCV is characterized by a positive stranded knA genome which has 40% beneforg at the polypeptide level to a HCV polyphotein. The antisense polynocleotide binds to cellular polynocleotides which exhance and/or are required for viral interviently, replicative which eshance and/or are required to viral interviently, replicative ability, to be otherwicity. The antisense polynocleotides may also be designed to bind with high specificity, to be of interased stability, to be stable and to have low toxicity, to be of interased stability. The anatomic masses with line and to have low toxicity. The composition also compute section is used for preventing HCV replication in a system. The posent sequence is encoded by a novel HCV cDNA sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition comprising a hepatitis C virus antisenso polyno bodide which is complementary to or corresponds to a sense strand of the virus genome, and selectively hybridises to it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The specification describes a pharmareutical composition which
                                                                                                                                     Hepatitis C virus; HCV; antisense polynucleotide; polyprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 59; DB 21; Lenath 2955; 34.5%; Pred. No. 4.50003
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                                                              Polyprotein encoded by sense strand of BCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1821 VILIPATEPTVPQTERNWKNHMGPFMSILO 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-1990; 20000EP-0109602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kuo G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    890S-0325338.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8908-0341344
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Best Local Similarity 34.5%
Matches 10; Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       course of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-566891/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORP.
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1821 VLLPAIKKTYKQIEKNWKNHMGPFMSILQ 1849
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                                                                                                            /label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton M, Choo QL,
                                                                                                                      Misc-difference 1949.
                                                                                                                                                                                                                                                             Misc-difference 2690.
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                                                                                              Misc-difference 1948
                      Misc-difference 1454
                                                                                                                                                                                           Misc-difference 2385
                                                                                                                                                                                                                                                                                       Wischdifference 2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-284418/38.
                                                                       Mise-difference 1877
                                                                                                                                                                                                                                          Misc difference 2502
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIP-) CHIPON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2955 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also AAQ05955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ05956
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                              Misc difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           epitopes
                                                                                                                                                                                                                                                                                                                                                                           16-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                               17-MAP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                         20-APR-1989;
                                                                                                                                                                                                                                                                                                                                                    19-SEP-1990
                                                                                                                                                                                                                                                                                                                             EP388232-A.
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 O, Gaps
                                                                                                                                                                                                                                                                           AAR70230 is the casewaite legalities forms (HT H,CW,FUH) protein from which the synthetic HCV antigens described in AAR70210 B70720 were derived. These synthetic antigons can be used to screen blood, or blood products for the presence HCV, they can also be used in various specific assays for the detection of HCV antibodies, and
                                                                                                                                                                                                        Synthetic antiques for the detection of hepatitis C virus antibodies—comprise partions of the HCV peptide sequence, for use in screening blood and blood products
                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 59; DB 16; Length 2891, 34.5%; Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                           10; Tude1s
                                                                                                                                                          Pollet D. Van Heuverswyn H;
                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatahas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus (HCV), autiviral agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1821 VLLPATKKTYKQIEKNWKNEIMGPFMSILQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus putative polyprotein.
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Misc-difference 9..9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR08124 standard; protein; 2955 AA.
                                                                                                                                                                                                                                                        Disclosure; Fig 1; 51pp; English.
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Misc-difference 176..176
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//abei-y or M
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                                                                        90EP-0124241.
                                                                                                90EP-0124241.
                                                                                                            90EP-0108611.
                                                                                                                                                                                                                                                                                                                                          antigens, or as immunogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                             Gonservative
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                                                                                                                                    (INNO ) INNOCEMETICS NV.
                                                                                                                                                           Deleys RJ, Macrtens G,
                                                                                                                                                                                  WPI; 1995-116946/16.
                                                                                                                                                                                                                                                                                                                                                                 Sequence 2894 AA;
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 Hepatitis C virus.
                                                                                                             14-DEC-1990;
                                                                        14-DEC-1990;
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                                                 22-MAR-1995
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                          EP644202-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide(s), antibodies and anti-sense polynucleotide(s) for diagnosis and therapy.
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Misc-difference 2349..2349
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Misc-difference 1471..1471
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1877..1877
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2385..2385
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2690..2690
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Best Local Similarity 34.59
Matches 10; Conservative
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Bits separate represents the entire hepatitis of virus polyprotein. BY is a member of the transmiss tamily not appears to encode a basic polyproteic demant ("\") if the N-terminal of the Wiral polyprotein, followed by two alyesprotein domains ("Hi", "EZ/NSI"), upstream of the necessivity all penes NSZ through NSS. See also AAQ39134 48, AAR3982 decembed and AAF90000 according
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14 SEP 1991; 310; 4759575.
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                                                                                                                        Boughton M. Weiner AJ:
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RMA viroaces frequently calible a high rate of spontaneous mortation, thus a virus is considered to be the same of equiv. To HCV if it exhibits a abbal homology of more than 70 percent with the HCV HT if a sequence indicated in the teatures table can immunicate ally minde proteins encoded by HCV. Additional amino acids or chemical aps. may be added to either end of the poptides for the purpose of the acids of the peptides for the purpose of the fact and the acids of the peptides where the world is a like an incidence of the poptides of the peptides for the used for the detection of a fibodies specific for HCV. They may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New synthetic peptides for detecting antibodies to hepatitis or virus - useful in e.g. ELISA assays, and for detection of HOV antiquens or as immunogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Composite hepatitis C vitus; BT-01/2De2/CHL; BCV; non-A non-B; synthetic antigens; blood screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 0.5%; Score 59; DH 14; Length 2894; Best Local Similarity 34.5%; Pred. No. 4.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deleys RJ, Maertens G, Pollet D, Van Heurerswyn H;
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||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| ||: :| 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2275. ...
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Z294 - 16
Z297
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/tabel= 17
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/label: 18
                                               1730..1749
/label 14
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/label-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1992.
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ability or chronicity. The antisense polynucleotides may also be designed to bind with high specificity, to be of increased stability, to be of increased stability, to be of increased stability, and to have low texicity the composition also comprises an agent which causes viral RNA to be inactive. The composition is used for preventing HCV replication in a system. The present sequence is encoded by a novel HCV cDNA sequence, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction PCF, amplify, primer, bepatitis C virus; HCV, asymptomatic, chronically infected; epitope; viral isolate; domain; immunological, cross-reactive; envelope protein; "accine; ap53(BVDV)/9p55, hog cholera virus, postivirus, NSL, flavivirus.
                                                                                                                                                                                                                                                                                                                                                                    Novel composition comprising a hepatitis C virus antisense polynucleotide which is complementary to or corresponds to a sense strand of the virus genome, and selectively hybridises to it -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The specification describes a pharmaceutical composition which comprises a hepatitis C virus (ACV) antisense polymorfectide. The HCV is characterized by a positive stranded RNA qenome which has 40% homology at the polypeptide level to a BCV polyprotein. The antisense polymorfectide binds to cellular polymorfectides which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%, Score 59; DW 21; Longth 2772; 34.5%; Prod. No. 3 90+03; Elyo 9; Mismatches 10: Indole 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1821 VLLPAIKKTYKQIEKNWKNHMSPFMSILQ 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 16; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92WO-US07683.
                                                                                                                                                                                                                                                                    Kuo G;
                                                                           16-MAR-1990; 2000EP-0109602.
                                                                                                                      89118-0325338
                                                                                                                                                                8908-0355002
                                                                                                                                            89115-0341334
                                                                                                                                                                                    90EP-0302866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 34.5%
Watches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               course of the invention.
                                                                                                                                                                                                                                                                    Houghton M, Choo Q,
                                                                                                                                                                                                                                                                                                              WPI; 2000-566891/53.
                                                                                                                                                                                                                              (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2772 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA75296.
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                                                                                                                      17-MAR-1989;
20-APP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993.
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EP1034785-A2
                                                                                                                                                              18-MAY-1989;
                                                                                                                                                                                      16-MAR-1990;
                                     13-SEP-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 59; DR 11; Length 2772;
34.5%; Pred. No. 3.9e+03;
.ive 9; Mismatches 10; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  edimpanzee with chronic HCV infection. A lambda gall library was chimpanzee with chronic HCV infection. A lambda gall library was screened with probes derived from previously isolated clones. The OPF is derived from the overlapping clones pida, cal67b, Cal56e, Ca84a, CA59a, F9-1, 121, 141, 11b, 71, 81, 34, 34, 46b, 37b, 75, 36, 81, 32, 34b, 25c, 14c, 81, 31, 33q, 39c, 35f, 19q, 26q and 15e. This polypeptide can be used to design probes. The detection of HCV nucleic acids, in screening programmes for the detection of HCV nucleic acids, in screening programmes polymucleotides can be used to inhibit viral replication.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by a cDNA compiled Hepatitis G virus cDNA clenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polypeptide(s), antibodies and anti-sense polymusimotide(s) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus, BCV; antisense polynucleotide, polyprotein;
viral infectivity; viral replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus DNA - used for producing probes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4: Mismatches
                                                                                                      Hepatitis C virus polypeptide from long ORF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1821 VILPATKETYKQIEKNWKNHMGPFMSILO 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB18540 standard; Protein; 2772 AA.
                                                                                                                                                Hepatitis C virus, antiviral agent
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                                                                                                                                                                                                                                                                                                                   90EP-0302866.
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89US-0341334.
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                                                                23-JAN-1991 (first entry)
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Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis and therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1990-284418/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2772 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ciral infectivity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ05956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus.
                                                                                                                                                                                        Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                   16-MAR-1990;
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17-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                     20-APR-1989;
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                                                                                                                                                                                                                                                                         19-SEP 1990.
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                        AAR08123;
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RESULT 192 AAB18540

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Gaps

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21.43 AA

Serportion

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using macrolide binding profeigs and analogues, useful for freatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resuptor to the production of the production of a harmonic method of the production of the production of a concentration of a managed macrolide binding protein the which has aftered matrolide-binding specificity relative to the which has aftered matrolide-binding specificity relative to the which has aftered matrolide which specificity protein the production of production of production of colline which specification of colline which specification of colline which specification of colline of protein the MRP. The MRP is selected from PRAP, an PKSG6 binding protein (see AAVESIT), a cyclophilin and a calcinouries a method why chosen from PKAP, EKRP, Cyclophilin ad calcinouries a method to the described of the production of the product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    selectively inhibiting proliteration of a transplanted haemalopoietic cell, a method for treating graff versus fast discouse by selectively inhibiting proliteration of transplanted haemalopoietic cells; and a method of promoting education of an and haemalopoietic activity of a baemalopoietic stom cell from a descri-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This polypoptide comprises FRAP (tori) protein. A claimed method
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41.4%; Pred, No. 4.5e-03;
31.9c - 12; Mismatches - 12; Indels - 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKAP; for1 profein; macrolide binding profein; graft versus host disease; stem cell; dene therap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2070 LIKTEDSSPRVRFAALLIVLALAFK KFNVIVITE 2194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HARD ) HARVARD COLLEGE. (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR08123 standard; protein; 2772 AA
                                                                                                      AAW56027 Standard; Protein; 2549 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of graft versus host disease
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                                                                                                                                                                                                                                                                                           (tirst entry)
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                                                                                                                                                                                                                                                                                                                                                                                        FRAP (torl) protein.
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV28518.
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                                                                                                                                                                                                                                                                                           28 - AUG - 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belshaw PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1998.
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                                                                                                                                                                                                   AAW56027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia.
         RESULT 190
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                                                                                                                                                            GdbS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hench RAFII (AAWALES) is a protein that interacts with the FK506-
Lin LLL proche/Cupangrin complex and modulates assembly of
rup may in cappiages results by the consistency proteins. Its amino
Pril sequence was detroit in a coMa chone (AAR) and other
its coil themay. The rapamyelusbinding domain of RAFII and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAPLI like problems (see also AAW0225-84) can be used in drous streeming assign to identify about a fair modulate the binding of up anythe Bradies problems with FK500 binding proteins. Such applies we be used to alter the order that and/or differentiation of a refer to assign early trees.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTICL page in Finding process PKBP (Emonosuppressive)
Califorder int. Myselber (Landse) and openist; cell profiteration.
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(154): Fred. No. 3,56:03;
                                                     14.4.4. Pulati
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                                                                                                                                                  12: Mismatches 12; Indels
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Zarel - Bapampelm-bin Hora domain
                                                     2. * LOKIBOSSBRVPBAATOVOATABROKERBNYTVIDE 2004
                                                                                                                                                                                                                                               2 " - CLKIPESSPRVPPAALLIVILALABRIKBNYIVILL 1194
                                                                                                                                                                                                                                                                                                                                       The certical species conditions by the key little 1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW days standard; Proteins 2549 AA.
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9405 - 25-735.
Lordy Mat d. Bentantity (1999) 1 Const. Consentity (1999) 1 Consentantity (1999) 1 Consenta
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the GST gene and the fusion protein expressed (see also AARBT31). The fusion protein was used in the isolation of a protein of mammalian origin which binds a glutathione-Stransferase (SST)-FK506 binding protein GST gene and corresponding but at the isolated from Molt4 cells using a complex of the tusion protein GST FKBP12 and rapamycin. The isolated protein molecular weights of 125, 148, 208 and 210 km. The isolated proteins have molecular weights of 125, 148, 208 and 210 km. They can be used for identifying an immunomodulatory, or an antitumour agent. They can also metabolites when complexed with FKBF. Antisense DRA ran be used for metabolites when complexed with FKBF. Antisense DRA ran be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein between jutathione's tranferase (GST) and SEP. The sep genewas amplified in five fragments using the primers given in AAT00756-69. The amplified SEP genewas inserted into a vector already containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents the sirolimus effector protein (SEP). The CDNA encoding this sequence was isolated from Molt. 4 human T-cell legbarmia cells (AFFC CPL 1582) and used in the production of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New effector proteins of rapamyein - which bind to a glatathione S transferase PK506 binding protein-rapamyein complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glutathione-S-transferase; GST; FK506 binding protein; FKBP; PCR; rapamycin; FKBP-rapamycin binding protein; Molt4 cell; amplify; fusion protein; GST-FKBP12; immunomodulatory agent; primer; antitumour agent; detection; antisense DNA; immune system.
                                                                                                                                                                                                                                                                       Query Match 0.5%; Score 59; DB 10; Length 2462; Best Local Similarity 34.5%; Pred. No. 3.30+03; Matches 10; Conservative 9; Mismatches 10; Indels 6
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diagnose HCV-induced NANBH, to raise antibodies for
                                      immunoassay or treatment, or to produce vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1821 VELPATKKTYKÇTEKNWKNHMCPFMSTLQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 16-29; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR81730 standard; Protein; 2549 AA.
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                                                                                                                                        Sequence 2462 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAT00770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FP676471-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR81730
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555x8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The peptides (claimed) can be used to detect heptitis C virus (MCV) antibody positive patients, post-franstusion hepatitis can be prevented by sereching a sample from a MCV antibody positive patient with the
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    /note= "claimed peptide reactive to HCV antibody"
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Pred. No. 3.36+03;
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                                                                                                                                                               Justy March 6.5%; Score 59: 14-10; Tenth 240; hogy Lent Similarity 44.5%; Prod. No. 4c+04; Marches 15: Conserration 9: Mismatches 19: Indets 1
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If is the sequence encoded in the open reading trame of hepatitis \dot{\rm C} virus (BCV) cDNA inserts in clones K9-1 through 15c. It is antiquarie and could be used in immanoassay readents and vacetnes and to detectate antiteduce useful in diagnosis and passive immunotherapy for BCV intection/rea A
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Hepatitis C virus (BCV); non A, non B hepatitis (HANBH)
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It is the sequence encoded in the open reading frame of hepatitis C virus (HVV) coMva inserts in clones 12f through 15e. It is antigenic and could be used in immunodasay reaqents and vaccines and to qenerate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence encoded in the hepatitis C virus (HCV) cDNA inscits in clones 12f through 15e.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence is the peptide encoded by the composite hepatitis C virus (HCV) cONA of AAH90331. The polypeptides are used to diagnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                           Hepatitis C virus gene - used for prodn, of polynucleotide probes, polypoptide(s) and antibodies for diagnosis, prevention and treatment of infection.
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34,59; Pred Nr 2 96+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; fig 32; 235pp; English.
                                                                                                                                               Houghton M, Chao QL, Kuo G;
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                                                                                    (CHIR ) CHIRON CORPORATION.
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                                                                                                                                                                                                         WPI: 1989-215054/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2261 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lord Similarity
es 10, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
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                                                                                                                                                                                                                                          N-PSDB; AAN90331
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                          18-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1989.
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Best Lead e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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48) TSLALSLAHELAPVETLABNELKETMKTSKESVEESFTEEAVLABLGLEBHTEVVLSATSA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMAS which possessed several erroneous main, avids The FNA viruses are used in vaccines against pollo. The screening method can be used during amplification of the source virus for vaccine prodn. to ensure maintenance of C at position 2493 in the viral genome i.e. increasing the attenuation. The new prod, overcomes the problem of errors introduced during replication of ss RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The protein sequence was deduced from the cDNA sequence of P3 policylars obtains. In Avillar, Start Sequence of a fact time RNA virus, i.e. the cDNA directs the plods, of a viable RNA virus which is phenotypically similar to the source virus. The tull length cDNA is phenotypically similar to the source virus transcription of pLED3 cDNA using TS RNA polymerase produced RNAS which possessed secent effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New vacatime against infectious pollo virus comprises RMA virus for producing RNA virus CDMA and viable RMA virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 59; DB 13; Length 2206;
21.0%; Pred. No. 2.8e+03;
ive 17; Mismatches 47; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Republiks Clinus, close 12t, clone 15e, probe, tapcine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Tatem JM, Wookslovy CL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 6; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 FELFKEHFSSEVTISNLLINLF 561
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                                                                                                                                                                                                                                                                              900S-0570000.
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nes 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AA022965.
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                                                                                       W09203538 A.
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                             Poliovirus.
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RNA virus; error reduction.
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                                                             AAR22210;
RESULT 181
               AAR22210
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          0.5% Score 59; Db 15; Tenqth 1764;
25.88; Pred, No. 2 10.53;
ive 12; Mismatches 42; Indels e
                                             Susserve at two
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This sequence represents a Hellcohaetter pytori differ protein of the investion. The polypepides can be used for preventing or treating the Hellcohaetter intertions, and austroducdend discusses associated with these intertions, including acute, chronic, and attophic mastrilis, and peptic ulter discusses, e.g. gastric and droobned in ers. they can also be used for the production of antibodies. The products can also be used to and diagnosis.
                                                                                                                                                                                                                                                                             GHPO protein; Helicobacter Intection; gastroduodomai disease; gastrifis;
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86.7%; Prod. No. 2.10003;
(ve. 11) Mismatches 8: Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INME) MERIEUX ORAVAN PASTEUF MERIEUN SERUMS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   True type 3 politovirus profein from LED4.
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                                                  AAW98354 standard; Protein: 1737 AA.
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970S-0833457.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-0506471.
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                                                                                                                                                                                                                                                                                                           poptic alcer disease.
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01 AFR 1997.
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RESULT 180
                          AAW98 154
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/note: "potential protein-kinase C phosphorylation site"
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/note= "potential protein kinase C phosphorylation
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//note- "potential casein kinase 2 phosphorylation
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/label= Phosphorylation
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                                                                                                                                                                                                                                                                 this sequence represents a Repartitis of thus (ReV) antides, combination of
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41.53; Prod. No. 9.2002;
ive 9; Mismatches 10; Indels 0; Caps
                                                                   Tailmais a Three Legalitis Carras antiques - used for detection of specific antibodies to diamose infection
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N POST-BUILDAND PSYMBOL
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This acquence represents a tusion protein constructed from the begatifies evirus core domain (which is situated at the carboxy ferminus of the tusion protein) and a c200 construct (a fusion of the NS3 and NS3 domains). This protein used in the construction of nevel confined to a five of accordance of immunological activity than any simple HCV antiden. An example of immunological activity than any simple HCV antiden. An example of immunological activity than specification comprises a first antiden containing at least W antiden actids of the C domain of the HCV polyprotein and a second antiden comprising at least. B amino actids of the NS3 domain, the NS4 domain, the S4 domain of the RCV polyprotein in the form of a fusion protein a physical mixture of board to a soild matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               It is the sequence encoded in the open reading trame of hepatitis 'viris cbNA inserts in clones 141,m 11b, 71, 7e, 8h, 4c, 40t, 47b, 6, \alpha, \alpha, and 18h, 32, 34b, 35e, 14c, 8h, 4t, and 4e, it is antiqueric and could be used in immunoassay requests and vaccines and to generate antihodies useful in diagnosis and passive immunoatherapy for BCV intection/row. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded in the hepatitis C virus (HVV) cDNA inserts in clones 14i, 11b, 7f, 7e, 8h, 33c, 40b, 37b, v5, 36, 81, 32, 44b, 25c, 14c, 81, 31f, 33q and 39c.
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34.5% Pred, No. 9.2002;
.ive 9, Mismatches 16: Indels (
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97 Mismatches
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Houghton M, Choo q-L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WFI, 1989 159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1766 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                               1021 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N PSDB; AAN92097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 · NOV 1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 · Ban 1988,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP318216-A.
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                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP92041;
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 178
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Choo Q, Houghton M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-00T-1988;
14-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-APR 1990,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5683864-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 · NCV 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                   AAW34481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-DEC
                                                                                                                                                                                                                                                                                                              RESULT 176
                                                                                                                                                                                                                                                                                                                              AAW34481
                                                                                                                                                                                                                                                                                                                                                                                XX COOCCOXX
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cutionres PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant antigens representing distinct antigenic regions of Hepatitis C virus (BCV) geneme, useful for detection of antibodies and antigens in body fluids of individuals exposed to BCV ^{\circ}
                                                                                                                                                         A specific antidenic region of the HCV genome is expressed as a chimeric fusion with E coll CMP-KDO synthetase (CKS) gene. The fusion profein page 3 can be used to detect antibodies and antigen in body fluids from individuals exposed to HCV e.g. in confirmatory, competition or neutralisation assays. The same amine acid sequence (i.e. AAR33571) is described in the specification as pHCV-205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV recombinant antiqen pHCV-205 amino acid sequence SEQ 1D NO:54.
                                                                             Hepatitis C assay using recombinant C-100 region antiqens - for detecting antibudies and antique in body fluids from infliduals exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                            0.5%; Score 59; DB 14; Length 992; 34.5%; Pred. No. 8.8e+02;
                                                                                                                                                                                                                                                                                                                                                      10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cusey JM, Dailey SH, Dawson AT,
toll, Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopatitis C virus; HCV; antiqen; detection; antibody
                            Casey JM, Desai SM, Devare SC, Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                 1821 VILLPAIRETYRQIEENWENHMOPPWSTLO 1849
                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 79-73; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69029 standard; Peptide; 992 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0179896.
96US-0646757.
96US-0572822.
90US-0614069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                        Local Similarity 34.5%
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desail SW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-122352/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ABBO ) ABBOTT LAB.
                                                      WPI; 1993-093940/Ti
 (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                       992 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lesniewski RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6172189-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -AUG-1991;
-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-NOV-1992;
10-JAN-1994;
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07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09 JAN-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB69029;
                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                        Matches
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the present invention describes recombinant Repatitis C virus (RCV) antigens (I). (I) is useful as a reagent for the detection of antibodies and artigen in body fluids from individuals exposed to BCV. The BCV assay uses reliable and efficient reagents and methods to accurately detect the presence of BCV antibodies in samples obtained from the individuals auspected by the ABS1379 and AABS001 to AABS002 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "c200 (amino acids 1192-1931 of HCV polyprotein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR primer, amplify, HCV, hepatitis c virus; antigen combination; NS:
C domain; S domain; NS5; HCV polyprotein; anti-HCV antibody; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note: "c22 (amino acids 2-120 of HCV polyprotein)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ċ
                                                                                                                                                                                                                                                                                                                                                                                                Longth 992;
                                                                                                                                                                                                                                                                                                                                                                                          0.5%, Score 59, DR 20: Longth 040
34.5%; Pred. No. 8.80+02;
.lvc 9; Mismatches 10: Indels
                                                                                                                                                                                                                                                            in the exemplification of the present invention.
Claim 3; Column 197-202; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1821 VLLPAIKKTYKQIEKNWKNBMGPFMS11.0 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV antigen combination pSOD/c200/core.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc difference 1..154
/note- "hSOD fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  801 viapavginwakletfwakhmwnfisgiq 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW34481 standard; Protein; 1021 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference 1..902
/note- "linker"
Misc-difference 903..1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0325338.
89US-0341334.
89US-0353896.
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RRUS-0191263.
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87US-0139886.
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RMUS-0271450
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                                                                                                                                                                                                                                                                                                                                                                                                      Oucty Match 0.59
Best Local Similarity 34.59
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note≈ "I
Misc-difference 160..899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 155.,159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIPON CORP.
                                                                                                                                                                                                                                                                                                                     Sequence 992 AA;
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Kuo G;

Mart : tex

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Gut ferrez RA:

hawson GJ,

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antiques (1). (1) is useful as a readeft for the detection of antihodies and autique in body fluids from individuals exposed to BCV. The BCV assay uses reliable and efficient readefts and methods to accurately detect, the presence of BCV antibodies in samples obtained from individuals suspected of having BCV infection. AARAZZZB for AARSTR1 to AARSTR79 and AAR69001 to AABSD02 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus (HCV) genome, usefur for detection of antihodies and antiques in body fluids of individuals exposed to {\rm H}^{\rm e}{\rm V}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes recombinant Hepatitis (*virus (HCV)
                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant antigens representing distinct antigenic regions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heparitis C virus; elfo antiqui; PKS fusion protein:
CMP-KDO synthetase; Immunodot assay; Non-A, non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.5%; Score 59: DB 22; Lorotth 973;
llarity 34.5%; Fred. No. 8.6e+02;
Concerpative 9; Mismalches 10; Indels
                                                                                                                                                                                                                                                                                                                  revare SG, Desai SM, Casey JM, Dailey SH,
Lesniewski RR, Stewart JL, Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Column 191-198; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1821 VLLFAIKKTYRQIEKNWKNHMCPFMSILO 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CKS-BOV antiqen insion profein pBCV-18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR33571 standard; protein: 992 AA
                                                                                                                                                                       9008-0572822.
9008-0614069.
9108-0748561.
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                                                                                 97118-0867611.
                                                                                                                    92US-0989843.
                                                                                                                                     94HS-0179836.
                                                                                                                                                                                                                          910S-0748566.
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Rest Local Similarity
Matches 16, Conserv
                                                                                                                                                                                                                                                                                 (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     973 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1991;
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             US6172189-B1.
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                                                                                 02-JUN-1997;
                                                                                                                     19-NOV-1992;
                                                                                                                                                        19961
                                                                                                                                                                       24 - AUG - 1990;
                                                                                                                                                                                                             21-AUG-1991;
                                                                                                                                                                                                                              21-AUG 1991;
                                                                                                                                                                                                                                               29-OCT (1991;
                                               09-JAN: 2001.
                                                                                                                                        10-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                              0.7 - NOV
                                                                                                                                                          0.1 - MAY -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 174
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 o; caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV recombinate and Lea pBPV 7x amino acid sequence 3Eg ID Not53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 republics busing using recombinant. The replan antidens too between my antibodies and intiden in body timids from individuals exposed to heppings by yours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A specific interpret region of the HVV percent is expressed as a chimnetic first or with E even thereto spuritelase (CAS) gener, the tistor protein pHV 12, can be assed to detect antibodies and antique in bedy linds from individuals exposed to HFV e.g. in confitmatory, competition of centralisation assays.
                                                                                                                                                                                                                                                                                                      Thro antique; TKS tusion protein; immunodot assar, Non A, non B Repatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spore 50 - 58 14; Length 973;
Prod. No. 8,6000;
*: Mismarohos - Lo; Indols
lo; Indels
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 9: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [82] VILPALKKIYKULEKNWKNHANFMSILU 1849
                                  142) VILPAIRKITREJEENWENBRIEFRATIQ 1843
                                                                                                                                                                                                                                                                      38S HeV and open basish protecting pHeV 7a7
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                                                                    78 - Singasytha (keetiwakaasanisa) a a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tiim ti Pide Ct ti Zuspir Endlish
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                                                                                                                                                             studing proteins of AA
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Locati Similarity 34,545
ass. Location Statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.547.53.71.47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.08-07485 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PrAMP and (thist entry)
                                                                                                                                                                                                                                    of 330, 1999 (1988) entry)
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185 T. S. 188 J. S. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WELL 1703 033940/11.
                                                                                                                                                                                                                                                                                                                         Sym had ases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARR ) ARR (LLAR)
                                                                                                                                                                                                                                                                                                        Hepatitis e vicus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatana of virus.
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21 AUG 1991: EL AUG. 19 EU

Section 18

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Sector Materials

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The primers (AAG55718-23) are used to design probes (AAR45745-18) for
the alpha-thA pelygocase gove (AAG5724). The gene lised I was
amplified using primers (AAG5725-26). This method of closing
alpha DAA polymerase is easy and effective allowing quick and easy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                        by amplifying using primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repailitis Classay using recombinant C-100 region antigens—for detecting antibodies and antigen in body fluids from individuals exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A specific antigenic region of the MCV genome is expressed as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 AIN SQLAMILERSVQTRAVBRQTPBISHTTHISPVPTIFFPAQFOLPWIN 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hopatitis C virus, C100 antique, CKS fusion protein, CAF nor synthetase, imbenedet assay, Non A, nor B lepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 59; DB 15; Length 882;
95.8%; Pred. No. 7.5e±02;
ive 8; Mismatches 28; Indels
                                                                                                                                                                                                                                                                           of specified sequence and cloning to hybridise probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terrare so, Eupprecht KR:
                                                                                                                                                                                                                                                                                                                                                                                                                                          production for genetic engineering research.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKS-HCV antigen fusion protein pHCV-72.
                                                                                                                                                                                                                                                          Cloning of alpha DNA pulymerase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         claim 5; Page 62-66; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR33569 standard; protein; 971 AA.
                                                                                                                                                                                                                                                                                                                   Claim 2; Page 8-12; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9108-0748566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92WO-US07187.
                                                                             92JP-0194713.
                                                                                                                   92JP 0194713.
                                                                                                                                                      (TAKI ) TAKAKA SHUZO GO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-Jun-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 30,89
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Casey JM, Desai SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WP1; 1994 094940/11.
                                                                                                                                                                                                WPI: 1994-061475/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (АВВО ) АВВОТТ БАВ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             depatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  882 AA;
                                                                                                                                                                                                                     N PSEUR; AAQSS724.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 - AUG - 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-AUG-1991;
JP06014780-A.
                                                                           80 - JUN - 1992;
                                                                                                                40-JUN 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9 +04087-A.
                                       25-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR33569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 170
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The present invention describes recombinant Hepatitis C virus (BCV) antiques (I). (I) is useful as a reagent for the detection of antibodies and antique in body floids from individuals expresed to BCV. The HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cut torrog RA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant antigens representing distinct antigenic regions of Hepatitis C virus (HCV) genome, useful for detection of antibodies and antigens in body fluids of individuals exposed to HCV .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       assay uses idiable and efficient reasonts and methods to accurately detect. The presence of HCV antibodies in samples obtained from individuals suspected of having HCV infection. AAB7221B to AAF3235, AAB51371 to AAB71379 and AAB69001 to AAB69032 represent sequences used
chimeric fusion with E.coli CMP-KDO synthetase (CKS) gene. The fusion protein pHCV 72 can be used to detect antibodies and antigen in body fluids from individuals exposed to HCV e.g. in confirmatory, competition or neutralisation assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCV recombinant antigen pHCV 72 amino acid sequence SEQ ID No:52.
                                                                                                                                                                                                                                                                                                                                   ċ
                                                                                                                                                                                                                                                              0.5%; Score 59; DB 14; Length 971;
34.5%; Pred. No. 8.6e-02;
Live 9; Mismatcher 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PH, PAWSON CT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C virus; HCV; antigen; detection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 17, Column 187 192, 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JM, Natley St
Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                1821 VLLPAIKKTYKÕIFKNWKNHMGPPMSILO 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                              780 viapavqtnwqklotfwakhmwnfisgiq 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB69027 standerd, Pepride: 971 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CaseT JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0867611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0179896.
96US-0646757.
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90US-0614069.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lesniewski RR, Stewart JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0748561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0748566.
91US-0748565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-APR-2001 (first entry)
                                                                                                                                                                                                                                                                 Query Match
Bost Local Similarity 34.5%
Matches 10; Cosservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desa: SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPT; 2001 122352/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           971 AA;
                                                                                                                                                                           971 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6172189-B1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 AUC-1990;
07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-AUG 1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Decare 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR69027;
                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB69027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME OF THE PROPERTY OF THE PR
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Score 59; DB 22; Length 971; Pred. No. 8.5e+02;

0.5%;

Query Match Bost Local Similarity

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It is the sequence encoded in the open reading trame of departitis \tilde{v} virus (\theta v V_{\rm c}) can insert in clones 40b, 47b, 45, 46, 81, 42, 44 and 2°c. It is an epitope which could be used a minimons asy reserved and vaccines and to generate antibodies usered in diagnosis and passive immenoifiering to the HeV intection/mon-A, non-H by attitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence encoded in the hepatitis C virus (BPV) cDNA inserts in chares 40b, 37b, 35, 36, 81, 32, 34b and 25c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone; DNA polymerase; hybridise; amplification; denetic endinection; PCK; polymerase chain reaction; restriction map; plesmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.5%; regre 69; lik lor Length 869;
44.5%; fred, No. 7.20:02;
ve. 9; Mismatches lit indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoperitis o virus (HCV); non-L, non-B kepatitis (HANBH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purified hepatitis C virus
- and associated nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Figure 14-A, 14-B, 14-C; 134pp; Ehdiist.
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JOHN WILLIAMENTAL LEMMENTHESTED 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8808-0271450; 08-122714
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                                                                                                                                                                                                                                                                                                                                                   AAP92029 standard; protein; 859 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guery Match 0.5%;
Hest Local Similarity 34.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88EP 0410922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-MAR-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Houghton M. Chao q-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1989-154274,022.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN92085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NoV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 NOV 1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP318216-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP92029:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invertion describes recombinant Hepatitis of virus (HWW) and rems (!). (!) is useful as a reagent for the detection of antibodies as an isometic body fields from individuals exposed to HCW. The HCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the properties is exacted by the open reading trains which extends through the reporties of the solub of AANOOGE. These antiques recent with notthedres in particular with month money heptitis (MANNH). They can be used to discusse HeV induced NANHH, to raise antibodies for immunoussay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepititis Titras, per readini trames temes 406; elsme 406; elsme 45; elsme 45; elsme 45; elsme 25; elsme 2
                                                                                                                                                                                                                                                     assay uses religible and efficient rearents and methods to accurately better the presence. I HEV antibodies in samples obtained from traditional sespected of better HEV interfeor, and 221H to AAF422 65. AAF45127 to AAF4127 and AAF60001 to AAF60032 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 departitis "virus race used for producot polymerboride probes, proypeptobe(s) and another for diagnosis, prevention and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leng Muton. (54) Series 59; 18 lb; Lonoth 858; 863; 1 2ni Similarity (4.54) Pred, No. 7.zerrz. Marches 10; Lonothines 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (*%) Shore for 18 22; langth 781;
44,5%; Prod. No. Fidenoz;
(b) 9, Minmarches 19, infeto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carteautes tit 14 to 14 Zo 14 4: euppe Endlish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in the exemplification of the present insention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PP extending through hepatitis cryical contact
three loss between Presentations of the and Presentations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a, Missairdes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [4] VILEALKRIVKÇIPKNWKNEMSETMETE, 1419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Set compared toward beautisatiquely
     Colonia Carlot Mappe Barrish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or treatment, or to produce vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAPS TV Standard: professor MSM AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           how the Kure St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8705 0122714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELLS CELLS THE VIEW TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jan. 2011. 1.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merst Dooring States in 1935.
Marchael Color Consentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WELL THREE ERS OF 42 NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THI AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HE TAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Part of the Service
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 % love 196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LK N W | 1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 N V 14441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boundhoon M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mark 11 1 A.
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AAI + 14+

The strategy

Sulofolobus solfataricus.

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1821 VELPAIKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                       Example 12; Figure 24; 63pp; English.
                                                                                                                                                                                                                                                                                                        AAB51372 standard; Protein, 781 AA.
                                   protein with E. coli enzyme CKS
                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0867611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0748561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                92mg-0989843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90MS-0572822.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9005-0614069.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0646757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lesniewski RR, Stewart JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-0748565
                                                                                                                                                                                                                                                                                                                                           17-APR-2001 (first entry)
                                                                                                                                                                                                         Ouery Match
Best Local Similarity 34.55
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Devare SG, Desai SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WP1; 2091-122352/13.
WPI; 1994-159120/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus.
                                                                                                                                                                                  781 AA;
          N-PSDB; AAQ62663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N PSDB; AAF32219.
                                                                                                                                                                                                                                                                                                                                                                                                             US6172189-BI.
                                                                                                                                                                                                                                                                                                                                                                                                                                              12091-Niii-co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-AUC-1990;
07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OFT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-TAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                              09-JAN-2001.
                                                                                                                                                                                   Sedneuce
                                                                                                                                                                                                                                                                                                                        AAB51372;
                                                                                                                                                                                                                                                                                        PESTLT 166
                                                                                                                                                                                                                                                                                               AAB51372
                                                                                                                                                                                                                                                                                                                                                  n; daps
                                                                                                                                                                                                                                                                                                                                                                                                                                              Promoter, expression, lac, hepatitis, virus, protein, core, HCV) CES, CTF CHE P. decay P. words, equiverente eyildylyf transferase; CMP-KDO synthetase; HTV, human immunodeliciency virus; al, openAria, envelope proteis, apAl; transmembrase protein
                                                             Hepatitis C assay using recombinant NSI region antiqens - for detecting antibodies and antiqen in body finids from individuals
                                                                                                                                                                                                                                                                             s 0.5%; Score 59; DB-14; Longth 781; Similarity 34.5%; Prod. No. 6.2000;
                                                                                                                                                                                                                                                                                               9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                  1821 VELPAIKKTYKQIRKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                                                                                           |: ||:: ::::| | || || |:| :1
585 viapavqtnwqkletfwakhmwnfisgiq 613
                                                                                               Example 2, Paye 60 63, 175pp, English.
                                                                                                                                                                                                                                                                                                                                                                              AAR52690 standard; Protein; 781 AA.
                    Devare SG;
                                                                               exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88US-0167067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88US-0167067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90US-0573103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9208-0835878
                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-1995 (tirst entry)
                                                                                                                                                                                                                                                                                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bolling TJ, Mandecki W;
                                                                                                                                                                                                                                                                                                                                                                                                                                HCV CKS-33-BCD antigen.
                   Dailey SH, Desai SM,
                                   WPI; 1993-093941/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
  (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                       Sequence 781 AA;
                                             N-PSDB; AAQ38251.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepatitis virus.
                                                                                                                                                                                                                                      proparations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 NOV 1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-PEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5 3127 57 A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 - MAY 1994.
                                                                                                                                                                                                                                                                                 Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 · AUG - ]
                                                                                                                                                                                                                                                                                                                                                            RESULT 165
                                                                                                                                                                                                                                                                                                  Matches
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Casey JM, Dailey SH, Dawson GJ, Gutierrez RA:
U JL, Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant antigens representing distinct antigenic regions of Hepatitis C virus (HCV) genome, useful for detection of antibodies and antigens in body fluids of individuals exposed to HCV ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  licker DNA sequences, 266 amine acids of the HCV NS3 region. 2 amine acids contributed by linker DNA sequences, 256 amine acids of the HCV NS4 region and 10 additional amine acids contributed by linker
                                                                                                                                                                                                                                     the nepalitis core virus protein (HCV) coding sequence was used in the construction of an expression vector designated pHCV-31. This vector allows the fusion of recombinant proteins to a CKS vector allows the fusion of recombinant proteins to a CKS or CTP-2MH-3 west, Femanoco 4.1 sounds of the CKS protein coding sequence in the construct lacilitates the detection and purification of heterologous proteins and gives tusion proteins which are expressed at high Densis. The HCV PYS-3-APM antiqual provinces of the amino acids of FKS, within amino acids contributed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
Prodn. of recombinant hepatitis virus core protein - as fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HCV recombinant antigen pHCV-31 protein sequence SFQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.5%; score 59; DB 15; Length 781; 34.5%; Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus, HCV, antigen, detection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
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AAP COLLE

CMP KDO synthetase; immunodor assay; Non-A, non B bepatitis

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immunoassay: pHCV-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-093940/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C Virus.
                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB
Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB: AAQ48236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 - AUG - 1992;
                                                                                                                                                                                                       21 AUG-1992:
                                                                                                                                                                                                                                                                    21 AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9 104 088 - A.
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                                                                 W09404087-A.
                                                                                                                                  04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR 43594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR33594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hoperitis Coffess Nanderson A, nonew Ropatitis; CMP-KDC synthetaser new structural protein; pePV via disenseis; PKS tusion protein;
Tit PMC school, Warms will know to TP 1457F Transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Simb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New recognition (NSS performance) for the hepartitis diassay for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9,54; Score Oc. 08 14; bondth 781;
9,54; Prod. No. 5,2e+62;
170 - 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reportitis Yeiras, NSA, Clearantiques CKS fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEVE MS on help protection encoded by sector pHEV-41.
                                                                                                        B.W. 1885 O. B.D. Tusi a protein encoded by pBOVOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE PUBLIC VERSION OF THE PRESENTANT OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tat stapasy mayking bakhmwa isata 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sir is unterflass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              example 25 Page 59 53, 164pp; Bredlish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAPAST 40-441-45 Production 784 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treatment of Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C 1087 - 11881 -
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                                       ($1.00 (810) AND ($1.15)
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                                                                                                                                                                                                                                                                                                                                                Report 11 is Virus.
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greeny Matich Best Local S

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AAR (45.71)

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The BRV CKE-ros-Edg expression sector pBRV 31 was constructed from a clone expressing the 4FC KES-BRD and shall designated pBFV-24) and a clone expressing the 4FC KES-BRD antique (designated pBFV-24) and BFCV EGG expression to produce produce pBFCV-29. The FFCV KES-44 and Inserted into pBFCV-29. The FFCV FRO Edge of the FFCV-29 and sometimes of EGG entrance coasists of ZG samino acids of TKS-43-BFCD adjusted edgesists of ZG septembers, ZG and no acids of the FFCV NS+4 region (amino acids of TKS-43-BFC) and and sequences, ZG and the FFCV NS+4 region (amino acids of the FFCV NS+4 region (amino acids of the FFCV NS+4 region (amino acids of the FFCV NS+4 region) and load additional amino acids contributed by linker INA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C assay using recombinant C to region autidous for detecting antibodies and antique in body finids from individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C Virus; non-A, non-B hepatitis virus: NANBH;
non structural protein; CMD-KLO synthetase; CKS tusion protein;
CTP;CMP-3-deoxy-manno-octulosomate cytidyjyl transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 59: FB 14: Length 281; 34.5%; Pred. No. 6.20·02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9: Mismatches 10: Indels
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                                                                                                                                                                                                                                             Casey JM, Tesai SM, Devare SG, Rupprest, KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1921 VILIPAIRKTYRQIRKNWRN9MGPPW411Q 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 87-89; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR33594 standard; Protein: 781 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0748551.
92W0-US07187.
                                                                          91US-0748566.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 4.5%
Mutches 10: Censervative
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The protein (mol.Wt. 90 kD), encoded by pHCV-31, is composed of Lwo-non-continuous coding regions located in the putative non-structural regions of HCV designated NS-3 and NS-4. Clone BCD represents the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C-terminal 256 amino acids of c100-3; the N-terminal amino acids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The polypeptide represents a distinct antigenic region of the HCV genome and can be used for the detection of antibodies and antigens for early diagnosis of HCV intection. The polypeptide can also be used to develop specific inhibitors of viral replication and for
                                                                                                                                                                                                                                             Hepatitis C virus; antigen; diagnosis; inhibitor; CMP-KDO synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins and representing distinct antigenic regions of the BCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label~ 33
/hote= "HCV region NS-3, amino acids 1192-1457"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- BCD
/hote- "HCV region NS-4, amino acids 1676-1931"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devare SG, Desai SM, Gasey JM, Dawson JJ, Lesniewski RF,
Dailey SH, Gutierrez KA, Stewart JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant heptatitis C virus antigens - produced as fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 59; DB 13; Length 781;
44.5%; Prod. No. 6.20:02;
ative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 11, Page 37-43; 115pp; English.
                                                                                                                                                                                                                                                                     CKS; HCV CKS-34-BCD; cl00-3; NANBHV.
                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                 AAR21565 standard; Protein; 781 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    linker
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                                                                                                                                                  09-JUN-1952 (first entry)
                                                                                                                                                                                                 HCV CAS-33-BCD - pHCV-31.
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/iabei-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992 066430/09.
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nes 10; Conserv
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RESULT 160
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                       AAR21565
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CKS methods of protein synthesis are known in the art, for inst. a cks method has been disclosed in EP A 0331 961. Six individual nucleotides representing AAS 11-150 of the HCV genome were liquated together and cloned as a 456 base pair ForeI-PamHI fragment into the FKS fusion vertex pinced in From FereI-PamHI fragment into the FKS fusion vertex pinced in From FereI-PamHI fragment into the FKS fusion vertex pinced in From FereI-PamHI fragment from sequences, and the first 150 AAS of ECV. To construct the plasmid pHCV-31, the 781 base pair EcoRI-BamHI fragment from pECV-23 representation the FFC BCD recombinant antiqen fragment from pECV-23 representation from FECV-31, axpresses HCV ECS Tecombinant antiqen which consists of 239 AAS of CKS, 33-BCD recombinant antiqen which consists of 239 AAS of CKS, 8 AAS contributed by linker DNA sequences, 256 AAS of the HCV NS3 region (AAS 1957), 2 AAS (AAS 1956-1931), and 10 additional AAS centributed by linker DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                               Sequence of fusion protein HCV CKS-33-BCD recombinant antiqen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repatitis Colrus CKS fusion protoin - produced using vector
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34.5%; Fred. No. 6.2e:02;
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9; Mismatches 10; Indels
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1821 VILLPATKKTYKQIEKNWKNHMGPFMSILQ 1849
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                  |: ||: ::::| | || || :| :| 585 viapavqtnwqkletfwakhmwnflsgiq 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR33632 standard; Protein; 781 AA.
                                                                                                                           AAR22208 standard; Protein; 781 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                91EP-0114296.
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                                                                                                                                                                                                                                                                                      CKS fusion protein; antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABBO ) ABBOTT LAROPATORIES
                                                                                                                                                                                                 (first catry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-089871/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                    encoded by pHCV-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               781 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ22963.
                                                                                                                                                                                                                                                                                                                                                                                                                                26-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1990;
                                                                                                                                                                                               23-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                              18-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                          EP475182-A.
                                                                                                                                                                                                                                                                                                                        Hepatitis.
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                                                                                         RESULT 161
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                                                                                                             AAR22208
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The present invention describes recombinant Hepatitis C virus (HCV) and beautions (1). (1) is set if as a realent for the detection of antibodies as district the finite and efficient expects to HCV. The HCV reserves relimite and efficient realents and methods to accurately intributed as suspected of azite HCV interior. ANY 22218 to ANY 2228, AARCOUNT ANY COURT OF ARROWS TO ANY 2228 and the exception of the presence of the presence of the ANY 2228 and ANY 2228.
Jakey JM. Pailey SH. Pakson JJ. Sutlerfer RAP
1 JJ. Espprecht Kes
                                                                                             New residential artifors representing distinct artigories regions of Heparitiss views (BPV) genome, useful for detection of antibodies and artigors in body fluids of individuals exposed to BCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herefits Casay shorters adjant, Correction and sense for betering any Rodres and antisen in body thirds from individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A specific anthemic region of the BV decome is expressed as a chimcon tasion with Ecolf OMP NDO synthetase (GKS) owner. The basica protein pHTV-red can be used to detect antibodies and antibute as noty findled from individuals are exposed to BV can in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repairis Cabas Claimanedor assay: New A. Ben Hebritis.
"We Kreingsteinser lamenedor assay: New A. Ben Hebratitis.
                                                                                                                                                                                                                                                                                                                                                                                         Corry Mitch. Control Startbardy 84.5kg Prod. No. 4.55502
                                                                                                                                                                                                                                                                                                                                                                                                              Fred. No. 4, *0*02;
3; Mismatches les Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "KS H"V in them took in protein pH"V-204.
                                                                                                                                                                 London of London Phys. English.
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Former SG. Lowert GMC Charge
Lossinowski PFC Stowart Co.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Character of the
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                                                    WPI: ZOOOT LEERT,
N PSOOR: AARTAGEEN
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                                                                                                                                                                                                                                                                                                                                                 Sequence
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AAR 11 11 11
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The present invention describes recombinant Hepatitis \ell vitas (BCV) antiques (I). (I) is useful as a reagent for the detection of antibodies and antique in body fluids from individuals exposed to BCV. The BCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casey JM, Dailey SH, Dawson GJ, Galierrez KA:
f JL, Rupprecht KR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant antigens representing distinct antiacnic regions of Hepatitis C virus (HCV) genome, useful for defection of antihodies and antiques in body fluids of individuals exposed to {\rm HCV}_{\odot}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          assay uses reliable and efficient reachers and methods to accurately detect the presence of HVV antibodies in samples obtained from the individuals suspected of having HCV interfion. AAF322H to AAF422. AAF3137 to AAF5137 and AAB69001 to AAB6032 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Selection
                                                                                                                                                                                                                                                                                                                                                                                                     S. 17.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HCV recombinant antiqen pHCV-204 amino acid sequence SEQ ID No.49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Obery Match
Best Local Similarity 34.5%; Prod. No. 4.4e+oz:
Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                       Score 59: 08-14; Lougth 513;
Fred. No. 4.4e+e2;
9; Mismatches To; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hepatitis C virus: HCV; antiqen; detection; untilendy
confirmatory, competition or neutralisation assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1: Column 179-184: 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1821 VELPATKKTYKÇIEKNWKNHMGPFMSTLQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             422 viapavqtnwqkletfwakhmwnfisqiq 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB69025 standard; Peptide: 614 AA
                                                                                                                                                                                                                                                                                   Ouery Match
Hest Local Similarity 34.5%:
Matches 10; Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Devare SG, Desai SM, Casey
Lesniewski RR, Stewart JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9208-0989843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94US-0179896.
96US-0646757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 900S-0614069.
910S-0748561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90HS-0572BZZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0748566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9708-0867611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91US-0748565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WP1, 2001-122352/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 613 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0S6172189 BI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02 - JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 - AUG - 1990;
07 - NoV - 1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-0CI-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 4 - N: JV - 1 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-JAN-2001.
                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR69025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB69025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \begin{array}{c} \mathbf{x} \times \mathbf{x} \\ \mathbf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELXEXELETXSX CCCCCCCCXXX
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1921 VILIPATERIYASTEKNWENHMGPPMSILQ 1849

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Levels of the HCV CKS-collo recombinant antique. HCV CKS-cillo antigen consists of 23% arina antis of CKS, eight amino acids court. Bolted by linker 23% sequences, 30% amino arias from grow camino acids 164-1941) and 10 additional amino acids region (amino acids 164-1941) and 10 additional amino acids contributed by linker DNA sequences. A 63th NlaTV-HaelII fragment was deleted from pHCV-24 (a plasmid which expresses the HCV CKS-collo antigen under control of the lac promoter). The pHCV-58 fusion protein (containing a 21 amino acid deletion, i.e. of HCV amino acids limit HEZDI was expressed at a significantly higher level than the pHCV-24 fusion protein.
                                                                                                                                                                                                                                                                Hepatitis C assay using recombinant NSI region antigens – for detecting antibodies and antigen in body fluids from individuals {\sf detecting}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV recombinant antigen pHCV-58 protein sequence SEQ ID NO:18.
                                                                                                                                                                                                                                                                                                                                                                                       The clone pBCV-58 was constructed to overcome poor expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 59; DR 14; Length 599; 34.5%; Pred. No. 4.2e402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hepalitis C virus, HCV: antigen; detection: antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1821 VLLPAIKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403 viapavqinwqkletfwakhmwnfisgiq 431
                                                                                                                                                                                                                                                                                                                                                  Example 8; Page 93-95; 175pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB51379 standard; Protein; 599 AA
                                                                                                                                                              Dailey SH, Desai SM, Devare SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91US-0748561.
91US-0748566.
91US-0748565
                                                                                                                                                                                                                                                                                                       exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0867611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9002-0572822.
9003-0614069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92ms-09843,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9405-0179896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0646757.
                                    92WO-US07188.
                                                                                91115-0748561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                       WPI; 1993-093941/11.
                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus.
                                                                                                                                                                                                                             N-PSDB; AAQ38258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5172189-B1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUN-1997;
                                       21-AUG-1992;
                                                                                21-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1991;
04-MAR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB51379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contributed by linker DNA sequences. A 53bp NialV-Hacill fragment was deleted from pHCV-24 (a plasmid which expresses the HCV CKS-follo antiqen under control of the lac promoter). The pHCV-58 rision protein (containing a 21 amino acid deletion, i.e. of HCV amino acids 1609 1620) was expressed at a significantly higher level than the pHCV-24 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        levels of the HCV CKS cl00 recombinant antigen. HCV CKS-cl00 antigen consists of 239 amino acids of CKS, eight amino acids contributed by linker DNA sequences, 363 amino acids from HCV NS4 reqion (amino acids 1569-1931) and 10 additional amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting antibodies and antigen in body fluids from individuals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatifis C Virus; non-A, non-B hepatifis virus; NANBH; non-structural protein, CMP KDO synthetase; CKS fusion protein; TTT.CMF i dear mannersetalescrate cytisfiff transferier;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The clone pHCV-58 was constructed to overcome poor expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 14; Length 599;
Pred. No. 4.3e+02;
                                                                                Hepatitis Civicus, NS3, C160 antigen, CKS fusion protein;
CMP-KDO synthetase; immunodot assay; Non-A, non-B hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repatitis C assay using recombinant C-100 region antigens :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCV C100DZ recombinant antigen encoded by pHCV-58.
                                           HCV-C100D2 recombinant antiqen encoded by pHCV 58.
                                                                                                                                                                                                                                                                                                                                                                                              Caser JM, Desai SM, Demare SG, Pupprocht RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 8, Fage 119 121, 206pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1821 VILIPATERIYEÇIRANWENHMÜPEMETLÜ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR33601 standard; Protein; 599 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exposed to hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.58;
                                                                                                                                                                                                                                                                        92WO-US07187.
                                                                                                                                                                                                                                                                                                                9108-0748566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-1993 (first entry)
    01-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inmunoassay, phov 58.
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI: 1994-094940/11.
                                                                                                                                                                                                                                                                                                                                                         (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          599 AA;
                                                                                                                                               Repatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ38243.
                                                                                                                                                                                                                                                                        21 - AUG-1992;
                                                                                                                                                                                                                                                                                                                21-AUG-1991;
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WP1; 1993-094942/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hepatitis C Virus.
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                         Safrija
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paily for this on protorin (Bolisti, 66 Kb) expresses at slinitizantly higher levels than the paily-44 tustion protorin. Payer's from prises a 21 inches orded deletion (W.W. anchos acids 1600–1620) in the extreme N regiminal portion of the HeV entries respected to the pHeV-24
                                                                                                                                                                                                                                                                                                                                                                                              Heparidis V virus, articlea, dramosis, inhibitor: AMP-KDM synthased
TRS: HEV AS STOCK, NANHHV; COE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the polypopolide represents a distinct antiaunic region of the BCV becomes and can be used for the ferring at any building and and after that the restry distinct on the belypopolide can also be asset to develop specific infiltitors of viral replication and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perhalmant Lepturins 'vins nations' produced as usion profession neglectors and representing distinct anticomic regions of the HOV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "EVV restion NSL amino acods 1569-1599
and Peri-1931"
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Chiley SH. Doterber MA. Stewart JD.
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Cive yr Mismatches (6)
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  Note: to all Simplering (4.5)
Matches (40) Conservative
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Hopatitis C virus; NANNH; nom A, nom-8 hopatitis; CMP-KD- synthetase;
nom-structural protein; pHCV-56; diagnosis; CKs Insion protein;
CHP:CMP-3-doxy-manne-e-talesemate cytidy)yl transferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The clone pHPV-58 was constructed to evertence point expression levels of the HCV CKS closs antique consists of 20 annine acids of eXS closs antique consists of 20 annine acids contributed by linker bNA sequences, 46 annine acids reading (amino acids 1569-1941) and 10 additional amino acids contributed by linker bNA sequences. A 646 p Native Back to the West was deleted by linker bNA sequences. A 646 p Native Back to the Colon antique under control of the lac promoter). The pHPV 68 closs antique under control of the lac promoter). The pHPV 68 amino acids 600-1620 was expressed at a significantly biomer level than the pHCV-24 Instead of the deletion, i.e. of HCV families acids 1600-1620 was expressed at a significantly biomer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tor hepatitis of assay for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 59; DR 14; Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches lot indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HCV ClOOD2 recombinant antique encoded by pHCV-18.
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1821 VILEAIKETYKÇIHENWENHMGPEMSILQ 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant NSS region antiaens t
detecting hepatitis C virus intections
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                                                                                                                                                                                                                                                               AAR34639 standard; Protein; 509 AA.
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Matches 10; Conservative
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0; Gaps
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                                                                                                                           The clone pHCV-57 was constructed to overcome poor expression levels of the HCV CKS-cl00 recombinant antiqen. HCV CKS-cl00 antiqen consists of 299 amino acids of CKS, eight amino acids contributed by linker DNA acquences, 363 amino acids from HCV NS4 region (amino acids 169-1931) and 10 additional amino acids contributed by linker DNA sequences. A 69bp Ddel fragment was
                                                                                                                                                                                                                                                                                                                      defected from $\text{phys.24}$ (a piasmid which expresses the HCV CKS-cl00 antiqen under control of the lac promoter). The pHCV-57 fusion protein (containing a 23 amino acid deletion, i.c. of HCV amino acids 1575-1597) was expressed at a significantly higher level than the pHCV-24 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mepatitis C Virus, non A, non'B hepatitis virus, NANBH,
nocraticatural protein, CMP KPO synthedase: CKS Ensien protein;
TELEME : decky mains it Ciles-date cytis; [7] Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 59; DB 14; Length 597;
34.5%; Pred. No. 4.2c+62;
iive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HCV C10001 recombinant antigen encoded by pHCV-57.
                                                               Example 8, Page 114 116, 206pp, English.
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exposed to hepatitis C virus
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Hes 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoassay; pHCV-57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Repatitis C Virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR 33600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dawson GJ, Gutlerrez RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C virus (HCV) genome, useful for detection of antibodies and antiques in body fluids of individuals exposed to HCV ^{-}
                                                                                                                                                                        Sden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant antiqens representing distinct antiqenic regions of
antigen under control of the lac promoter). The pHCV 57 fusion protein (containing a 23 amino acid deletion, i.e. of HCV amino acids 1575-1597) was expressed at a significantly higher level than the PHCV-24 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    HCV recombinant antigen pHCV-57 protein sequence SHQ ID NO:16.
                                                                                                                          / Match
Local Similarity 34.78, Fred. No. 4.2c+02;
Los 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatit_s C virus; H∩V; antiqen; determion: antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Devare SG, Desai SM, Casey JM, Dairey SH,
Lesniewski RR, Stewart JL, Rupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 8; Column 91-94; 167pp; English.
                                                                                                                                                                                                     1821 VLLPATKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                        401 Viapavqtnwqklerfwakhmwnfisgiq 429
                                                                                                                                                                                                                                                                                                                      AAB51378 standard; Protein; 597 AA.
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96US-0646757.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  597 AA;
                                                                                             597 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hepatitis C virus.
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                                                                                             Sequence
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Length 597;

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Hepatitis C assay using recombinant C-low region artifices : 0.1 detecting antibodies and antigen in body fluids from individuals
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                                                                                                                                                                                               New recombinant NSS region antigens theteeting hepatitis C virus infectious
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92WO-US06964.
                                910S-0748565.
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Hest Local Similarity 34.70.
These 10; Conservative
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                                                                                                        Dailey SH, Desal SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Casey JM, Desai SM,
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                                                                      (ABBO ) ABBOIT LAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        597 AA;
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21-Aug-1992;
                                  21-AUG-1991;
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The polypeptide represents a distinct anti-dense region of the BEV persons and an her seed to the detection of an following and arbitrary represents of BV interview. The polypeptide can also be seed to be pelypeptide can also be seed to be pelypeptide can also be seed to be pelypeptide can also be
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64.50; Sware for the by Lorath 597; bost Lorat Santourity (44.50; Pred. No. 44.2000z; Marthe Marthes III). Novementative of Mismatches III; Index.

therapeutic purposes.

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1921 VILLYSKRYKESHERMKNIRMSBYRSTEF 1849 4 d. vouparefringklettwarhimmitisaig 42)

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bischosure; Fia 42. Page MS-87: 115pp; English.

10-17-300

regare 80, lean SM, chaep 3M, leased 50, lashbaski 8K, tableg 8H, appropriate 8A, Stewart 55,

WELL LESS MANAGEMENT

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The clone pHCV-57 was constructed to overcome poor expression antique consists of 29 amino acids of EKS, cital the HCV EKS cloud antique consists of 29 amino acids of EKS, cital amble acids of contributed by linker DNA sequences, 44 amino acids from BCV NS contributed by linker DNA sequences, 44 amino acids from BCV NS contributed by linker DNA sequences. A 69bp late Intamment was dicket a from pHCV 21 a plasmid which expresses the BCV ES cluud antique under control of the lac promoter). Be pHCV-57 tasion, amino acids 1275 1593 was expressed at a significantly higher level than the PHCV-24 fusion protein.
tor hepatitis Cassay for
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CMP-KDo synthetuse, immunador assuy, Ron A, nan B hepatitis
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34.5%; Fred, No. 4.2e+02;
Live 9; Mismatches 10; Indels
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The present invention describes recombinant Hepatitis C virus (BCV) antigens (I). (I) is useful as a reagent for the detection of antibodies and antigen in body fluids from individuals exposed to HCV. The HCV assay uses reliable and efficient reagents and methods to accurately detect the presence of HCV antibodies in samples obtained from individuals answerted of leving HCV infection. AAR32218 to AAR32181 to AAR51379 and AAR6901 to AAR69032 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                               Dovare 3G. Desai SM. Casey JM. Bailer SM. Paween SJ. Optionnes RA:
Lesniewski RR, Stewart JJ., Pupprocht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant antiqens representing distinct antiquair regions of Hepatitis C virus (HCV) genome, useful for detection of antibodies and antiques in body fluids of individuals exposed to HCV ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hepatitis C virus; antigen; diagnosis; inhibitor; CMP-KDO synthase;
HCV recombinant antigen pHCV-63 amino acid sequence SEQ ID NO:48.
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34.5%; Pred. No. 4.2e+02;
ive 9: Mismathbos 10; Indels 0;
                                 Repatitis C virus; RCV; antigen; detection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in the exemplification of the present invention.
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96US-0646757.
90US-0572822.
90US-0614069
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91US-0748565.
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Matches 18 Conserva
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                                                                     Hopatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hepatitis C assay using recombinant C-100 region antigens—for
detecting antibodies and antigen in body fluids from individuals
exposed to hepatitis C virus
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34.5%; Fred. No. 4.2k-52;
[or. 9, Missetches, 10, Indel*
                                                      0.5%; Secre 59; DB 22; Length 592;
34.5%; Fred. No. 4.26.62;
Live 9; Mismatches 10; Indels
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hes 10; Conservative
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Matobos 16, Conserv
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MP KPO synthetuse: Pemma det ussay: New A. dansb beparatis.
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antigens (1), (1) is useful as a reagent for the detection of antibodies and antique in body thoids from individuals exposed to RCV. The BCV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New recombinant anticons representing distinct anticonic respects of Hepatitis C virus (HCV) genome, useful for detection of antibodies and antiques in body fluids of individuals exposed to \rm HCV .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             defect the presence of HCV antibodies in samples obtained from findividuals suspected of having HCV interfer. AFFYZZIM 10 AMESI379 and AAMSONOL to AMESI370 and AAMSONOL to AMESI370 and ANGONOL to AMESI370 and ANGONOL to AMESI370 and AMESI3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    assay uses reliable and efficient reagents and methods to accurately
                                                                                                                            A specific antiquate region of the HCV account is expressed as a chimical table with E.soli MF EF (1914) of the table with the based to detect antibodies and antique in hely fluids from replyidate exposed to HCV e.a. in confirmatory, competition or neutralisation assays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes recombinant Repairies of virus (ReV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOV recombinant antiqen pHOV 62 amino acid sequence 359 ID Ne:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Storre 59; DR 14; Longth 592;
34.5%; Prod. Ro. 4.20002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in: habits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hopatitis C virus, MCV, antiquos detections antibody.
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Lesniewski KK, Stewart JL, Eupprecht KK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 16; Column 174-178; 167pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1821 VILPATERTYRQIEKNWENHMGPPNSTLQ 1849
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                                                                     Claim 1; Page 53-55; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB69023 standard; Peptide; 502 AA.
exposed to hepatitis C virus
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910S-0748561.
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9008-0572822.
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Matches 10: Conservative
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                                                                                                                                                                                                                                                                                                                                                 592 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB69023;
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Querry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 145
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                                                                                                                                                                                                    The present invention describes a recombinant protein which consists of three continuous regions (N-terminal region, internal region and continuous regions and the above three regions is selected from the three hyalabanate synthase (HAS) modified proteins HASI, HAS2 and HAS3 (e.g. a protein made from HASI and mine acids 1 to 71, HAS2 and made has a research reagent for blochemical research and medical decelomet. The intention for blochemical research of internessed or lewested activity, AAY78127 (e.g. AAY78142 represent specifically claimed examples of recombinant proteins from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a recombinant protein which consists of three continuous regions (N-terminal region, internal region and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A hyaluronate synthase modified protein – useful as a research reagent
                                                                                                                useful as a research reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; murine; hyaluronate synthase; modification; HAS1; HAS2; HAS3; tessearch teagent, bicchemical research, medical development; chimoric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              N.B. The present sequence is not given in the present specification, but is derived from sequences given as specified in the claim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant chimeric hyaluronate synthase modified protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 0.5%; Score 59; DB 21; Length 553; Local Similarity 28.6%; Pred. No. 3.8e+92; Local 14; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 < VIQDLATLEEELQPEKKI KSHQKI,SPTLKNIJ,SCVYSCPSYTAKDLMKV 1021
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                                                                                                                                  for biochemical research and medical development
                                                                                                                A hyaluronate synthase modified protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78127 standard; Protein; 573 AA.
                                                                                                                                                                        Maim 12; Page ; 30pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page -; 30pp; Japanese.
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                                      (SEGE ) SELENGARD ROCYO CO LITO.
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98JP-0193788.
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                                                                          WPI; 2000-140125/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55 4 AA;
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24-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 - JUN 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
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Human, secreted protein, immunestimulant, immunesuppressant; virucide, antibu-1-131, antifusjal, vyl static antialinematic; dermatological, antidaotic; antiastimulatic; antialinematic; protocodide, antidyrold, immune deficiency; severe combined immunedeficiency; SUID: infection, HVV, hepatitis, malaria; autoimmune disorder; systemic lupus; connective tissue disease; multiple sclerosis; erythematosis; rheumatoid arthritis; autoimmune pulmonary inflammation; astima; Guillain-Barre syndiome; autoimmune thyroidills, myastboid atmais autoimmune thyroidills, myastboid atmais autoimmune thyroidills, and atmais autoimmune thyroidills, and atmais antidisease; autoimmune inflammatory eye disease; allergy.
C-terminal region) where one or two regions among the above three regions is selected from the three hyaluronate synthase (HAS) modified proteins HASI, HAS2 and HAS3 (e.g. a protein made from HASI amilio acids 1 to 71; HAS2 and HASI amino acids 410 to 583). The protein is useful as a research reagent for blochemical research and acidical development. The invention provides a HAS modified protein of increased or lowered activity. ANY 9127 to ANY 9142 represent specifically claimed examples of recombinant proteins from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                       N.B. The present sequence is not given in the present specification, but is derived from sequences given as specified in the claim.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted protein clone pg195_1 protein sequence SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steininger RJ, Spaulding V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jacobs K, McCoy JM, LaVallic ER, Collins-Racic LA, Evans C;
Merberg D, Treacy M, Aqostino MJ, Steininger KJ, Spaulding V
Wong GG, Clark HF, Fechtel K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0 5%; Score 59; DR 21; Length 573; Best Local Similarity 28.6%; Prod. No. 40:02; Matches 14; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         923 VIQULATIFEFIOFEKKI KSROKLSETIKNI LSOVYSOPSYTAKDUMKV 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nutritional, chemokine, immune stimulating or suppressing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY94928 standard; Protein; 590 AA.
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98US-0096815,
98US-0099229.
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04-SEP-1998;
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AAY78137 standard; Protein; 553 AA.
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Best Local S
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Prod. No. 3,800023
                                                                                                         73 VIQUIALIFEEDPEKKERSEPRISSILENGIS VISTESTEREMEN 1921
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C-terminal region) where one of two regions among the above three
regions is selected from the three hyaluromate synthase (HAS) meditied
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Recombinant chimeric hyaluronete synthase modilied protein #10.
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for biochemical research and medical development
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three continuous regions (N-terminal region, internal region and
C-terminal region) where one or two regions among the above three
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                                              tor biochemical research and medical development
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28.6%; Pred. Mo. 3.86+02;
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                                                                                                           Claim 15, Fage 1, 30pp, Japanese.
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(SECT ) SECTINAGAND AUGIO IN LILL.
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three continuous regions (N-terminal region, internal region and C-terminal region) where one or two regions among the above three regions is selected from the three hydraconate synthase (HAS) modified proteins HAS1, HAS2 and HAS3 (e.g. a protein made from HAS1 amino acids 1 to 71, HAS2 amino acids 52 to 379 and HAS1 amino acids 410 to 589).
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                                                                         and medical development. The invention provides a HAS modified protein of increased of lowered activity. AAY78127 to AAY78142 represent specifically claimed examples of recombinant proteins from the present
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to 71, HASS amino acids 52 to 379 and HASI amino acids 410 to 583).
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                                           The protein is useful as a research reagent for biochemical research.
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Pred. No. 3.80+02;
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The present invention describs a recombinant protein which consists of three continuous regions (N-terminal region, internal region and collecterminal regions). Where the collections and regions among the above three regions is selected from the three hydriconate synthase (RAS) modified proteins HAS1, HAS2 and HAS3 (e.g. a protein made trom HAS1 amino acids 1 to 71, HAS2 amino acids 52 to 379 and HAS1 amino acids 4 for to ^{\rm F}). The protein is useful as a research reason to biochemical research and medical development. The invention provides a HAS modified protein of increased or lowered activity, AAY78127 to AAY78142 represent aggregifically claimed examples of recombinant proteins from the present
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Mouse; murine; hyaloromate synthase; moditication; HAS1; HAS2; HAS3; roscareh reagont; biochemical research; modical development; chimetre.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant chimeric hyaluromate synthase moditied protein #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match (0.5%) score 59: 08.21; Londth 952; tocal Similarity 28.6%; fred, No. 4.Ke+02; we 14; Conservative [1]; Mismarches 24; Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78140 standard: Protein: 5'2 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page -: 30pp: Japanase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SECK ) SEIKAGAKU ROGYO CO LII.
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                                                                                                                                       Chimeric - Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A hydrograph synthase medities protein—msetul as a research reasent for biochemical research and medical descripment
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of accessed or covered actacly, AAV78127 to AAV78142 represent
specifically claimed examples of recombinant proteins from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Morsey Brillian Applications synthesis modification, HAST, HAST, HAST, research respects to adequate because the second research medical development; chimeric.
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28.58; Prod. No. (1800.2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     os ingalion boli kekkanor piklokrani or peljolytikoljavi bol
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Posservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
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                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                 AAY68492
                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a Helicobarter pylori GHFO protein of the invention. The polypetides can be used for preventing or treating Helicobarter infections, and eastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic diseases, e.g. qualtic and daodenal diseases, e.g. qualtic and daodenal disease. They can also be used for used for the production of antibodies, the products can also be used for
                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                    New isolated Helicobarter polynucleotides · used to develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic axid encoding hydlaronan synthase 2 or 3 or their active fragments - used for treating arthritis, in wound repair, for
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                                                                                                                                                                                                                                                                                                                                               0.5%; Score 59; DB 19; Length 552; 34.9%; Pred. No. 3.80.02;
                                                                                                                for the diagnosis, prevention and treatment of Helicobacter
infections and qastrointestinal diseases
                            Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
                                                                                                                                                                                                                                                                                                                                                                            indels
                                                                                                                                                                                                                                                                                                                                                                                                     1918 KLFDWAKTEDAPKDRIJTFYNDAPCIAEKIKGLFTLFAGHLVKPFA 1963
                                                                                                                                                                                                                                                                                                                                                                                                                      Marine, Agaluronan synthase 2, HS 2, Ayaluronan;
 (INMR ) MERIEUX CRAVAX PASTEUR MERIEUX SERUMS
                                                                                                                                                                                                                                                                                                                                                                          6; Mismatches
                                                                                                                                                            Claim 8; Page 1788-1791; 2054pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spicer AP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 29; Pages 60-61; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW50009 standard; Protein; 552 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murine hyaluronan synthase-2.
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es 16, Conservative
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                                                                                                                                                                                                                                                                           detection and diagnosis.
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                                                         WPI, 1998 512293,46.
                                                                                                                                                                                                                                                                                                      552 AA;
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                                                                        N PSDB; AAX14534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hyaluronic acid.
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three continuous regions (N-terminal region, internal region and creation) where one or two regions among the above three regions is selected from the three hydrirenate synthase (BAS) modified proteins BASI, BASZ and BASS (o.g. a protein made from BASI amino acids 1 to 71, BASZ amizo acids 52 to 379 and BACI amizo acids 410 to 587). The protein is useful as a research reagent for biochemical research and medical development. The invention provides a BAS modified protein of increased or lowered artivity. The present acquence represents mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A hyaluronate synthase modified protein – useful as a research readont for biochemical research and medical development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a recombinant protein which consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; aurine, hyaluromate synthase; modification, HASL, HAS2; HAS3; research reagent; blochemical research; medical development.
HA can be used to treat arthritis or perforated car drums, protect eyes during susperly, deliver ands, prevent post-operative scarring or addression formation, heal wounds and perent restenois following balloon angioplasty. Modulation of HA production in vivo may be useful in, of Chance disease, mesothalional, Wilm's tumour and outdoms associated with inflammation of lung and Eidney, all of which are associated with elevated levels of HA in tissues or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%, Score 59; DB 21; Length 552;
28.6%; Pred. No. 3.86+92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            923 VIQNIATEPPROPERSHQRI SPTERNI I STVYSCPSVIAKNUMKV 1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           973 VIONIATUPRELOPERRISHORISPITRALIFALIS
                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 59; DB 19; Length 552; BB.6%; Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse hyaluronate synthase modified protein HAS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatrhes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY68492 standard; Protein; 552 AA
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Matches 14; Conserv
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                                                                                                                                                                                                                                                                                                                                      Sequence 552 AA;
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AAY 45445 standard: Protein: 479 AA.

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W 11. T. A.  TRANSPORTER

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The present investion describes recombining Beptitis \psi virus (BVV) and antiques (I). (3) is useful as a reason, for the detection of antibodies and antique in body links from individuals exposed to BVV. The BVV assay uses reliable and efficient journals and methods to arrelatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Now recombinant antiques representing distinct antiquent response of Repatitis C virus (BCV) genome, useful for descettes of antiboda seam antiques in body thinds of incividuals exposed to BCV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   defect the presence of HEV antibodies in samples ofreined from individuals suspected of haring HEV intection. AMFXL2FF to AAB51379 and AAB59001 to AAB69042 represent sequences used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Desai SM, Casey UM, Dalloy SH, Taxson GJ, Gulletter FA:
KR, Stewart JL, Eupprecht KR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 69; 08.2±; Lonath fla;
34.5%; Frd. Ro. (.40-02)
(9) Mismarches ltd. Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the exemplification of the present insention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW98815 standard; Protein; 552 AA.
                                                                                                                                                                                   9408-0179896,
9608-0646757,
9008-0572822,
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                                                                     9705-0867611.
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910S-0748566.
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                                                                                                                                                   92US-0989844.
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                                                                                                                                                                                                                                                                                                                                                                                                                    9108-0748565
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(1)
(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      local Similarity 34.59
es 10; conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptic ulcer disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABBO) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 512 AA;
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                                                                                                                                                                                                                        -MAY 1996;
-ABG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01 APR 1998;
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                                                                 02 JUN 1997;
                                                                                                                                                                                                                                                                                                                                          21-AMG-1991;
21 AUG 1991;
                                                                                                                                              19 - N: W - 1992;
10 - JAN - 1994;
                                                                                                                                                                                                                                                                                                      07-NoV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                        29-m(T-1991;
09-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Devane SG,
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                                                                                                                                                                                                                                                                                                  Mesperatory diseases pheamonia; bronchitis; heart disease; saregidosis;
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                                                                                                                                                                                                                                                                                                                                                   singsitis: purplent of itis media: erythema modesum: pharyngitis;
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It is the polypoptide sequence encoded in the combined open reading frames of the hepatitis C virus (HCV) cDNA of clones 35, 36, 81 and 32. It is an epitope, portions of Which could be used as Emmunoassay reagents and varyings and to generate and inclinative aseful in diagnosis and passive immunotherapy for HCV infection/uon-A, non-B hepatitis.
The sequence is encoded by the combined open reading trame of hepatitis C virus cDNA (see AAN90310). These artigens react with antibodies in patients with non-A non-B hepatitis (NANBH). They can be used to diagnose HCV-induced NANBH, to raise antibodies for immunoassay or treatment, or to produce vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Polypeptide encoded in the combined open reading frames of clones 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SdbD 10
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34.5%; Pred. No. 2.90~02;
ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 59; DB-H0; Length 460; 34.5%; Pred. No. 2.5k+92;
ivc 9; Mismatches 10; indole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1821 VELPATETYEQTERNWENHMONTMSH.Ø 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88US-0271450; US-122714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 13; Figure 9; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP92024 standard, protein, 460 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton M, Choo q L, Kuo G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-1990 (first entry)
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Matches 10; Conservative
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Matches 10, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 1989-159274,722
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                                                                                                                                                                                                                                                                                                                                                     Sequence 460 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sales
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       combined open reading frame, clone 35, clone 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 c.ì
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1644 INPULATVORKERIGIESQATURÇTALITLELLIGENFOREDP 1688
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The invention relates to a novel system for producing pelykethes particularly 12., 14. and 16-membered ring macrolides from a desired starticularly 12., 14. and 16-membered ring macrolides from a desired startic unit. The biosynthesis of polyketides is initiated by a group of chain-forming enzymes known as polyketide synthases (FKSs) which are multienzyme complexes consisting of a set, or module, of enzymes which catalyse polyketide chain extension. The system of the mornally possess them, thereby controlling the starter units used. The normally possess them, thereby controlling the starter units used. The confidence and a controlling malany, a substituted malany is substituted malany. The sidure for transfer to a chain extension module. The substituted actly residue for transfer to a chain extension module. The substituted actly residue for transfer to a chain extension module. The substituted actly residue for transfer to a chain extension module. The substituted actly residue for transfer to a chain which effects domain is preferred any transfer and this site, may provide the domain, and an acyl carrier protein domain (AFF). The Relates and this site, may provide the domain, and the active site, and the invention are used to produce polyketides, particularly 12., 14. and 16-membered ring produce polyketides, particularly 12., 14. and 16-membered ring and a cratter units, or with unusual starter units, which minimises the formation of by-produces containing a different contact or propionate) starter units, or with unusual starter units, and the contact or propionate or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           andesired or different starter units, and also allows the incaperation of unusual starter units, the system allows the identification of polykerides which may have exhanced properties or profess no make bioactivity, sequences AAV77259-Y77288 represent PKS CLF or KS domains of a variety of actibomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polyketides which minimises the formation of by-products containing an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        starter unit. The polyketides prediced have use as peténtial anthelminthies, insecticides, immunosuppressants, antifungals or antibacterials. The present invention provides a system for preducing
                                                                                                                                                                                               Novel methods for preparing new variant polyketides, for use as anthelminthies, insecticides, immunosuppressants, antifungals or antibacterials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 59; DB 21; Length 421;
50.0%; Pred. No. 2.5e+02;
EVO 3; Mismatches 7; Indels
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                                                                                   Leadlay PF, Staunton J, Cortes J, McArthur HAL;
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                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2A-D; 97pp; English.
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Protein identification, signal transduction pathway: metabolic pathway, hybridisation assay, genetic mapping; gene expression centrol; promoter;
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                                                                                                                                                                                                                                                                                                                           This sequence represents the KS domain amino acid sequence of the grandish profession of the grandish of the macrolides of the invention. The macrolides are 14-monher marrolides that incorporate an acetate starrer unit so that, has a 12-monher marrolides that incorporate an acetate starrer unit so that, has a 12-monher profession of down, 15-monher marrolides are produced by a process which mismisses the fermation of by products
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tive 3; Mismatches 7: Indels
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                                                                                                                                                                  Leadlay PF, Staunton J, Cortes J, McArthur BAI;
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                                                                                                                                                                                                                                                                                                Claim 15, Fig 2, 78pp, English.
                                                                                                           (BIOT - ) BIOTICA TECHNOLOGY LTD.
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01-APR-1999;
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Polyketide: nerrolide, biosprthesis: polyketide synthase: PKS:
multienzyme complex; loading module: ketosynthase domain; KS: CLF domain;
decarboxylation; acyl carrier protein domain; ACP: anthelminthic;
insecticide; immunosuppressant; antitudal; antibacterial.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Silver in
                                                                                                                                                                                                                                                                                                                                                                                                               Overy Match (0.5%) Score 59: 106.21) Londth 414: Rest Local Similarity 26.7\%; Prod. No. 2.50002; Matches 12; Conservative 10; Mismatches 24: Indexs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptomyces violaceoruber polyketide synthase KS demain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY77279 standard; protein; 421 AA.
        9908-0155659,
9908-0156659,
9908-0156458,
9908-0156596,
9908-0157753,
9908-0157753
                                                                               990S-0158029.
990S-0158242.
990S-0158369.
                                                                                                                                 990S-0159295.
990S-0159329.
990S-0159330.
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990S-0159584.
990S-0160741.
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990S-0160815.
990S-0160980.
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990S-0161404.
990S-0161405.
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99US-0161993.
99US-0162142.
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99US-0159294
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99US-0161459.
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                                                                                                                                                                 99US-0159331.
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22 - SEP - 1999;
24 - SEP - 1999;
26 - SEP - 1999;
26 - SEP - 1999;
65 - orf - 1999;
66 - orf - 1999;
66 - orf - 1999;
67 - orf - 1999;
12 - orf - 1999;
13 - orf - 1999;
14 - orf - 1999;
                                                                                                                                                                           14 - m.H - 1999;
14 - m.H - 1999;
21 - m.H - 1999;
22 - m.H - 1999;
25 - m.H - 1999;
25 - m.H - 1999;
                                                                                                                                                                                                                                                                                                                                                      1996;
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26-00T-1999;
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98GB-0014006

29-JUN-1998;

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990S-0139456
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990S-0139463
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990S-0134941.
990S-0135124.
990S-0135353.
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990S-0138540.
990S-0138847.
990S-0139119.
990S-0139453.
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99US-013944.
99US-0139455
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990S-0139817.
990S-0139899.
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99US-0132485.
99US-0132486.
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99US-0134218.
99US-0134219.
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99HS-0128714.
99HS-0129845.
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                               25-FEB-2000; 2000EP-0301439.
                                                                             9908-0123548.
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18-JUN-1999;
18-JUN-1999;
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09-APP-1999;
16-APP-1999;
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14-MAY-1999;
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          06-SEP-2000,
                                                                                                     25-MAR-1999;
20-MAR-1999;
                                                                                                                             01-APR-1999;
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28-APR-1999;
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06-MAY-1999;
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                                                                              09-MAR-1999;
                                                                                                                                                                           19-APP-1999;
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                                                       25-PER-1999
                                                                                                                                                                                                                                                                                                 06-MAY-1
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Purified hepatitis Coting (HUV) and parified or recombinate HCV nucleic acids (NAs), considing HCV polynuclectides or epitopes, and polypetides are claimed. HCV is a cansative agent of non A, non B hepatitis (NANHH). The NAs may be used to design phose for defin, of HCV NAs in samples. The polyhebitism is a familiar of the polyhebitism is because an immunocherapy. To produce antibodies useful for diagnosis and passive immunocherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein Identification; signal transduction puthway, metabolic pathway,
Lybildication cosa,, genevic supplies, genevators in control, promoter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.5%, Score 59, DB 10; Length 382;
Best Local Cimilarity 44.5%; Pred. No. 2.20+02;
Matches 10; Conservative 9; Mismatches 10; Indels 9; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein tragment SEQ ID NO: 15604.
          Non A non B hepatitis, probe; varcine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The purified virus may also be used in vaccines.
                                                                                                                                                                                                                                                                                                                                                                                    and assorted nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                           36 2, 139pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1821 VELDATERIYEÇE FINMENHMITEMSILQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1..27
/lubel 334
28..42
/label*adaptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG15375 standard; Protein; 414 AA.
                      passive immunotherapy; antiqen.
                                                                                                                                                                                                                                                                                                              K40 G;
                                                                                                                                                                 /label-extra
                                                                                                                                                                                                                                                                                                                                                                         Purified hepafitis C virus -
                                                                                                                                        /label NANB
                                                                                                                                                                                                                                      88EP-0310922.
                                                                                                                                                                                                                                                             88US 0271450.
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                                                                                                                                                     385
                                                                                                                              43..377
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                                                                                                                                                                                                                                                                                                                                   WP1: 1989-159271/22.
                                                                                                                                                                                                                                                                                     (CHIR-) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                          Example, Fig. 36 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 382 AA;
                                            Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN92104.
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                                                                                                                                                                                                                                      18 - NOV - 1988;
                                                                                                                                                                                                                                                             14-NOV-1988;
                                                                                                                                                                                                              51 MAY 1989.
                                                                                                                                                                                      UP318216 A.
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                                                                                                                              Region
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AAP90182;
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Keqion
                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                      RESTILT 121
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                                            AAP90182
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                                                                                                                   the exatentia is emptises an HTV initiate from the C foundin (prof. 22 AAR-OTS), and at least one HTV initiate from the NS3 (prof. C3C AAR-OTS), NS4 (prof. Clan - AAR-OTS), S (prof. S2 - AAR-OTS) or NS5 (AAR-OTS), building.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The introductions may in the tens of a fast as protein, a simple physical mixture, or the fit tribual intlates comment, bound to a solid mathix. They are prot. prop. by recombining DNA to thinkes (primers are intens in AALL271) [1273], but can be synthesised or isolated from HTV water things who was enable;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s inc
                                                                                                                                                                                                                                                            School School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substitute as at synthetic Hepatitis {}^{\prime} Virus antiques {}^{\prime} provide more effective diagnosis at Noa A. NoarB Hepatitis
fittings fitting in Pracing of Failty, esp. is immuneasing reaching, being a to a report of safet specific and intring your outly and land into HVV in the above, all fitting in diffuses and characteristic of acute and characteristic characteristic and characteristic bins may be achieved of HIV, HILV, appartitis B virus and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non A non B hoporti's girds, WANBHY, WYV, and been, detection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7,540; Secto 5a; 54,17; Longth 460; 44,540; Pred, No. 2, Lorez; 10; Indels 10; Indels
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41,10 Prof. No. 2,5002
100 9: Mishatelies (S) Indels
                                                                                                                                                                                                                                                                                                     TACL VICEARREYRUGENWENRWIPENS INC. 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [AZ] VIJPATKKITKITIKINKKNEGSHIMITL 1849
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No. Coservative
                                                                                                                                                                                                                                                            diagnosis: antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heaterstan M.
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                                                                                             treponenta pallidum.
                                                                                                                                                                                                                                   Stat 24 (1883)
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                                                                                                                                           11 . AA.
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                                                                                                                                                                                                                                      Brist 1.71
Matches
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Sequence of the carboxy-terminus of the fusion polypeptide choice of
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                                                                                                                                                                                                                                  Hopatitis ? Virus, tasion polypoptide; prober vaccine: n a.A.m.a b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hepatitis Clyicus gene - used for produ. of polymorleofide profess, polypeptide(s) and antibodies for diagnosts, prevention and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Scope 59; 58 10; Length 882; 84.5%; Fred. No. 2.20+02;
                                                                                                                                                                          e terminas of superexide dismetase (100 tusion polypeptide).
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                                                                                                                                                                                                                                                                                                                                                                                 Location/gnai::iors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88GB-0027024.
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AAP90182 standard; protein;
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9903 0145085.
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15-SEP-1999;
16-SEP-1999;
20 SEP 1999;
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-AUG-1999;
-AUG-1999;
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- AUG - 1999;
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03 - AUG - 1999;
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24-SEP-1999;
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29-SEP-1999;
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991. KSHÇKLIGDTERNELSOVIYOPSTARDI MKVIQIVIMBRATI SQLIJIMADQLI PYTQYEP. 1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis C vitus: C-106 3 construct, peptide fragment; immuncassay; reagent; probes; antibodies; HIV; HTLV; hepatitis B virus; Treponema pallidum; open reading frame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence is a fragment of the sequence given in BP-418216. Pragments of the HCV C-100-3 construct react specifically with antibodies to hepatitis C virus. These peptides are useful as assay reagents for diagnosis of HCV infection, allowing a decrease in talse positives of known methods. DNA sequences encoding the peptides are useful as hybridisation probes for detection and/or determine of HCV. Antibodies raised to the peptides are useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Open reading frame of the hepatitis C virus C-100-3 construct.
                                                                                                                                                                                                                               ch 0.5%; Score 59; DB 21; Lonath 357; l Dimilarity 23.7%; Prod. No 2^{\alpha+\alpha}2; Index 14; Concervative 14; Mismatches 31; Index 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide(s) for hepatitis-C virus detection - their use in immunological tests, and single test for the detection of different epitope(s) from different pathogens
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91DE-4112743.
91DE-4120281.
91PE-4121431
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 990S-0160768.
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19 MAY - 1999;
21 MAY - 1999;
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has been modified using the BepMi excision linker CA-3 which is one of a group of linkers designated blacks.

Within the scope of the hyvantion, this sequence was used to within the scope of the hyvantion, this sequence was used to illustrate a novel mathet of meditying PNA. PNA libraries expressing these modified polypoptides can be used to analyse the relationship between structure and function. Modified beta-lactames inharries can be used to determine the susceptibility of a particular antibiotic to hydrolysis ic. neatralization by mutant engines. Since all possible combinations of mutations were represented within the scope of the invention a meaningful sample could be achieved. The method of the invention allows the neasurement of successful transformants which contains a mitation linker, to determine the used to calculate the present in the library. This can then be used to calculate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gone expression control, promoter;
                                                                                                                                                                                                                                                                                                                                      probabilities that the most and the least common codon combinations are present in the library. The libraries can also be used to produce sets of modified polypeptides such as bronnenss, eq. human growth hormone, in order to detect and anlyse structure/function relationships.
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                                                                                                                                                             The sequence given is the beta-lactamase (bla) gene product which
                                                                                                                                                                                                                                                                                                                                                                                                                                     Overy Match 0.5%; Score 59; DB 13; Length 286;
Hest Local Similarity 22.7%; Pred. No. 1.5e±02;
Matches 15; Conservative 15; Micmatches 36; Indels
                                                                                    Novel DNA modification method and prodn. of modified DNA
                                                                                                libraries - used to determine effect of modification on interaction of encoded product, e.g. enzyme with target
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                                                                                                                                     Disclosure; Fig 10; 98pp; English.
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1999;
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                                                                                                                                                                                                                                                                                                                                                                          1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 JUN 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :1 - .TITN - 1 999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-JUN-1999;
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                                                                                                                                                                                                                                                                                              MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                      1999;
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                                                                                                                                                                                                                                                                                 19-MAY-1
20-MAY-1
21-MAY-1
24-MAY-1
25-MAY-1
27-MAY-1
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23-APR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Figure constant Arabi Lesis chairman sequence determined bas transment; Side pereter auggins (doorfit valon) promotery structural order UIRs antanislated requests expression control.
Fine the star Arden gass facilized sequence determined DNA transmits SPE, penetic mapping adentification parameters structural nearly UDS unitaristated regions expression control.
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19.8%; Pred. No. 1.20+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.20002;
6; Mismarches 12; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plust SEF encoded polypophide sequence SEG List 1 Not13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 lippitch ldvspilatavipilasivhasta 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tann 14; Pare 543 544; *** App. English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AABLA bela stochard: Poptidos 253 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ON TAND TAND COURS OF DELICITIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * 41,8e17.d* 19e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alexandric No. Property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Junety Materia
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHILE LOSDO 457 O'DO/4 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CART CHART ( HART)
                                                                                                                                                                                                                                                                                                                                                   With the Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14 273, 25000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---
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The present invention describes polymorlectides, such as complete chNA sequences and/or sequences of genomic DNA enempassing complete across, political and general increases the finally referred to the assequence-determined DNA transments (SDSB). Their work plants and Arabidopsis thatham. The SDBs are promoters, structural across, untranslated regions (UTRS), or 3' termination sequences. They can be used for expressing a gene product and controllind expression of a target gene, either as a promoter, a structural gene, an OHR or as a 3' termination sequence. They are also useful as tools for generic mapping, and identification of a particular individual, lant or terminating a group plants with a common trail. AAASH4 to AAASH4 and AABA465 in AAASH4 in the polymorphical in the polymorphical by them given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sare contra
                                                                                                                                                                                                                                                       Now corn plant and Arabidopsis thalians sequence actermined INA tragments, useful for expressing gene products and for controlling expression of a target gene \dot{\cdot}
                                                                                                                                      Alexandrev N. Brover V. Chen X. Subtumatian C. Treakhan MES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          beta-lactamase; BspMi excision linker; buman growth hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; score 50; 58.21; Lenath 253;
13.8%; fred. No. 1.2c+02;
fve. 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 iippiidtidvspllatavlqtlqsivbqstq2^{\rm C3}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             333 ILHGISETYDVSPLLRYMLPHLVVSIIHHVTG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key Location/Qualitiers
Misc-difference 194..198
                                                                                                                                                                                                                                                                                                                                                            claim 14; Page 342; 674pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR22598 standard; Protein; 286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zlabel: CA: 4
07-JAN-2000; 2000Wn-US00466.
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                                             99US-0115293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotic; transformants.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 43.89
es 14, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blad31 mutation (8).
                                                                                                                                                                                                                WP1: 2000-465970/40.
                                                                                           (CERE-) CERES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli.
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                                             08 - JAN - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web 207090 - A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                     Zhend L:
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RESULT 112
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                                                                                            AAY37675
                                                                                                                                                                   This sequence represents a human hyaloronan synthase (HOEFCII). HOEFCII polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the HOEFCII gene using probles containing the HOEFCII mutations in the HOEFCII gene using probles associated with HOEFCII matatace by determining HOEFCII polypeptide lovels. HOEFCII polypeptide to screen for agonists and antaquists which bind HOEFCII polypeptide by observing the binding, or stimulation or inhibition of HOEFCII activity. These can be used in treatment to activite (agonist) or inhibit (autaponist) HOEFCII activity in addition to direct administration of antisense sequences to prevent expression, or HOEFCII polypeptides to treat conditions associated with a lack of HOEFCII probein. Gene therapy may also be used to affect endomine and HOEFCII probein. Gene therapy may also be used to affect endomine and useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for inducing an immune response to immunise and prevent discases, and for isolating HeBFCII clones or parity, jug HEBFCII polypeptides by alfinity, chromatography, HOBFCII polypeptides on the administered directly or as a various to inconduct against disease. Diseases diagnosed, prevented or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treated include chronic renal failure, inflammatory discuses, myocardial ischemia, cancer, rheumatoid arthritis and cirrhotic liver disease. The HOBERGI polypeptide is also useful for mapping the gene to a chromosome,
                                                                                                                                                                                                                                                                                                                                                            qene therapy; immune response, vaccine, chronic renal failure; cancet,
inflammatory discases, myocardial ischemia, theumatoid arthritis, human
cirrhotic liver disease; chromosome mapping; linkage analysis
                                                                                                                                                                                                                                                                                                                                      Robbell, hyainronan synthase, diaquosis, detection, discuse, imbalance,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Epalacosan spathage (MeMPCM) polypoptide and polymentostide useful as diagnostic reagents and for prevention and treatment of cancer and chronic renal failure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             allowing gene inheritance to be studied through linkage analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            th 0.5%; Score 59; DB 20; Length 241; Cimilarit; 28.6%; Pred, Mc, 1.1e+02; 14; Conservative 11; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         973. VEQUATATETERIQRERELLAS REALISMALENTESCOVSCESVERFIARDEMY 1021
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AAW76768 standard; Protein; 241 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 16; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98EP-0303991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US 0865273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nambi P. Fullen M. Shu Y.
                                                                                                                                                                                                                                         15-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                           Human BUEFC11 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI: 1993-001400/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY 1997,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP881294-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1998
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                                                                                                                                                                                            AAW76768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [reca]
                                                                                               RESULT 111
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of Chlanydia trachomatis (see AAED1425). The polypeptides can be used as vaceines against Chlamydia trachomatis Antisonse and thrown sequences can also be used to control growth of the microordanism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY36754 Y37949 are encoded by open reading frames (ORFs) of the genome
                                                                                                                                                                                                                                                    Vaccine, eye disease, conventional trachema; nonendemic trachema; paratrachema; inclusion conjunctivitis; qenital disease; perihepatilis; nongomococcal uretritis; epidymitis; cervicilis; salpingitis; batthelinitis, parametath; venoreal lymphegranulematesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases such as conventional trachoma, nonendemic trachoma, paratrachema, and inclusion conjunctivitiss quental diseases such as nongeneococcal urctritis, epidymitis, cervicitis, appinglis, perihepatitis, appinglis, pneumopathy in breast leading infants: and venereal lymphogramicanis. The polypeptides of the invention may be of use in treating these diseases.
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29 2%; Pred No. 1 26+02;
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                                                                                                                                                                                             Chlamydia trachomatis surface exposed protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 1302-1304; 1755pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geneme sequence of Chlomydia trachomatis
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AAY37675 standard; Protein; 250 AA
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the present incention describes projuccientides, such as complete (MMA) supercess ind/or separates of actually box encompassing complete genes, particularly actually and/or interestic regions, collectical referred to as sequence determined that interestic regions, collectical referred to as sequence determined that Incompletes, Structural plants and matricus interestical regions (WIPS) or of referred to a queez, and or or products, Structural genes, and that expenses that have regions (WIPS) or of referred to a queez, and that a complete sequence in the property of an expense of the or or or entire that a product or or or entire to the force of the plants with a common trait. AAA7843 to AAA78640 property the sequences and projectically individual plant or for collective the sequences and projectively the specifically (MAZARA) to AAA78640 projectical invention, a particular developed by them diver in the
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performs on a new society in the control of the complete properties of the control of the co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SdPS
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fromments, useful for expression arms products and for controlling express) as of a larger per-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig. She are also prographine sequence SES List 1 Not14.
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Atabidopsis (fallens, the SDEs are premited as structural across, untranslated regions (UERs), ct of termination sequences. Incy can be used for expression a gene product and centrollica expression of a target gene, either as a prometer, a structural above, an UER of as of fermination sequence. They are also useful as fools for genetic mapping, and identification of a particular individual plant or for clustering a group of plants with a common trait. AAA784 to AAA386, and AAA4665 to AAB25099 represent the specifically claimed polynocleotide sequences and polypeptides encoded by them eiter in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is the peptide encoded by the confised open reading frame of hepathitis C virus (BCV) cDAAS in closes of and F (see AANT E). The polypeptides are used to distincts Builder all NANEH, to take antibodies for immanoassay of freatment, of to produce vareines.
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                                                                                                                                                                                                                                                                    Hepatitis C virus; open reading frame; clone 36; clone Ml; probe;
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34.5%; Fred. No. 1.1e+02;
ative 9; Mismatches 19; Indels
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44.8%; Fred. No. 1.1e+a2;
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                                                                                                                                                                                                                                                                                                                                                                                                                     AAP90148 standard; protein; 247
                                                                                                                                                                                                                                          Hest Local Similarity 44.8%;
Matches 14: Conservative
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06-SEP-2000.	C - Other Substitution		25 PER-1999;	05-MAR-1999;	09-MAR-1995;	23.MART 1999;	29-WAR 1999	01 - APR - 1949;	06-APR-1999;	08 - APR - 1999;	16 APR-1999,	19-APR-1999;	21 APR 1999;	23-APR-1999;	24-APR-1999;	28 APR 1999;	30-APR-1999;	30-APR-1999;	04-MAY 1999,	05-MAY 1959,	06 - MAY - 1999;	05-MA1 1777, 07-MAV-1696.	11 MAY 1223	14 - MAY 1999	14 - MAY - 14994	14 - MAY - 1939;	14 - MAY 1999.	18-MAY 1999:	19-MAY-1999;	20-MAY 1999;	21-MAY-1999;	24-MAY-1999;	25-MAY-1999;	27 - MAY - 1959;	28 MAY 1999;	01-00N-1989;	04 - IIIN 1999:	07-JUN-1999;	08-JUN-1999;	10-JUN-1999;	10-JUN 1999;	15557 - NOO- 57	16 - JUN - 1999;	17 - 1015 1999;	18-JUN-1999;	18 JUN 1995,	18-JUN-1999;	18-JUN-1969;	18 55M 1999;	18-JUN 1999,	1000 01 NIII-81	18-JUN 1995;	18-JUN 1999;	18-JUN 1999;	18 JUN 1993)	21-00M 1999;	23-JUN-1999;	23 JUN 1999,	24-JUN-1999;	78-70B 1999;	29-38H 1999;	30-JUN-1999;	01-301-1999;	02-JUL-1999; 02-JUL-1999;
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RESULT 105

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                                 the polynogither may respect by soil behave synthesis transport for global (1991), at some president technology.

The usest task in records resultivity and is more specific than assure the polynoptide choice. (Breithallo), see that Angiette desired Andrews AAPLEAGES.
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It is encoded in the open reading trame of a composite necessition energy and proposed from overlapping hepatitis ? Virtuas (HV) cMAN in electors 81. 1-2, and 91, isolated using a synthetic sequence equivalent to a transment of HCV cDNA in clone 5-1-1. It is an epitope, portions of which could be used as immuneasing readents and vaccines and to accorate antibodies useful in diagnosis and passive immuneatherapy for HVV infection/from A, non B hepatitis.
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Bybeidisation assay; genetic mapping; gene expression control; promoter;
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AAP92018 standard: protein: 528 AA
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choo q-L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1989-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N PSDB: AAN92074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1044405-AZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 - Nº V 1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-Nov-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 - oryr - 2000
                                                                                                                                                                                                                                                      02-MAR 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 - MAY - 1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Honghton M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP418216-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Querry Match
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                                                                                                                           AAP%2018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG40309
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Matches

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RESULT 101

AAE 52015

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The synthetic peptide p1689 represents amino acid residues 1689-1805 of the hepatitis C viral antiqen. The peptide may be used in an assay to detect antibodies to HCV and thus to diagnose chronic HCV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10. Indels Or Caps
Hepatitis C virus; NANBH; assay; antibody; p380-JH1; p380-J; p3801A;
                                                                                                                                                                                                                                                                                                          Assay for detecting presence of antibody to hepatitis \mathbb C viral antigen - by contacting sample with polypeptide contq. at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunological assays for hepatitis C virus antibody - by using polypeptide(s) contg. epitope(s) of hepatitis C virus antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 59; DB 14; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ciűű-3; hepatitis C virus; immunoassay; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred, No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1821 VELPATKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 13; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR13354 standard; Protein; 118 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1: Page 45; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P1689 HCV antigen (1689-1805).
                                                                                                                                                                                                                                                                                                                                                one epitope of virus antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90AU-0068390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0610180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ABBO ) ARHOTT LABORATORIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             890S-0456152.
                                                                                                                                                  92WO-US07813.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.5%;
                                                                                                                                                                                   9145-0760292
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                                                                                                                                                                                                                                                 Lesniewski RR, Leung TK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Casservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             See also AAR33861-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1991-238393/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                               WPI; 1993-117564/14.
                                                                                                                                                                                                                  (ABBO ) ABBOTT LAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
                                                                                                                                                                                   16-SEP-1001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1989;
                                                                                                                                                  16-SEP 1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AU9068390-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 HTM-1991.
                                                                                    WO9306247-A.
                                                                                                                   01-APR-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR13354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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(X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            It is the putative sequence encoded in the open reading frame of hepatitis C views (HCV) clnM insert in clone 81. It is an epitope, portions of which could be used as immunoassay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for
                                                                                                                                                                                                                                                                                                  Sequence of the polypeptide encoded in the hepatitis C virus (HCV) cDNA insert in clone 81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Caps
                                                       Gaps
                                                       ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5%; Score 59; DB 10; Length 117;
34.5%; Pred. No. 40;
Live 9; Mismatches 10; Indels
               Score 59; DB 10; Length 117;
Pred. No. 40;
                                                     9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                  Hepatitis C virus (HCV); non-A, non-B hepatitis (HANBH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and associated nucleic acids and polypeptide(s)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypoptide p1689 comprising HCV viral antiqen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1821 VICEATERISECTERNWERRESTRUCTURE 1819
                                                                                      1821 VLEPAIKKIYKQIEKNWKNHMSFFMSILQ 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               880S-0271450; US-122714.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 viapavqtnwqkletfwakhmwnfisqiq 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCV intertion/non-A, non-B hepatitis.
                                                                                                       Claim 13; Figure 4; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR33872 standard; peptide: 117 AA.
                                                                                                                                                                                                      AAP92019 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton M, Choo q L, Kao G,
                      0.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88EP-0310922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Purified hepatitis C virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Rest Local Similarity 34.5%
Mutches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                    02-MAR-1990 (first entry)
                                    Local Similarity 34.59
es 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR.) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1989-159274/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAN92075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV 1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-NoV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                               11-MAY-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                    EP318216-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR33872;
                   Query Match
Best Local e
                                                                                                                                                                                                                                       AAP92019;
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RESILLT 102

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AAR 13872

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F. dinticalis (8) Languaghatinin hash (AAP96011) was identified as the product of the holf open (AA) 180/41 [Soluted as an ECOPV FILLING OF COLOR AND THE HAPPER AND THE HOLTON OF POTTONS OF IT.

ASSOCIATED AAP FOOT 24), our be obtd. From transformed most ceils and used as a creating 24), our be obtd. From transformed period is and used as a creating 18, period Manage or animals arthred period in all and a second of the about the transformed and the second of the presence of animal period and the detect the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        presence of anti-P. Bradish's antibodies and to raise monoclonal and bodies for dienostro apple.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rementialitie protect periodos al diseases vaccines haga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Land 2 M. Jayine 1, Patti JM, Proquiske Fox A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE CIAINTERCONNECTIVE ON TANK 17 CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name to Private 1412 Notes English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAWebind standard; Profein; 2628 AA
Zimen Surjegilde
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHES COLUMN
                                                                                                                                                                                                                                                                             2455 - 15 C
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(UVEL ) ONLY FLORITA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 SEC 1995
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                                                                                                                                                                                                                                                                                                                                                                  8 . . . . . . A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Chitchell
                                                                                                                                                                              14. (C. N.)
                                                                                                                                                                                                                                                                             Hear Cools
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mar 11.4 S
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this sequence is encoded by a Porphyremeans dintitude of the invention. This sequence represents the bank haemadoblinin protein. The polypeptides are used to produce antibodies to ordanisms associated with periodomtal disease. The antibodies are also used in purification and identification procedures, the areas and polypeptides are used as vaccines against periodomtal disease.
                                                                                                                                                                                                                                                                                                                                                                                                 sdry to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hepatitis C virus gene —used tor prode, of polynamics probes, polypeptide(s) and antibodies for diagnosis, prevention and treatment of infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence is the pertide encoded by the hepatitis of this kery cloud insert in DNA Bi (see ANNSCOOK). The polypoptides are used to diagnose BCV-induced NANBUL to raise antibodies for immunoassay or treatment, or to produce vaccines.
                                                                                                   Isolated Forphyromonas aintivalis genes — encedita haemaduittinin.
                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 60; DR 19; Jenuth 2028;
40.0%; Pred. No. 2.7c+03;
                                                                                                                                                                                                                                                                                                                                                                                                 1nde l's
Lautz M. Lepine G, Tatti JM. Proquisko Fox Ad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of hepatitis C virus con insert in DNA 81.
                                                                                                                                                                                                                                                                                                                                                                                                 6; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1568 QIALYILKILCKNEGAENROPEVPULXIAVKLIAP 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Repatitis C virus; DNA 81; probe; vaccine
                                                                                                                                                    Claim 1; Column 91-110; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP90136 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure: 114 4: 235pp: English.
                                                                                                                   and/or protease poly:poptide(s))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88GB-0027024.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87US-0122714.
                                                                                                                                                                                                                                                                                                                                                                              40.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR ) CHIRON CORPORATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Henghton M. Obec QL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 1989-215054/30.
N-PSDB: AAN90305.
                                               WPI: 1998-582627/49.
                                                                                                                                                                                                                                                                                                            2628 AA:
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117 AA:
                                                                  N PSDB; AAVSBB75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pan troglodytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1987;
                  Tumwasorn S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2861 VON-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1989.
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                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP90136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 100
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The present invention relates to a method for determining the effect of a test sample on unverginess exposing an acceptor substrate for UGUT to a labelled donor in the presence of the test sample and UGGT. The method is useful for determining UGGT activity. In particular, the method is useful for determining UGGT activity. In particular, the method is useful in glucosyltamisterase assay and kinetics measurement for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           folded glycoproteins. The present sequence was used in a sequence bomology comparison with rat UGCT (see AAF60732 and AAB72436) which was used in the method of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                determining BBCF activity, BGST is a soluble envyme of the endoplasmic reticulum which catalyses the addition of a qlucose residue onto asparagine-linked oligosaccharides, which are present on incorrectly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          656 LICVANÇKMIELLADMINLGDPSSMLKMVPPI I SVOERPSPNLPQYVTFHVILSVLVSCC 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UL : Ligssmakysfælradfrekregjeilælladlisenbehnimileperkneverprifælli 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining the effect of a test sample on UDP-qlucose:qlycoprotein
glucosyltransferase (UGGT), useful for measuring UGGT activity,
comprises exposing an acceptor substrate for UGGT to a labeled donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haemagglutinin, hagA, periodontal distant; surcines antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 0.6%; Score 60: DH 22: Length 1447; Best Local Similarity 27.3%; Pred. No. 1.1e+03; Matches 18; Conservative 14; Mismatches 34: Endels 1
                                                               UCCT; UDP-glucose.glycoprotein glucosyltransferase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                    Tessier DC, Dignard D, Bergeron JJM, Thomas DY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porphyromonas gingivalis strain 381.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR96030 standard; Protein; 2628 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Logation,/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P. ginqivalis haemagglutinin hagA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure, Fig 9; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                    (CANA ) NAT RES COUNCIL CANADA.
                                                                                                                                                                                                                                                                                                                    99US-0376330.
                                                                                                                                                                                                                                                                  27-JUL-2000; 2000WO-CA00883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                     Schizosaccharomyces pombe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the presence of UGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WFI, 2001 218359/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1447 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               716 SSLKET 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               735 sspkrs 740
                                                                                                                                                                    WO200112845-A1.
                                                                                                                                                                                                                                                                                                                       18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-1996
                                                                                                                                                                                                                    22-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR96030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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This protein comprises novel mouse related adhesion focal tyrosine kinase (RAFTK), an intracytoplasmic protein tyrosine kinase (FTK) involved in the modulation of cell growth and differentiation. Its amino acid sequence was adduced from a cDNA clone (see ANVI7801) isolated from a mouse brain library. It shows 95% homology with human RAFTK (see AAWAR372). RAFTK may be expressed in fost cells or in transquence animals and used to raise antibodies and to screen for compounds capable of modulating RAFTK interaction with cellular proteins. Agents that modulate RAFTK are used to control growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ಚರ್ಚ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding vertebrate related adhesion focal tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               induced, inhibition of apoptosis where this is induced by radiation, chemotherapy or neurodegenerative disease, and also for explanding cells for transplantation, treating conditions associated with meribary-eryte abnormality, or a thrombony-oppania, and control of platelet aggregation.
                                                                                          EAFTE, related adhesion foral tyrosion kinse, mouse, protein protein tyrosine kinase, ETK, etc. stockly constituted differentiation, cell adhesion; cell migration; regulation; signal transduction; metuatasis, cancer, leukacaia, thromboo; topachia, therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mediated diseases, e.g. cancer or leukaemia, where apoptosis is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             differentiation, haematopoiosis or survival of cells (claimed) (especially mast cells, melanocytes and megakaryccytes), or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase - useful for, e.g. regulating growth, differentiation, adhesion and migration of cells, used for treating metastuses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             adhosion (especialy tocal adhosion formation), migration, phagocytosis or motility of cells, particularly for treating metastases. Typical applications are in treatment of immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 60; DB 19; Length 1009;
23.3%; Pred. No. 6.6c+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse related adhesion foral tyrosine kinase (RAFTK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14, Mismatches 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BETH-) BEITH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Paye 145-148; 167pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avraham H. Avraham S. Groopman JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB72445 standard; Protein; 1447 AA
                                                                                                                                                                                                                                                                                                                                                                               97WO-US14093.
                                                                                                                                                                                                                                                                                                                                                                                                                              9705-0816462.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9605-0703623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10, Conservative
  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-169174/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1009 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV17801
                                                                                                                                                                                                                                                                            W09807870 Al.
                                                                                                                                                                                                                                                                                                                                                                            12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                              3-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-AUG-1996;
17-AUG-1998
                                                                                                                                                                                                                               Mus spretus.
                                                                                                                                                                                                                                                                                                                            26 FEB-1998.
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Identifying agents that bind and modulate protein tyrosine kinase z - useful for inhibiting migration, adhesion or activity of monocytic cells, particularly for freatment and prevention of osteopolosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rights, is a recently described member of the tenth albeston kinase family. A claimed method for identifying compounds (1) that bind to, and, a medical section of a compound then bettermining binding opticially any change test compound, then determining binding and opticially any change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevent monecytic cells from dyradina extracellular matrix. These are potentially useful for treatment and preventian of osteoporosis and intlammation, or generally any condition associated with
                                                                                                     Protein tyrosing kinase 2: PVBZ deney mense; pudescorrected adhesion kinase beta: related adhesion tyrosine Kinase; tocal adhesion kinase; liqand; monocyte; estequenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in activity. The method is used to identify (i) that present adhesion of momocytes to substrate, inhibit osteoclast mobility or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is the amino acid sequence of motion protein tyrosine Kidase (PYKZ), deduced from a cDNA sequence (see AAA494545) and itself control of a newsystem of the STA are named and related adhesion to a linase beta and related adhesion to all tyrosine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The method is based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.68; Seore 66; DR 19; Length 1609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :ndels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fred, No. 6,6e+02;
14; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mote- "proline rich domain"
Murine protein tyrosine kinase 2 (PYKZ).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tormation in monocytes and macrophages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Znote "Kinase domain"
701..767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualitiers
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res 10: Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAV49608.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sale
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                                                                                                                                                                                                                                                                    Protoin tyrosine kinase ii PYKII menser eell adhesion Kinase betar
relited idaesten leesi tyrosine Kinase; todal adhesion Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the amount of radiolated tyrosine measures. The result is supported with this measured in the absence of rest compound. Madulitors of PYK2 are perentially useful for controlling the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w.edg. Secretor (dr.19), indigital languages (3.3%). Prod. No. f.fering.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is a protein with neurite elongating activity,
                                                                                                                                                                                                Neurite, elongation, anti-dementia, memory, improvoment, chicken, mearon fibre, repair, seuron cell, activation, learning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A protein with neurite elongating activity – useful as an anti-dementia, memory-improving or neuron fibre-repairing agent
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"claimed truncated protein"
                                                                                                                                                                                                                                                                                                                                                         "claimed truncated protein"
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                                                                                                                                                                       Chicken derived neurite elongation protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
                                                                                                                                                                                                                                                                        becation, gradities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 2-3; 24pp; Japanese.
                                                                                   AAR97123 standard; Protein; 687 AA
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                                                                                                                                                                                                                                                                                  Misc difference 551
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Local Son
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                                                                                                                AAR97123;
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                                                       RESULT 92
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RESULT 93

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by expression of a human cancer associated antiqen precursor coded for by a nucleic acid molecule (NAM). The method comprises: (a) contacting a biological sample isolated from a subject with an agent that specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for diagnosing a disorder characterised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        binds to the NAM, an expression product or a fragment of an expression product complexed with an HLA molecule; and (b) determining the interaction between the agent and the NAM or the expression product as a determination of the disorder. The products and methods can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the diagnosis, monitoring, research, or treatment of conditions characterised by the expression of various cancer associated antiqens. The invention provides nucleic aedia sequences and encoded polypeptides which are cancer associated antiqen precursors expressed in human breast cancer, repail cancer, relon cancer, quastric cancer, prostate cancer and
                                                                                                                                                                                                                                                                                                    breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated cancer associated nucleic acids and polypeptides isolated using sera from cancer patients, used to develop products for the diagnosis, monitoring or treatment of cancers
                                                                                                                                                                                                                                                                    Cancer associated antigen; diagnosis; research; treatment; human;
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Pfreundschuh M, Sahin U, Scanlan MJ, Stockert E;
                                                                                                                                                                                                      Renal cancer associated antiqen precursor sequence.
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AAY07064 standard; Protein; 862 AA
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Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                             prostate cancer.
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17-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the professe was as the smallest in eader to center it (partially) insulance of professe the topological professe with a professe with modified professe; it is not professe with modified professe gibt errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               System Geographics (Advisor) (1994), Freds, Nov. 2, Pere2, 99. Mismarches (17), Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 MENTEVNSLASS CRITICAL PROGRESS CAVIDAGE REAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Lashyinking partition is a second and the contraction of the contrac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jackson of professors and contract of demonstrations.
                                                                                                                                                                                                                                                                                                                                             The leaves are a ledge of English.
                                                                                                                                                                                                                                                    became sequence of the Inglia parentholiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ors to surery from 25 and 4 app. English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHON ) PHONE POTTENY FORER SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Productive general production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12FF ..... 49.54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity (4,48)
Matches (4) Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 731, 1994 (Tiles entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please Roy Printers A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klaymore my was last tax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WP1: 1939 457842740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serpendent 141 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33462 NEL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 N.S. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D. JAN 1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transfer Fr
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The present adjusts represents a rew polarity; PMP-2 is a statement. Pattering distinct regions: a morth domain, a system of the domain. But a remained in the domain and a cytopicasmic domain. By No orbiting the eyoplasmic tall domain. PCLP. Homology is shown to CDA in the eyoplasmic tall domain. PCLP. Homology is shown to CDA in the eyoplasmic tall domain. PCLP. Polypeptides and nucleit acids are useful for diagnosing and freeding (PDA) discuss associated ATD, selectin mediated kinding oversis, including acute and dream in mediated kinding oversis, including another and die useful in assays for selectina for therapestre acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podocalyxin-like protein, e.g. useful for diagnosing and freating discuses associated with selectin mediated binding events
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLE-2: podovalywim like protein; selectin; ligand; brmann;
inflammation; autoimmune disease; tissue rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score for DB 200 Tenath full;
43.4%; Pred. No. 3.40002
0.6%; Stope 60; 38 15; Lepath, 561;
62.9%; Fred. No. 2.86+0.;
tye 8; Mismarches Let indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homan podocalyxin-like sialomucin PCLP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..32
Znote "siqual peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note "mature protein"
                                                                                                                  1137 NCKMSHCAQTVSSVPEGTSVNAEGVRTEL 1165
                                                                                                                                                   138 nafathraal (aschygeakeas) marke sek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualitiers
                                                                                                                                                                                                                                                                                                                         AAY31741 Standard; Protein; 605 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 7; Fiq 1; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            980S-0111654,
980S-0074489,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99W0-US01780.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.4%;
                                 17.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22 NoV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.3
Matches 15, Conservative
                           Best Local Similarity (7.9)
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REGG ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43..605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen SD, Sassetti CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 1999-540141/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 605 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB: AAX87926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W-1941464-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lo DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 - AUG - 1999.
                                                                                                                                                                                                                                                                                                                                                                                     AAY +1741;
         guery Match
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Setro to

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Chlamydia pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                               (CHIR-) CHIRON SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                     513 AA;
                                                                                                                                                                                                                           N-FSDB; AAR12221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-NOV-1998;
WC9924578-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 4661-NUL-E0
                                                                                                                                          14-JAN-1998;
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                      20-MAY-1999.
                                             09-OCT-1998;
                                                                    01-SEP-1998;
                                                                                          14-NOV-1997;
18-NOV-1997;
                                                                                                                   27 - NOV - 1997;
                                                                                                                             10-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY35274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [555]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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DF
This sequence is encoded by a Purphynomias singularist case of the invention. This sequence represents the hagA haemagglutinin protein. The polymorphides are used to produce antibodies to organisms associated with periodontal disease. The antibodies are also used in purification and identification procedures. The genes and polypeptides are used as vaccines against periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sdep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis: Neisseria gonorrhocae; antigen; vaccine;
treatment, Meisseria intection, meningitis, septicaemia, gonorrhoa.
                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Porphyromonas gingivalis genes - encoding haemagglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%, Score 60, Ob i9, Length 497,
40.0%; Pred. Mc. 2.46.02;
tye 6; Mismatches 15; Indels
                                                                                                                    Haemayqlutinin protein; periodontal disease; vaccine; haqA.
                                                                                                                                                                                                                                                                                                                                    Han N, Lantz M, Lepine G, Putti JM, Progulske-Fox A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis antiqen encoded by ORF139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1668 STABITIERICIERISABHHTGTIVPVONTAVELTAF 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Column 37-44; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY38786 standard; Protein; 513 AA
                        AAW69483 standard; Protein; 497 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        and, or protease polympoptide(s))
                                                                                                                                                                                                                                                  88US-0241640.
91US-0647119.
                                                                                                                                                                                                                                      950S-0570311.
                                                                                               Maemaqqlutinin protein hadA.
                                                                                                                                                                                                                 9508-0570411.
                                                                                                                                                                                                                                                                           9405-0353485.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-00T-1999 (tirst entry)
                                                                     22-DBC-1998 (first entry)
                                                                                                                                           Porphyromonas qingivalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                  (UABR-) UAB RES FOUND.
                                                                                                                                                                                                                                                                                                             (UYFL ) UNIV FLORIDA.
                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-582627/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Cimilarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      497 AA;
                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV58870.
                                                                                                                                                                                                                 11 - 040; - 1995;
                                                                                                                                                                   US5824791-A.
                                                                                                                                                                                                                                        11-DEC-1995;
                                                                                                                                                                                                                                                    08-SEP-1988;
                                                                                                                                                                                                                                                                25 - JAN - 1991;
                                                                                                                                                                                                                                                                           09-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                    Tumwasorn S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                          20 OCT - 1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY38786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Onery Match
                                                AAW69483;
 RESULT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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            AAW69483
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Respiratory disease, paramonia, bronchitis, heart disease; sarcoidosis: sinusitis; purulent otitis media; erythema nodosum; phorynditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequences AAY38499-Y38944 represent Neissoria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and N. gonorrhoeac antigenic proteins. They are encoded by open reading frames (GRES) AA711972 212358. The antigenic proteins, their fragments, their nucleic acids and antibodies are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis, prevention (as vaceines) or treatment of Neisseria infections, such as meningitis, septicaemia and genorithe. Both organisms are closely related. Fragments of the nucleic acids are useful as hybridisation probes and antisense reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 qeetaaaarrsammeglafilpfmespeersagetilyppwisslpfilonga 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 CVPLAFORT DEHVERFLAFMERFORT VTKSVKVFARTROSSAOLIKVILLAFYA [22]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 60; DB 20; Longth 513; 34,5%; Prod No. 2 504.02;
                                                                                                                                                                                                                                                                                                                                                                                                 Grandi G, Masignani V. Pizza M, Pappuoli P. Scarlato V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6, Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amiss grid segmen of a Chlomydia proumoniae, protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 329-330; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY35274 standard, Protein, 541 AA.
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                                                             97GB-0019016.
97GB-0023516.
97GB-0024190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 980S-0107078.
97FP-0014673.
98WO-IB01665.
                                                                                                                                                                   97GB-0024386.
97GB-0025158.
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immunity. The attendated barrenium retains sarture antibens present on the Virilent organism and thus is a good immuneren.

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p. Pred. No. 1,4692;
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A portion (AAR96025) of P. qinqivalis (B. Laemanelutinin hadA (see also AAR96040) was identified as the product of clone SLZ (AAL9040) isolated from a P. qindyalis (B. quemic library. The haemaqqiatinin can be obtd. from transformed host cells and used as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a vaccine to protect humans or animals against periodontal discuse. 
Expression in Salmannella cells allows probn, or a live varcine. 
The backmandiation can also be used to detect the presence of anti-p, analysis anti-bodies and to raise monorload anti-bodies.
                                                                                                                                                                                                                                                                                                                                                                             Haemaqqlutinin; haqA; periodontal disease; vaccine; antibody.
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40.0%; Fred. No. 1.48-02;
UNF 6. Mismatches 15; Indees
                                             Query Match
Best Local Similarity 47.8%; Prod. No. 1.90***;
Matches 11; Conservative 4; Mismatches 8; Indees
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    P. qingiyaiis haemaqqintinin hadA.

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Matches 14: Conservative
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Sequence 427 AA:
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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РК 28-SEP-1099; 9908-0156458. РК 29-SEP-1999; 9908-0156596.	04 - oct - 1999;	05-001-1939; 06-00T-1959;	07-cert-1999;	08-001-1999; 12-001-1999;	13-OCT-1999;	- 2 OM - 1995; - 3 OM - 1999;	14 oct 1999;	14 -00T -1999; 14 227 1444;	14 -oCT - 1999;	14 -007F - 1999; 10 - 67F - 1666;	21 - OCT - 1999;	21-00T-1999;	21 - OCT - 1999;	21 -00T - 1999;	21 - 00T - 1999;	22-071-1999:	32 - 001 - 1999;	25-oct-1999;	18661-130-6 <b>7</b>	46661-100-97	PR 25-001-1959; 950S-0161360.	26 - OCTF - 1999);	28 Oct 1999;	82	10 S166 4661 150 67	). 6.8. (). (S. ()	Best Loral Challail, 28.59, Fred. No. 1.3e-02, Watches 11, Conserrative 11; Mismatches 24; Indole 9; Caps 0;		Q7 12.2% FOR EXPERIENCE VPG PERSON (Q4 HHRALLE DATA VALUE FOR VEHICLE 18.2%)	(a) 212 kdg hydrigation i Equations Fitting an image objection of the		RESULT 83	AAV22584		AC AAG21584;	on by 17-oct-2000 (liest entry)	Arobidos: =		KS - Protein idealitication, ciamal translation pathway, metabolio pathway; KS - betaidsation assum arotin membina rape skampakan bulta), premilor		XX OS Arabidopsis thaliana.		PN EP193405-A2. xy	PD 06 - SEP - 2000.	XX SELEMBL-2000 - 2000	100004	25-FEB-1999; ocwar-10000	09-MAR-1999; 09-MAR-1999;	PR 23-MAR-1999; 99US-0125788. PR 25 MAR (999, 9900 0126204).	

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping, as a sapression control; promoter; termination sequence.
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eve 11; Mismatches 24; Indels
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                        11; Mismatches
             Pred. No.
              28.68;
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RESULT 79

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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypelides in the series of the permenting or treating thelicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic quatritis, and peptic ulter diseases, e.g. gastric and duodenal ulters. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                      GHPO protein; Helicobacter intection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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            AAW98814 standard; Protein; 275 AA.
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                                                                                               H. pylori GHPO 1381 protein.
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Best Local Similarity
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Problem populations is signal transduction publicate metabolic pathways hybridus that issues genetic mappings gene expression controls promoter, termination sequence.
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Query Match 0 6%, Score 60; DB 21; Lenath 266; Best Local Similarity 28.6%; Pred. No. 95; Matches 14; Conservative 11; Mismatches 24; Indels 0; Gaps

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Protein identification; signal transduction pathway; metabolic pathway;
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Query Match
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the Rattus norvedicus belwan inc 560 which correspond to alternatively spliced unc 56 transcripts, and a homan one 563 cobx which shares homelogy with the Rattus norvedicus unc 568 cobw. Also described are assays based on protein-protein interactions between the unc 5 protein and a variety of different interacting proteins. The unce 56 variant cobnas and unc 568 common are useful in methods for identifying compounds which reduce or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Three variants of homen and 50 cDMAs (as 5CL, and 5Cs and and 5C8) and a homen unce 5HS1 cDMA, asolul in yeast two hybrid experiments for identifying unknown lumina cDMAs which encode proteins that interact with the human unce5C protein.
                                                                                                                                 Three variants of human une 5C cDNAs (une-5Cb, une-5Cc and une-5C8) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibit the lethal phenotype associated with the expression of the uncession of the uncession of the during the deads of the search of the search of the search of the constant of the constant of the constant of the constant of the following that interact with the human nuces of protein. AAC90914 to AAC90971 and AABS0646 to AABS0693 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    376 KEHHERATLIKISLKRENLASILLASILLISYSSQERMESNEVSLINEQFLPLIFILES 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; Caenorhabditis elegans; UNC-5; splice variant; nematode Worm;
                                                                                                                                                  a human unceSHSI cDNA, useful is yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact with the human unceSC protein -
                                                                                                                                                                                                                                                                                                                  The present invention describes 3 variants of human unc-5C cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.68; Score 61; DB 22; Length 731; 27.1%; Pred. No. 40:02;
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Van Criekinge W. Roelens I. Bogaert T. Verwaerde P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Mismatches
                                                                                                                                                                                                                                                             Example 4, Page 119 121, 246pp, English.
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Best Local Similarity 27.19
Matches 16, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
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                                                 WPI; 2901-016508, U.
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                                                                                N-PSDH; AAC90919
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represent human broast, gastric and prostate CAAP protein sequence respondively. CAAPs have extractation of the buman CAAP proteins, peptides, nucleic
                                              The pergraf ferentian describes 2 markets of bunner and for dBMAs (unc-50b, unc-50c and unc-508) which correspond to alternatively spliced
                                                                                          une-5C transcripts, and a human unc-5HS1 cDNA which shares homology with
                                                                                                       the Kattus norvegious unc-SHSI coNA. Also described are assays based on partering protein interacting between the mer's partering and a varioty of different interacting proteins. The unc-St variant coNAs and unc-SHSI coNA are useful in methods for identifying compounds which reduce or inhibit the lethal phenotype associated with the expression of the unc-S death domain in yeast They are also useful in yeast two hybrid experiments for identifying unknown human coNAs which encode proteins that interact with the human unc-SC protein. AAC90914 to AAC90971 and AAMSOGAS to AAMSOGAS are present sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding breast, gastric and prostate canter associated antigen procursors, useful for diagnosing and treating a condition characterized by expression of an abnormal amount of a protein, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prostate cancer associated antigen precursors (CAAP) respectively. AABF3237 to AABF3472 to AABF3470
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27-14; Pred No 1-66+03;
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              Claim 37: Paye 110-118; 246pp; English.
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protein-protein interaction: ifentification.
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42.48; Prod. No. 1.15+32;
tige 6; Mismatches 13; Indels
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990S-0142154.
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99US-0123180
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12.4%; Pred. Ro. 1.1e:02;
.ve 6; Mismatches 12; Todels 0; Caps
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9408-015836.
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9408-01595841.
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9908-0157117.
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990S-0161992.
990S-0161993.
990S-0162142.
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9908-0154018.
9908-0154039.
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990S-0161360.
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9908-0155659.
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990S-0158232,
990S-0159293,
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99US-0150566.
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sequences AAAAAAA22-AAAQAS represent proteins used in a newel method of predicting the folded structure of proteins, by aligning sequences of homologous proteins and using patterns of evolutionarily conserved and varied sequences to assign positions. Positions in the alignment are assigned to the surface or inside of the folded structure, active sites,
                                                                                                                       and parsing segments. Secondary structural units are assigned by identifying periodicity in the assignments, and assembled into globular
                                                                                                                                                          form using distance constraints imposed by disuffide buildes, active site assignments and co-variation analysis. The predicted secondary structures are useful for identifying antigenic sites on a protein understanding the interaction of a protein with other molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               relationship between structure and function. Modified beta-lactamse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence given is the beta-lactamase (bla) gene product which has been modified using the BspWl excision linker MC-3 which is one of a group of linkers designated blad?
Within the scope of the invention, this sequence was used to lithistante a novel method of modifying DNA. DNA libraries expressing these modified polypeptides can be used to analyse the
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                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 61; 08-20; Length 259;
21.7%; Pred. No. 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             259 AA;
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This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and qastroduodenal diseases associated with these infections, including acute, chronic, and atrophic qastriitis, and peptic ilder diseases, e.g. qastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
mitheratics can be used to determine the susceptibility of a particular antibiotic to hydrolysis to incurrilisation by matant enymes. Since all possible combinations of mutations were represented within the scope of the invention, a meaningful sample could be achieved. The method of the invention allows the nessurement of successful transformants which contain a mutation linker, to determine the number of different colonies probabilities that the most and the least common codon combinations are present in the library. This can then be used to calculate the probabilities that the most and the least common codon combinations are present in the library. The libraries can also be used to produce sets of modified polypeptides such as hormones, etc. human growth hormone, in order to detect and anlyse structure/function relationships.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
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                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Helicobacter polynuclectides - used to develop products for the diagnosis, prevention and treatment of Helicobacter
                                                                                                                                                                                                                                                                                                       0.6%; Score 61; UB 13; Length 286;
22.7%; Pred. No. 77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (INMR.) MEPLEUX ORAVAX PASTETTE MEPLEUX SERUMS.
                                                                                                                                                                                                                                                                                                                            Best Local Similarity 22.7%; Pred. No. 77;
Matches 15; Conservative 17; Mismatches
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the present sequence represents a midE polymoptide. The polypoptide is easily for at his send in the respirite increased activity or expression of midE to treat that respirite increased activity or expression of midE to this seem to represent the mide and in varcines. The polypopties and for recombinant (or in viz) production of the midE is used for recombinant (or in viz) production of the midE expression of any properties and primers, between mutations in midE encoding encoding sequences, or measuring the expression of midE encoding encoding sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               susceptibility), also for serotypine or chromosome identification. Tiscuss which may be distincted our freshed are particularly intertion by S. rare is, but may also be intertion by Helicobarter pyiori, and assectified corers and throns.
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                                                                                                                                                             WPTS LONG ADMAZZEN
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                                                                                                                                                                                                                         27 Airk 13335
                                                                                                                                                                                                                                                                                                                                                        2 AT 1 1991
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invention can be used for producing transgenic plants with higher locals of protein content (e.g. 2 to 5 fold increase) and higher levels of essential amino acids. The present sequence represents the ASPI protein
                                                                                                                                                                                                                                                            The present inzention describes transcenic plants (A) comprising a determinance which encodes a protein comprising an amphibibility alpha their over a beta pleated sheet, that produces more protein per tissue weight of root, tuber, seed, lear, stem, edible portion, flower or whole plant than a normal plant. The preferrod protein is an arrificial storage protein designated AB which has been designed as a nutrificial protein for humans. Products and methods from the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prediction; secondary structure; alianment; evolutionary conservation; homology; periodicity; co-variation analysis; antiaenic site; site directed mutagenesis; interaction.
                                                                                                                                                              Transgenic plants containing dense exceding profeius comprision amphiphilic alpha helices or teta-phoated sheets to increase profein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633 THPLERGWEBALENVIKSTRFORLFOVANGRMIELLADMINIGHPFSMLR 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 61; DB 21; Length 92;
32.0%; Fred. No. 15;
17e 9; Mismarches 25; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Predicting the folded structure of proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 257-260; 113pp; Enalish.
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                                                                                                                                                                                                                                Claim 9; Page 86; 111pp; English.
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             980S 0056056.
                                                                                                                                                                                               production in plant tissues
                                                                                                                                                                                                                                                                                                                                                                                                                              from the present invention
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein kinase #16.
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                                             (DEME-) DEMEGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BERNA) BENNERS S.A.
                                                                                                                             N-PSDB; AAZ35977.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 92 AA:
             27 - APR - 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 MAR 1992;
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234 AA;

Sequence

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cardiovascular disorders e.g. cardiar arrest, coretrowascular disorders e.g. cerebral isotheria, andiodenesis, nervous system disorders e.g. Alzheimer's disorders e.g. andiodenesis, nervous system disorders e.g. corneal infection. The polypeptides can also be comilar disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to mainfain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT36254 T37345 are encoded by open reading frames (OREs) of the genome of Chlamydia trachomatis (see AA261425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisonse and riboryme sequences
                                                                                                                                                                rhemolaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content. Ifpid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. Assert to AAP22315 and AAB2008 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine, eye disease, ocaventional trachoma, nonendemie trachoma, paratrachoma, inclusion conjunctivitis, ential disease; perhepatitis, nonendemocoveal uretritis, epidymitis, cervicitis, salpingitis; bartholinitis, pneumopathy, venereal lymphogranulomatosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases such as conventional trachema, nonendemic trachema, paratrachema, and inclusion conjunctivitis, qenital diseases such as nonquencenced usertitis, epidymitis, cervicitis, salpingitis, perimpathy in breast feeding infants; and venereal lymphograculomatesis. The polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can also be used to control growth of the microorganism. Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 52; DB 21; Length 225; 41.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein which is specific to Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  919 VVTSLLINLGSPVKEVRRAALQCLQALSCVASPFYL 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 1273, 1755pp; English.
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97FR-0016034.
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Best Local Similarity 41.7%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                 226 AA;
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                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein (TXREG) sequences. The antagonist and an agonist of the proteins of the invention are used to treat disorders associated with decreased or increased expression or activity of TXREG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated polypeptide with a human transcriptional requiator protein sequence is useful for the diagnosis, prevention and treatment of disorders associated with the immune, reproductive and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to human transcriptional regulator
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O
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0.6%; Score 62; DB 20; Longth 234;
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Similarity 41.7%; Prod. No. 1.70+02;
A: Mismatches 15; Indels
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                                                                                                                                                                                                                                                                             Human; transcriptional regulator protein; IXREG.
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                                                                                                                                                                                                                                                 Human transcriptional regulator protein #4.
                             9; Mismatches
               Pred. No.
                                                            1018 LMKVLQGVNGEMVLSQLLPMAHQLLEKI 1045
                                                                           72 imdilqglsngl+lqqilglsdvlleei 99
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                                                                                                                                                              AAB61304 standard; protein; 615 AA
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             42.9%;
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                             Conservative
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               Best Local Similarity
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                                                                                                                                                                                                                                                                                                            Homo sapiens.
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Matches 15;
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 Ouery Match
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beterologous robe which coroles a project römprisha an amphipaille rights deix of a fort pieces also protein per tissue width of robe tibles seed, heat stem cellic portion. However tissue width of robe tibles seed, heat, stem cellic portion, however or whole plant than a round plant, the preferred protein is an artificial status protein designated ASPM which has been designed as a next fifted by prefer protein to humans. Products and methods from the present annextion on persent for producing transporic plants with higher levels
                                                                                                                                                                                                                                                                                                                                                                                                                     1178 OOKREPSKOLKESSOO ESSE EVOSSYWDRVILLELLQHEKKILRSTQIILVITIENILGEC 1237
                                                                                                                                                       the profession to be a parently active proteins by inserting the DNA into an expression event a rate of transferd faint animal ecils with animal and event expression event of the which a event the biologically active protein is placed under the control of alpha-feroprotein gene enhancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                         81: PHILPPERIIIPETTPHOTIAGASPAAASPAAAPSTA 1418ALSSALTOPILIPUTDA 1869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the present invention destribes transferre plants (A) comprising a
                                                                                                                                      the DNA encoding this protein may be useful ton
                                                                           This profess sequence is its the sequence alread to AARZ entropy
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                                                                                              that Ali at position whos is replaced by Val.
This protein specifically binds to the enhancer of the alpha-
                                                                                                                                                                                                                                                                                                                                 pirks Some 64: 16:23: Longth 2783;
27:08: Pred. No. Lietos
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usedal the produced tradogical and be protein
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AAY561 standard: Errodous 17s AA.
                                     Main 44: Page 7: 24pp: English.
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                                                                                                                                        tertogerate in aemo.
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                                                                                                                                                                                                                                                                               Section 198
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Rest Local
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AAF22316 to AAF22363 encode the human secreted proteins given in AAFC2316 to AAF32363 encode the human secreted proteins have and polypeptides homologous to them. Human secreted proteins have extirities based on the tissues and edit by epera are explessed in. Brangles of activities and produced immunosapprossive, antiarthrities antirheumatic; antiproliterative, cytostalic; cardiant; vascitopic; cerebroprotective; nootropic; renjoyatestic; antiproliterative opportunetrial; the polymered on the proteins can be used to prevent, freat or ameliorate a medical condition in e.g. humans mice, rabbits, goals, horses, cats, does chickens of sheep. They are also used in diagnosting a pathological condition of sheep the include autohomous discusses e.g. themesed or treated include autohomous lisesses e.g. themesed arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiozascular disorder, cardiac arrest; cerebrizascular disorder;
cerebral ischaemia; angiodenesis; nervous system disorder; unfertion;
Altheimer's disease; ocular disorder; colucal intertion; wend beained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungicide; ophthalmological; vulnerary; gene therapy; newplasm; antoimmune disease; rheumatoid arthilis; hyperproliterative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: Scoreted protein; diagnosis; immnosuppressive; antiarthritie;
                                           essential amino acids. The present sequence represents a specifically claimed FDNPL tetrameric protein from the present insertion.
of protein content (e.g. 2 to 5-fold increase) and migher resels of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hyperproliterative disorders e.g. neeplasms of the breast of liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anticheumatie; antiprolificative, eytostatie; eardiant, vasetrepie;
eerebroprofective, mootropie; neuroprofective; as ikaesertal; virs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            956 IDHLISEARETTSPAAYVIQUATUFEELQPERELESBQRISELIENID, LOOA
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 24.5%; Fred. No. 27:
Matches 12; Conservative 15; Mismatches 22: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB63120 standard; Protein: 226 AA
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                                                                                                                                                                                         Sequence 172 AA;
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DNA encoding protein binding to alpha-fetoprofein gene enhancer -
                                                                                                                                               Enhancer; alpha fetoprotein; homeodomain; zinc-finger.
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/note= "homeodomain"
                                                          AAR23963 standard; Protein; 2783 AA.
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443 .476
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/label= zinc-finger
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      870 tetilglg 877
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                                       RESULT 57
                                                AAR23963
                                                                                                     TTPP OQYAMINETINING SYNCEVOTSTWOPTH PITTOHISTICKER PSYNTHETIST 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This protein specifically binds to the emhancer of the alphar fetoprotein gene. The DNA encoding this protein may be useful for the prodm. of biologically active proteins by inserting the CMA integral an expression vector and co-transfecting animal cells with another expression vector in which a gene for the biologically active protein is placed under the control of alpha-fetoprotein gene enhancer and promoter.
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i.1097
                   apel zinc-finger
3..155
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679..711
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Bost Local Similarity 27.9%
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AAW4 co.c.

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The present sequence is that of a human cytoplasmict isolency; thus synthetase. The cDNA encoding for the cytoplasmici isolency if the cNA synthetase, as factated from a human feeth cDNA library. The cluMa can be expressed using expression vectors to produce the corresponding recombinant protein. The protein can be used in assays to test substances known to inhibit the isolency itwa synthetases of pathogenic cramisms. Also, expression of the isolencyl-tRNA synthetase in a testor strain can be useful for restinal substances which are capable of inhibiting its activity.
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Best Local Similarity 28.3%; Fred. No. 3.60-02;
Matches 15; Conservative 10: Mismatches 28; Indels Conservative 10: Mismatc
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                                                         Human cytoplasmic isolencyi (FNA synthetase.
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Two hybrid assay, fusion, transcriptional activator, interaction, matrix, array, screening, reporter gene; identification. Legrain P. Fromont-Racine M. Cho R. Davis R. Lockhart D; /note- "DNA binding domain of GAL4" /note- "Yeast YMR117c protein" /note- "Encoded by TGA" Location/Qualifiets Yeast GAL4/YMR117c fusion protein. 980S-0003335. 980S-0154972. 99WO-IB00048. Saccharomyces cerevisiae. 148..378 1..147 (INSE ) ENG PASTEUR. (STRD ) UNIV STANFORD. Misc-difference 378 (AFFY-) AFFYMETRIX. 06-JAN-1999; W09935256-A1 06-JAN-1998; 17-SEP-1998; 15-JUL-1999.

servening polynucleatides with whole genome oligonucleatide or polynucleotide arrays -

Example 1; Page 36-37; 41pp; English.

This sequence represents a yeast GAL4/YMR117c fusion protein. YMR117c is a yeast OBP (open reading frame) which was found by two hybrid analysis to interact with the U2 shRNP-associated splicing factor, prpllp. This was used in grotel two hybrid screening methods for the identification of GAL4) Tused to a first test protein (e.g., YMR117c protein). A second by the sion protein contains a second test protein that potentially interacts with the first test protein. If the two test proteins interact, they bring the two domains of the transcriptional activator into close bring the two domains of the transcriptional activator can then bind to the corresponding transcriptional activator binding site on the reporter gene, thus effecting reporter gene transcription, and causing a detectable signal to be produced. The two hybrid assay can be used to test a large number of proteins simultaneously to determine whether they colinguarieotide probe marrix. Together, the probes encompassed all the coding sequences on the yeast genome, enabling the him district from locations and the genes encoding parties proteins to be identified. The methods of the invention thus allow large scale screening for DNA sequences that have functional utility and avoids the systematic sequencing of DNA inserts of interest that is required by prior art nucleic acids by direct hybridisation to Eight-density oligopuelectide arrays. Two hybrid assays exploit the ability of a pair of interacting proteins to bring a transactivation demain into class proximity with a DNA-binding site which regulates the expression of a reporter gene. The assay employs chimeric genes which express two types of fusion protein, one hybrid protein, contains a transactivation domain (e.g., that of interact with a particular protein. Such a two-hybrid assay was performed with a vector containing the yeast GALA/YMRITS DNA sequence and the colones encoding interacting proteins were selected. The DNA inserts of the partner proteins were amplified and hybridised to an methods. The methods can be used to screen polynacleotides, especially those from a host organism whose genome has already been sequenced.

AAC9799; to AAC98763 encode the human colon cancer associated proteins, called human colon cancer antigons, given in AAB5234 to AAB54006. The human colon cancer antigons can have expectative, cardiovarive, muscular; or uncolon cancer antigons can have called to a cancer antigons. The colon cancer antigon polynucleotides, can he used in game herapy. The colon cancer antigon polynucleotides, proteins and antibodies to the proteins are useful for the provention, treatment and diagnosis of calcon cancer antigon polynucleotides, polynucleotides, proteins and antibodies for the proteins are useful for the provention, treatment and diagnosis of calcon disorders, such as colon cancer. The polynucleotides may be used in diagnostics and research, sorb as for chromocome identification, and alsorders, such as colon cancer. The system disorders, muscular disorders, reproductive alsorders, immune system disorders, muscular disorders, reproductive adsorders, immune discusses, and cardiovascular disorders AAC98774 to AAC98772 and AAB5007 represent sequences used in the exemplification of the present

752 AA;

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Colon cannot associated gene sequences, referred to as colon cancer antisens, useful for the treatment, prevention, and diagnosis of colon disorders such as colon cancer.
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0 6%; Sooro 63; DR 20; Length 378; 31.5%; Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence - heb AA.
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PESOLI 5. AARIE171

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registance to issectivides have led to a resurrence of mataria in many parts of the world, and there is a pressing need for vaccines and new and pharps. AAA70078 to AAA70287 and ABBINHA to AABINHA to APBINHA in the result of and protein sequences given in the protein in the which are not specifically mentioned within the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the present invention describes proteins and their framents (1) encoded by chromosome 2 of the human material parasite. Flashedium talciparin, Also described are: (1) mucleotide sequences (1) encoding (1); and (2) vaccines against P. talciparum intection, comparised (1) or (1).

(1) and (1) are useful for the development of vaccines against antibody raised to immunoaeus comprished the sequences of (1), are useful in the detection of intection with P. talciparum. Fitthermore, (1) (especially when they are fillins or secreted or mentione profession).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can aid the identification of drugs to freat or prevent P. falciparum intection, or they can be used to identify drug resistance in P. falciparum. Sequencing of the Plasmodium chromosome 2 and the subsequent identification of proteins encoded by it will help to expand our understanding of parasite biology, a process hampered by the complexity of the parasitic lifecycle, and provide now fargets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vaccine and drug development. Parasite resistance to drugs and musquite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparamo chromosomo 2: Johan Malafia palabite: Vaecitee
antimalarial; malaria; protozcacide: infection; insecticide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteins encoded by chromosomy 2 of the human malarial parasite, Plasmodium faleiparum, usefui as antimalarial Zacotnes and in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; score 64; DB 21; Langth 1979;
21.1%; fred. No. 5er92;
ive - Zv; Mismatches - 34; indets - 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gardner M. Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 70-75; 577pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diagnosis of P. falciparum intection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42721 standard; Protein; 478 AA.
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New isolated human set-10 polypeptides Example 3: Page 85-88; 91pp; English.

666 AA;

Sednence

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225 agterywri 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                              AAY 22470;
                                                                                                                                                                                                                                                             RESULT
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                                                                                                             QQ
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                                                                                                                                                        δ
This sequence is an epitope tagged version of a human sel 16 protein of the invention. The human sel 16 proteins of the invention are isolated from hippocampus and mammary gland. The polypeptides can be used to alter presenting function. Compounds which inhibit either the expression or the artificity of the kaman sel-10 polypeptides may reverse the effects of mutations to presenting (PS 1) or FS 2, and therefore may be useful for the prevention or treatment of Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to human sel.10. The sel.10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel.10 polypoptide expression. The sel.10 polypoptides are also useful as drapped for expression. The sel.10 polypoptides are also useful as trapped for decreasing antibody levels in the treatment of Alzheimer's already to decreasing antibody levels in the treatment of Alzheimer's already to production level of Abeta. The polynucleotides are useful for developing the assays for identifying against sepable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                          50 TOLRELLGIDPSFEORRAPLFSQLAKTLERSVQTKAVNKQLDRNISLFLIHLSPYFILKP 109
                                                                                                                                                                                                                                                                                                                                                  New human sel-10 polypeptides and their encoding polynucleotides,
                                                                                                                                                                                                                                       Govery Match 0.6%; Score 64; DB 20; Length 666; Best Local Similarity 27.5%; Pred. No. 1e \cdot 02;
                                                                                                                                                                                                                                                                                 40, Indels
                                                                                                                                                                                                                                                                                 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    St. 10, human, Alzhelmer's distase, Abeta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3: Page 108-112; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-terminal mychis tagged sel-10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB5920 + standard; protein; 666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAA ) PHARMACIA & UPJOHN CO.
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                                                                                                                                                                                                                                                                                      19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Curney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-102404/11.
                                                                                                                                                                                                                                                                                                                                                                                                             110 AUKCLEWLI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 agterywri 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pauley AM,
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB59203;
                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sel 10, human, presentlin, Alzheimer's discuse; PS-1; PS-2; hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 901 SELLOTIOPSFROPEAPLESQLAKTLERSVQTKAVNKQLDENISLFLIHLSPYFLLKP 109
                                                                                                                       50\ \text{TCLEFLLGIDPSFEQFFAPI.FSQLAKTLERSVQTKAVNKQLDENISLFLIHLSPYFLLKP}\ 109
                                                                                                                                                                                165 sgpekilaldelidszeptyykhmmyvizyyfgrdfist)pkolalyvisflopkdliga 224
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Matches 19; Conservative 10: Mismatch.
0.6%; Score 64; DR 22; Longth 666;
27,5%; Prod No 15+02;
                                  Bost Local Similarity 27.5%; Prod No 10+02;
Matches 19; Conservative 10; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cterm V5 his tagged sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; Page 79-83; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY22470 standard; Protein; 669 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gurney ME, Li J, Pauley AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-US26820.
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                            27.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; mammary gland.
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                                                                                                                                                                                                                                               110 AQKCLEWLI 118
                                                                                                                                                                                                                                                                                                           225 aqterywri 233
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      Query Match
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Sel-10; human; presentitin; Alzheimer's disease; PS 1; PS 2; hippocampus;
                                                                                                                                                                                                                                                                                                                    the invention are useful for raising monorional or polyclonal antibodies useful in diagnost c assays for detecting set 10 polypeptide expression. The same lo polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of alzheimer's aftering the production level of Abeta. The polymorleopides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                 New human sel-10 polypeptides and their encoding polymacheotides, useful for raising antibodies for detecting sei-10 polypeptide expressing and as drap targets in the treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                      The present invention relates to human sel-10. The sel-10 proteins of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 IGLEBLIGIOPSFEQFEAPLFSQLAKILERSVÇIKAVNKÇLDENISLFLIHLSPYFLIKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; score 64; DB 22; Length 627; 27.5%; Fred. No. 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human C-term mychis taqqed sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
                                                                                                                                                                                                                                                                 Claim 1; Page 60-64; 115pp; English.
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                                                      (PHAA ) PHARMACIA & UPJOHN CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0068243.
                9908-0428877.
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Matches 19, Conservative
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                                                                                            Pauley AM, Gurney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-458026/38.
                                                                                                                                WPI: 2001-102404/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 AA;
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                09-10N-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               this approach represents a bumon set to protein of the invention. This serporce is specifically a bumon hipperampal set to protein. The pelipoper for the resolution at the present in time i compounds which taking extrem the expression at the entire true imman set in pelipoper set to the extremal polypoper of the entire true in the properties of motorious to present in I (PS-1) at the entire may be useful for the prevention or treatment of
                                                                                                          Set in harma presentition Altheimer's disease; PS 1: PS-2: Lippertampus;
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WP1: 1999-1596-26,709. N-PSD4G-AAX-099.

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Sequence

Query Match

RESULT 43 AAY 22469

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AAB59201 standard; protein; 626 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-102404/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            626 AA;
                                                    110 AQKCLEWLI 118
                                                                                     224 aqterywri 232
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                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                       RESULT 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sel 10, human, presentito, Alzheimer's disease; FS-1; FS-2; hippocampus;
                                                                                                                                                                                                                                                             Gaps
                                                                                      11. Serratia marcescens (smahsp70 - AAR03932). The proteins having bomolog, to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                     548 FSSEVIISNLLINLFQRAELSKNGEWYEVLKIAADILIKEEILSENDQLSNQV 599
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                                                                                                                                                                                                                            0.6%; Score 64; DB 11; Length 605;
                     Xenopus laevis (x170 - AAR03928);
Homo sapiens (humhsp70 - AAR03929);
Gallus gallus (chkhsp70 - AAR03930);
         Rat rattus (rathsp70 - AAR03927);
         6. Rat rattus (rathsp70 - AAR03927)
7. Xenopus laevis (x170 - AAR03928)
8. Homo sapiens (humhsp70 - AAR0392
9. Gallus gallus (chknsp70 - AAR039
10. Zea mays (mzehsp70 - AAR03931);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40,
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                                                                                                                                                                                                                                           32.7%; Fred. No. 89;
tive 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human omyc-N-sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY22469 standard; Protein, 626 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0068243.
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                                                                                                                                                                                                                                                Local Similarity 32.77
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapy; mammary gland.
                                                                                                                                                Mycobacteria species.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                               bub AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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50 TGLEELLGIDPSFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENTSLFLIHLSPYFLLKP 109

Matches

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The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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Protein encoded by construct 6myc-N-sel-10.
                                                                                        Sel-10; human; Alzheimer's disease; Abeta.
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Sednence
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                                                                                                                                                                                                                                                                                                                                                5 - 1-31 EBLOCK FROM SERVERAM SEGIAN SERVERANDER AV NEGRINSKALSKELI HESPYRILKP 109
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                                                                                                                                                                                                                                                                                                                              0: Gaps
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27.54; Pred, No. 86;
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                                                                                                                                                                    New isolated brain sel-to polypoptides
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                                                                                                  (FRAA ) PRABMATTA 4 URT GIN OF
                                                                                                                      Surney MF. Li J. Pauley AM;
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N PSERRE AAX 1977 11.
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Proteins homologous to heat shock proteins from Trypanosoma cruzi - used
                                                                                                                                                                                                                                                The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sol-10 polypeptide expression. The sel-10 polypeptides are also useful as dust targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Alberta. The polymorfootides are useful to december a sasays for identifying automic of idea are useful and the biological pathways that lead to Alzheimer's disease.
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New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fig. 2 provides an alignment of heat shork proteins from a variety of organisms: 1. M.hyopneumoniae (Mhyhsp70 - AAR03422);
2. Bacillus meqaterium (Bmehsp70 - AAR03423);
3. E. coli (GnaX - AAR03924);
4. T. cruzi (tc?0kd - AAR03925);
5. T. cruzi (AAx03926);
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27.5%; Fred. No. 86;
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                                                                                                                                                                                   Claim 1; Page 64-68; 116pp; Erglish.
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les 19; Conservative
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AAB01204;

RESULT

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Sel-10; human, presentlin, Alzheimer's disease; PS-1; PS-2; hipperampus;
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27 5%; Prod No 86;
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                                                                   AAB59198 standard; protein; 589 AA.
                                                                                                                                                                                                                                                                                                     Human mammary sel-10-1 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pauley AM,
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RESULT 39
                                           AAB59198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human GTPuse associated proteins, polynucleotides, and antibodies, useful for diagnosing, preventing and treating valious diseases such as atheroscierusis, cancer, acquired immune deficiency syndrome (AlDS), asthma, and autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory disorders, immente system disorders, cancer, AIDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 TGLEELLGIDPSFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENISLFLIHLSPYFLLKP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for treatment or prevention of diseases associated with GIPAF such as cell pioliferation disorders, autolmmune disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            brain tumbour tissue. This protein is expressed in mervous, reproductive and quastrointestinal tissue. The GTFPF proteins may be used to define and antiqunists and artiqunists of GTFPP activity and to generate antibodies to GTPAP. This means the GTPAP proteins may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guanine uncleotide binding protein; GTP binding protein, Grprotein, Grprase; GrPrase associated protein; GTPAP, cell profiferation; autoimmure, inflammatory, lammure system disorder, cancer, AIDS, acquired immune deficiency syndrome; asthma; atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is human GTPAP-29 protein. This sequence was derived from a cDNA library of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 64; DB 21; Length 589;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 27.5%; Pred. No. 86;
Matches 19; Conservative 10; Mismatches 40, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arthuitis; systemic lupus crythematosus, psoliasis, humman.
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                                                                                                                                                                                                                                                                                                                                                                                        Human GTPase associated protein-29.
                                                                                                                                                      AAB01204 standard; Protein; 589 AA.
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99US-0127990
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                                                                                                                                                                 this sequence represents a feman set to protein of the insention. This sequence is specifically a basan mammary set 10 protein. The polypeptides sequence is specifically a basan more from Compounds which inhibit either the expression on the activity of the haman set 10 polypeptides may reverse the effects of mutations to presenting (1984) or PS-2, and therefore may be useful to the presention of treatment of Alzheimer's
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This sequence represents a human metally protein of the invention. This sequence is specifically a human mammary selely protein. The polypeptides can be used to alter presentlin function, Compounds which inhibit either
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                                                                                                                          50 TOLERLIGIDPSFEQFEAPLESQLARTLERSVQTKAVNKOLDENISLFLIHLSFYFLLKP 109
                                                                                                                                                                               97 sapekilaldelidsceptqykhmmqyiepqfqrdfisllpkelaiyvlsflepkdllqa 156
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0.6%; Score 64; DB 22; Longth 559;
27.5%; Pred. No. 79;
tive 10; Mismatches 40; Indels
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27.5%; Fred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human mammary sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Page 60-63; 91pp; Erglish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY22466 standard; Protein; 569 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Surney ME, Li J, Pauley AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47US-0068243.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US26820.
                                    Best Local Similarity 27.5%,
Mutches 19, Cosservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPT; 1999 458026/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
es 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AQKCLEWLI 118
                                                                                                                                                                                                                                                                                                                 157 agterywri 165
                                                                                                                                                                                                                                                         110 AQKCLEWLI 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX99702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammary qland;
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The present invention relates to human sel-10. The sol-10 proteins of the invention are useful for raisina monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-30 polypeptide oxpression and sel-10 polypeptide expression and sel-10 polypeptides for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of Alzheimer's altering the production level of Abero. The polymerleadides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                      New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-19 polypeptide expression and as drug targets in the treatment of Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 TGLEELLGIDESPEQFEAPLFSOLAKTI EPSVOTKAVNKQIDPNISLFI I HI SPYFILKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 27.5%; Pred. Mc. 78;
Mutches 19, Conservative 19; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human mammary sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 68-71; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY22467 standard; Protein; 559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAA ) PHARMACIA & UFJOHN CO.
                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97HS-0068243.
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                                                                                             09-JUN-1999; 9975-0328877.
                             23-MAY-3000; 2000W0-11S09814
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                                                                                                                                                                                                                                       Pauley AM, Gurney ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-458026/38.
                                                                                                                                                                                                                                                                                                              WPI; 2001-102404/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 AQKCLEWLI 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 aqterywri 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX99702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09932623-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY22167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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sequence is specifically a human hippocampal sel 10 protein. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression of the activity of the human sel.10 polypeptides may reverse the effects of matations to presentlin. (FS 1) or PS-2, and therefore may be useful for the prevention of treatment of the prevention of th
                                                                                                                                                                                                                                                                                Sel i0, human, presentitu, Alzheimer's discase, FS-1, FS 2; hippocampus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a human sel-10 protein of the invention. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TOLEELLGIDPSFEQPEAPLFSQLAKTLERSVQTKAVNKQLDENISLFLIHUSPYFLLKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 64; DB 20; Length 553; 27.5%; Pred. No. 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                             Human hippocampal sel-10 protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 24; Page 50-53; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB59195 standard; protein; 553 AA.
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AAY22463 standard; Protein; 553 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney ME, Li J, Pauley AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0068243.
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                                                                                                                                      29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 27.5%
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 1999-458026/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 AQKCLEWLI 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX99701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200075328-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WC9932623-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC 1997;
                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1999.
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                                                                      AAY22463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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RESULT 34 AAB59195

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this sequence represents a human selet0 protein of the invention. This sequence is specifically a human hippocampal seleto protein. The projectives can be used to after presentlin function. Compounds which inhibit either the expression or the evitting of the buman seleto polypoptides may reverse be effects of indications to presentline! (PS-1) or PC 2, in their of reay be useful for the precention of the action.
the invention are useful for raished monocional or polyclonal in the discussion of the assays for defecting select passays by depending select passays to describe expression. The select problems are also useful as dranges for decreasing at the edge levels in the treatment of Alikelmer's discusse. It is also useful for identifying agents capable of alterior the production level of Aberta. The polymerbotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      % TOLERIESTOPSFEGFRAFITERSV_TRAVINGITENISTFLIHESPYFILKP 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%: Score 64; DR 22; Dangth 540;
27.5%: Pred. No. 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Greety Match 0.6%; Score 64; 16 20; length 545; Best Loral Similarity 2^{7.5}x_1 fred, No. 76; Matches 19; Conservative 10; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human hippocampal seleto protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated button set to polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaim 24; Page 54:56; 91p.s. English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY22464 Standard; Protein; 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      burney ME. Li J. Pauley AM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1708 Junia 821 C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    presy Match, 0.6%;
Best Local Similarity 27.5%;
Matches 15: Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78W--US26820.
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N PSDB: AAX99701.
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                                                                                                                                                                                                                                                                                                                                              540 AA;
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                                                                                                                                                                                                                                                                                                                                              Section
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The prosent invention relates to human sel-10. The sel by proteins of the invention are useful for idising monechonal or pelyclonal and manibodices useful in diagnostic assays for deterring sel 10 polypeptide expression. The sel 10 polypeptides are also useful as drag targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of aftering the production level of Abeta. The polymurfeotides are iselvitor developing assays for identifying agents capable of interfine with the biological pathways that lead to Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human sel-10 polypeptides and their cheodina polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the troutment of Alzheimer's disease
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50 TOLGELLGTDPSFEQFEAPLFSQLAFIFFSVGTRAVNRQLDFNISHFIHLSFYFFLEP TOY
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83. sypekthalderlidsceptqyklamqyklepgfqrdr(stlpheln)yelerlepbdllqu 142
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tes 19; Conservative 10; Mismatches 40;
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Human mammary sel-10-3 protein.
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Pauley AM, Gurney ME,
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                            WPT; 2001-102404/11.
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Matches
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  This sequence represents a human set 16 protein of the insention. This sequence is specifically a human manusary set 10 protein. The polypoptides can be used to after presentlin function. Compounds Which inhibit either the expression or the activity of the human set 10 polypoptides may reverse the effects of mitations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 TOLBELLOIDESPEQPEAPLESQLAKTLERSYQTKAVAKGIDPNISLFLIHLSPYFLLKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 64; DB 20; Length 540;
27.5%; Pred. No. 75;
                 Set 16, human, presentitin, Alzheimer's discuse; PS 1; PS-2; mammary qland, therap.
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                                                           Homo sapiens.
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The present increase decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for raising amperional or polyclonal or decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for facility and agents capable of a decreasing antibody levels in the treatment of Alzheimer's disease.

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Construction the production terrol of America The polyclonal control of the bological pathways that lead to Alzheimer's disease.

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         The present invention provides an antibody which reals with a classac product of vimentin but not with the intact protein. This can be used to detect appropriate, which may then be used as an indicate of the progression of the progression of discusses such as systemic impass crythematosus, autoimmane basembly the anaemia, Bussedow's discusse and acquired immunodaticioney
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9.34; Pred. No. 61;
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Marches 10: Object 21: Mishalches
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sequence is specifically a human nippocampal selely protein. The polypeptides can be used to alter presentlin function. Compounds which making tether the expression or the archigity of the human selely polypeptides may reverse the effects of motations to presenting 1 (PS i) or PS-2, and therefore may be useful for the prevention of treatment of
                                                                                                                                                                                                                     Sel-10; human; presentlin; Alzheimer's disease; PS-1; FS-2; hippocarptus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a human sellic protein of the invention. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TYLEELLGHPSPEQPEAPLPSQLAKTI PPSVQTKAVNGG OFNI SLFLHHLSPTFLLKP TOY
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                                                                                                                                                                                            Human hippocampal sel-lu protein sequence.
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27.5%; Fred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated human sel-10 polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mammary sel-10 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 24; Page 57-59; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY22468 standard; Protein: 540 AA.
                                                                                                    AAY22465 standard: Protein: 540 AA
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2121 VPHQCQYTIQQLETVLGEP 2139
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                       245 Igaqiqeqbeqidedeskp 264
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Hest Local Similarity 27.5%
Matches 19; Conservative
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                                                                                                                                                               29-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                                                        19-DEC-1997;
                                                                                                                                                                                                                                                                         HOMO Sapiens
                                                                                                                                                                                                                                                                                                   W09932623-A1.
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                                                                                                                                   AAY 22465;
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7
                                                                                    AAY22465
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WPI; 2001-149349/16.
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                                                                                                                                metabolic disorders
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N PSDR, AAA09307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exhibits significantly reduced expression in the Tochls of individuals with high codar police specific ide (immanoshobulin E) ievers. The genewas isolated from I cells from individuals allergic to cedar pollen using the differential display method. Pollinosis-associated gene 795 has homeology with the human vinentia gene. The invention also relates also constructs and homeology mignetism; perlinosis associated gene 795 to expression constructs and host neils comprised perlinosis gene 795; to expression nucleae actuals, pollinosis associated gene 775; to expression of pollinosis and probes.

Optimized associated gene 795 to makers and probes. On pollinosis-associated gene 795 to makers and probes. Adaptive the protein encoded by the gene, methods of detection of pollinosis-associated gene 795 nucleic acids, and a method of sucception daggers in integrals. The invariant additionally encompasses mathods gene 795 nucleic acids. The invariant of allergic disease by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       measuring the expression of pollinosis-associated gene 795 in pollen antigen-stimulated T-cells in the presence of a test compound relative to a control. Pollinosis-associated gene 795 is useful in the diagnosis of allegic diseases and in the screening of drug candidates for the treatment of such diseases. The present sequence represents a protectin encoded by human pollinosis associated gene 795.
                                                                                                                                                                                                                                                                                                           The invention relates to the human pollinosis associated gene 795 which
                                                                                                                                                        Pollinosis-associated gene 795 undergoing significantly low expression
in subjects with high crdar pollen-specific 19E levels, useful in
diagnosis of allergic diseases and screening drug candidates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caps
  Obayashi 1, Imai Y, Yoshida N, Oquwa K, Matsui K, Takahashi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIE: Interacting fretein; vimentin; protein complex; cytostatic, antiviral; neuroprotective; cardiant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2090. ALABKI KENYIVLI PBS (1947 AF) MEDPPE VEHÇIZIKTI DOL ETVIJEP. 2139
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                                                                                                                                                                                                                                                           Page 64-67; Claim 13; 73pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY92335 standard; Protein; 466 AA.
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                                                                                WPI; 2000-687343/67.
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                                                                                                        M PSDB, AAC64226.
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                                                                                                                                                                                                                                                                                               AMT92331 37 were isolated in a modified yeast two hybrid system using NIKI protein as "bait". These are known sequences which are NIKI interacting proteins. The invention concerns purified complexes of a NIKI protein interacting protein; where the interacting protein is chesen from Trkh, protein pherythen are lapha, 173-3egislon, alpha-tropomyosin, wimenfun, point, first from 18-2, IP-3, NIKI (also referred to as Nek2) is a human homologue of the Aspergillus nidulans mitotic requision, NIMA kinase. NIKI is a serine/Altheonie-specific kinase and is thought to play a key role in cell-typic creats leading to the onser of mitosis. The complexes, their derivatives and NIKI or NIKI is a mitosis, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody reacting with a cleavage product of vimentin but not with
the intact vimentin, useful for detecting apoptosis and the grantity of
cleavage product of vimentin or as a reagent for immunohistochemical
New complex of a NiKl protein and a NiKl protein interacting protein, useful for treating cancer, hyperprollicrative disorder, negredogenerative disorder, cardiomyopathics viral infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences, one are useful for treating or premeding a disease or disouder included abstract levels of the complex or protein. Such disouders include cancer, hyperproliferative disorders, can be not declared to disorders, candisoners, candisoners, candisoners.
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                                                                                                                                                                                                                               Example 1; Page 145-147; 172pp; English.
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Matches 16; Conservative
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Streptocassus pneumoniae Seud's protein.

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endometrium during the hyperplasia, adenocarchnoms or proliferative phase of the endometrium. The presence and quantities of those proteins can be detected using 25 gel electrophoresis comparison of cell lysates. The proteins can be used as biochomical markers to detect the phase of the endometrian and can be measured in leady fluids, obviation the need for endometrial biopsies.
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14E: immanoalobulin E; redar pallon alloray; T-ceil; reduced expression;
detection; diagnosis; drug servening; allergic disease.
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Endometrium, hyperplasia, aderocarcinoma, proliterative phase;
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diagnosis of hyporplasia and adenocarelloma
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                             2D gel electrophoresis; detection.
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                                                                                                       Homo sapiens.
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                                                                                                                                                                      W09810291-A1
                                                                                                                                                                                                                                                                                                            05-SEP-1997;
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                                                                                                                                                                                                                                         12-MAR-1998
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The present sequence represents a protein from Streptococcus pneumoniae. The nuclear acid sequence enroding the Streptococcus purumoniae protein can be useful in zacrinos for inducing protective antibodies against. Streptococcus pneumoniae, for treatment or presention of intection can promoned, a fit is media or meninditis, protein assed on the nucleic acid are amplificate a acid. As also feel is a satisfied the streptococcus intection. By usual hyperidisation or amplificate a acid. As a series of their articles in structural meningers in a series of their articles. The protein are used to detect specific and the detect specific and the acid in meningers. As the detect series of their articles in structural meningers which hind the protein are used to detect act responsibility or particles and for passible temporal in the controller and for passible temporal in the first can be acid. The protein are used to form the controller and for the protein are used to the controller and for the controller and to a toxin). Vaccines are administrated every by input in the controller and toxin and the protein are controller.

Nucleic acid encoding antiquency peptide(s) from Streptoroperus preumoniae - or their epitope containing fragments, useful in protective or theighwaite vaccines, and for diagnosis

Claim 11: Page 76. lidpp. English.

7.1 And 1.4

News ONL Hromorky) As WPI: 1998 272224/24. N PSDR: AAV27386.

(HUMA-) HUMAN GENOME SOIL INC

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AAW54 551 Standard; protein; 465 AA.

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AAWS4 CS13

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19. Mismatehes Pred, No. 400

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Querry Match

0.63 Search 15 DR 19: Length 450;

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library following screening with a partial tobacco beta-1,3 glucanase clone. The amino acid sequence is identical to that of the tobacco extracellular beta-1,3 glucanase_PR36 (which has been partially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta 1,3 glucanase
                                                                                                                                                                                                           ن
                                                                                                                                                                  0.6%; Score 64; DB 12; Length 343;
31.0%; Pred. No. 39;
Lice 8, Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "extracellular beta-1, 3-glucanase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extracellular beta-1, 3-qlucamase, chitimase, antifungal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cornelissen BJC, Linthorst HJM, Mclehers LS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana sp. extracellular beta-1,3-glucanase protein
                                                                                                                                                                                                                                                    1428 VLAAAYGEKDAILEADTEFWESVCCEESVQHQIQSLMNILQY 1469
                                                                                                                                                                                                                                                                          Bol JF, Cornelissen BJC, Linthorst HJM, Meleher.
Meulenholf EJS, Sela-buurlage MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transgenic plant; synergism; tobacco.
                                                                 characterised). See AAQ12897-Q12900.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See the office of the second
                                                                                                                                                                                                                                                                                                                                                                                               AAW31298 standard; Protein; 343 AA.
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                                                                                                                                                                                        Best Local Similarity 31.0%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYLE-) RIJKSUNIV LEIDEN.
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                                                                                                            343 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-JAN-1991;
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                                                                                                              Sequence
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                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW31298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New transgenic plants expressing chitinase and qlucanase have improved resistance against pathogenic fundi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cornelissen BJC, Melchers LS, Meulenhoff EJS, Sela-buurlage MB:
Vloemans AA, Woloshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ċ
                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinase; transgenic plant; beta-1,3-qlucanase; antilungal; plant resistance; pathogenic fungi; fungal resistant plant.
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81.0%; Prod No. 39;
Lyc 8; Mismatches 21; Indels
DR 18; Length 343;
                                                                         21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of an extracellular beta glucanase.
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31.0%; Pred. No.
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Matches 13; Conservative
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Best Local Similarity 31.09
Matches 13; Consorvative
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Isolated polyportate with a boman transcriptional regulator protein sequence is useful to the disaposis, presention and treatment of this they issued will the immune, reproductive and cardio-assenbar

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Set E. Yezh H. Sand YI., Barsafan MF.,

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Polynucleotides, polypeptides, antibodies, agonists and autagonists from
the present invention may be used to treat immune disorders by activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation, cancers, cardiovascular disorders, monrological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, adontsts and antaqunists may be also be used in drug screens. AAC76449 to AAC78457 and AB842240 represents sequences used in the examplification of
AA37507 to AAC78448 encode the human cancer associated proteins given in AAB43898 to AAB44249. The proteins can have activities based on the issues and cells the acmes are expressed in Example of activities include: cytostatic; protein and include: cytostatic; protein and include: cytostatic; and anticometry immonomediator; antichtable activities antichtable and antichtable; antichtable antichtable antichtable activities antichtable and antichtable activities antichtable antichtabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or inhibiting the prolliferation, differentiation or modulisation of immune cells, to treat disorders of harmatopoietic cells, antoimmune disorders, allegic reactions, qualt versus host disease and organ rejection, modulate harmostatic or thrombolytic activity, modulate
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Bol JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cuery Match 0.6%; choice 64: 48-21; Length 264;
Best Local Similarity 31.1%; Fred. No. 27;
Matches 14; Conservative 11; Mismitches 20; Indels
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Sela-Bunrlage MB, Vloemans AA, Woloshuk CP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
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N PSDB; AAQ12899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 - JAN-1991;
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Human, 37 EST, expressed sequence tag: secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs of polyA! RNAs derived from 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR 21, Նորցքի 136;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1790 EKITSEMGSASQANIFITSLKKTLATTLAFFVLLFAIKKTYKOIE 1834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; SEQ ID 5511; 71pp + CD-ROM; English.
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hybridisation assay; demetic mapping, deme expression control, promoter,
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Best Local Similarity 37.55
Matches 15; Conservative
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method for increasing the resistance of a core protein to proteolytic decreasing the congrises luxing or inserting onto or into the Core protein a stabilished poligieptide or formula [(6)ga)X(5)gb)Y(6)gb)Z(b) where sign, settly of general (8 sequential 6)g residues and X, Y, Z are between 1 of X, Y and Z reed not be identical from a repeat to a repeat. Alternatively a nucleic and encoding the stabilishing polypeptide can be finded onto or inserted fits a nucleic acid encoding a core protein. The finance of the profess and the invention are more resistant to destand for by protein. The proteins the profess can be used for freating actolimmure diseases,
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                                                                                                                                                                                                                                           Pusion protein; stabilishna polypeptide; proteolytic degradation; resistance; ball life; autoimmune disease; inflammation; nitro drou; RappaR revel for protein; inflammatory bowel disease; in vivo imagina; nitroredectase protein; enzyme therapy; prodrud therapy; protease; samewer; pathological condition; (RappaB.
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hybridisation assay, genetic mapping, gener expression control; promoter:
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Matches 16; Conservative 25; Mismatches 42; Indels 0: Gaps
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This represents a haman (IEEE/MIAPLHEEE (CI) polypeptide that is involved in mitosis and cell cycle promoters for ell cycle specific recommisses and selects IATA-less core promoters for cell cycle specific denses. The 'I protein plays a role in establishing gene expression patterns necessary transfering in mitogin through the cell cycle progression through necessary transfering found regulator of cell cycle progression through a 22M. The product is on the ease for a role in the necessary transfering for the ease for a role in mitosis of cell cycle profusesion and treating disorders associated with alterations in mitosis of cell cycle profusesion, becreased CI gene expression can be used to rest cycle profusesion, becreased CI gene expression can be used to real cycle profusesion and profusesion because the configuration of the cycle profusesion has been dependent on a stable by used to identify genes whose expression has dependent on a SI protein. Increase Ci is a Alice of the english which cell profule in a SI protein.
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AAY44264 Standard: Protein: 1199 AA 22-MAR 2000 (1118) 007181 AAY44LMA AAY44263 RESERVE 1 

Human TENSO/MIAFILLS: essential for mitosis.

Human, CLEBS, protection of Loyele resultator, mitosis, memphasia, clebs glassia, distribution disorder; hyperplasia, dysplasia, clebs.

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ARIA NOMINA (MINIO)

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Novel requirement protein, useral to diagnose and treat ceil proliferation disorders, including cancer WPI: Zudo life524/ld. N-PSDR: AAZZOGOS.

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The present sepence is a homan HF15/ZhAFH1150 protein. Which is required for a homan cell to enter mitosis. In particular,

990S-0135629

Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay, genetic mapping, gene expression earrol; promoter; crefs07hTAFILI50 is an essential cotactor for TFILD-Appendent transcription. CIF130 negatively regulates CIF150 thereby inhibition mitosis or cell cycle progression. CIF150 has a CIF130-binding domain and is used to screen compounds that interfere with the binding of CIF130. CIF130 is used to diagnose and treat proliferative disorders including hyperplasias, neoplasias and dyspiasias. 3458 14.10. SQFEMIQVEWVETHTSPQFFHERTT SVSTPRSQFFSRMFLEEVVEGGGTTT 1.14.0. 467 smethilight astassibly smooth (spins) | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 Score 67: UB 21: Length 1199; Pred. No. 93; 7, Mismatches 26; Indels Arabidopsis thaliana protein tragment SEQ ID No: 67800. AAG53267 standard: Protein: 188 AA 990S · 0134256. 990S · 0134218. 990S - 0134219. 990S - 0134221. 990S - 0134370. 9908-0134941. 9908-0135124. 9908-0135353. 35,38; 9908-0130510. 9908-0130891. 9908-0132863. 0.68, 9905-0126264. 9908-0126785. 9908-0128714. 9908-0129845. 99US-0130449. 99US-0131449. 99US-0132048. 99US-0132407. 99US-0132484 99US-0132485. 2000EP-0301439 990S-0123548 99US-0127462 99US-0130077 99US-0132486 950S-0132487 99US-0121825 99US-0134768 18-OCT-2000 (first entry) Ouery Match Best Local Similarity 35.3% Matches 18, Conservative Arabidopsis thaliana. términation sequence. 1199 AA; EP1033405-A2. 25 - FEB - 2000; 1666 1666 1666 :666 16,6,6 16661 24-APR-1999; 24-APR-1999; 16661 01-APR-1999; 16,66 19-APR-1999; :666 16.66 1666 555 :666 16,6,6 16661 MAY-1999; 06-SEP-2000. 09-MAR-1999; 16,66 25-MAR-1999; 24-MAP-1999; 1505 21-APR-1999; 1999; Sequence AAG5 3267; MAY - 1 MAY - ] 28-APR-40-APR-30-APR-MAY -MAY -06-APR-08-APR-16-APR-MAY-AAG53267 3 RESULT 556666**X**3 

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14-NOV-1997;
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                                                                                                                                                                                                                                                                                                                       \operatorname{Proteins} from Neisseria meningitidis and N. generrhoeae useful for diagnosis, treatment and prevention of infection
                                                                                                                                                                                                                                                                                                                                                                                                       and N. gonorrhoeae antiqunic proteins. They are encoded by open teading frames (OKES) AA211972 212358. The untiquinc proteins, their incleic acids and antibodies are used for
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18-NOV-1997;
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Amino acid sequences AAY38439·Y38944 represent Neisseria meningitidis and N. gonorrhocae antiqueic proteins. They are creeded by open reading francs (ORE) AAX11972 213358. The antiqueic proteins, their modified and a side antiqueic proteins.
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transcriptional regulator, benign proliferative disease; dysplastic;
                                                                                                                                                                                                                                                                                                                                                                        Proteins from Neisseria meningitidis and N. gonorrhoeae useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY29083 standard; Protein: 1199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 332; 524pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 2; Page 78; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human CIF150/hTAF11150 protein.
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97GB-0024190.
                                                   97GB-0025158
97GB-0026147
                                                                                                             98GB-0000759
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                                                                                                                                                                                                                                Grandi G, Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-444069/37.
                                                                                                                                                                                                                                                                                   WPI; 1999-327407/27.
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                                                                                                                                                                         (CHIR-) CHIRON SPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX91483.
                                                                                                                                                                                                                                                                                                                  P-PSDB; AAY38789
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                                                      27-NOV-1997;
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                                                                                       0-10pc - 1997;
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fransgenic plants in which flowering is suppressed by a tissue specific eytotoxic gene product, useful for the production of wood for use as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents the Arabidopsis anamous-like (Adl.) 2 protein. The AGL2 promoter is used to produce transactic plants of the invention, which are characterized by suppressed theorem. The plants are transformed with a construct comparising a float lorgan selective regulatory element (e.g. AGL2 premeter), specializely linked to a mortectified sequence encoding a cytotoxic generatively linked to a mortectified sequence encoding a cytotoxic generatively linked to a mortectified by the progeny). The plants may be stown for either benean consumption of to use as a raw material in industry. When there are prefixed process consumes 20 38 of the energy of a typical plant, it is advantageous to suppress flowering in order to improve wood and lumber yields, suppression of flowering may be desired to eliminate the production, of allergic public, or to prevent police discumination.
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treatment; Neissoria infection: meninditis; septicaemia; gonorthea.
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18.18; Pred. No. 9.4;
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                                                                                                                                                                                                                                                                   Amino acid sequence of the Arabidopsis AGLZ protein.
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biadder tamour and identi leation of therapeutic avents
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    n. 7 s.; serve 71; bit 20; length 368;
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Protein: 248 AA.
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WPI; 1998-230317/20.
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N-PSDB; AAV24135.

DNA sequence encoding BARD1, B123, BE14, BE31 or BE445 - which as breast cancer antigen, BRCA1, binding proteins are useful to identify patient having or at risk of developing cancer

71s/14/sure, Park 287/288, 348pp, English.

preparation of the recombinant breast cancer antigen, BRCAL binding proteins BARL, BRIS, BRES HILL BRIST or a composition for the detection of a HARDL BISS, BES, HILL BEST or BRIST, or a composition for the sequence, specifically a wild type BARCL composition for the detection or purification of BRCAL, useful to identify a patient having, or at antisk of developing cancer. BARLL can be used in the preparation of an antisk of antibody, and in the detection and purification of an protein. BARCL HILL BRIST or BRA45 can used in the identification of a binding protein agonist or antagonist that alters the binding of BARD1, B123, BE2, BE34, BE31 or BE445 to BE741 or the biological activity of the BE741 BARD1, B123, BE2, BE34 or BE445 complex. The antibodies can be used to detect BARD1, B123, BE2, BE14, BE31 or BE445, a specific anti-BARD1 antibody can be used to identify The sequence is that of a protein which can be used in the a patient having or at risk of developing cancer.

515 AA; Sequence

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23.9%; Score 2585; UB 19; Length 515; 99.0%; Pred. No. 0; tive 0; Mismatches 5; Indels 0;
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1690 VPVI XTAVKI TAPEPKPEKNVI GSALLCTAFVTSTLEALATPQLPSI MPSLLTTMKNTSF 1749 

1750 IVSSEVYLLSALAALQKVVETLPHFISPYLEGILSQVIHLEKITSEMGSASGANIHLER. 1809 

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2110 LAELMEDEGEEVERQCQKTIQQLETVLGEPLQSYF 2144

AAB43598 standard; Protein; 343 AA. AAB43598

AAB43598;

(first entry) 08-FEB-2001 Human cancer associated protein sequence SDQ ID No:1043.

Human; cancer associated gene, cancer antiqen; detection; cancer; diagosis; extratit; proliferative relaborary; immunomodulator; antidiabetic; antiarthritic; antiarthritic; antiviral; antidialmatory; antiarthric; antiallerate; autibacterial; cardiant; dermatoriogizal; neuroprotective; threadedytic; coaquiant, notropic; vasaropic, antiparation; gene therapy; inflammation; immune disorder; anti-order; harmonial; evel disorder; anti-order; anti-order; all-lengthric; cardiovascular disorder; anti-order; anti-

Homo sapiens

WG200055350-A1.

21-SEP-2000.

08-MAR-2000; 2000WO-US05882.

12-MAR-1999; 9902-0124270.

(HUMA-) HUMAN GENOME SCI INC

Ruben SM; Rosen CA,

WPI; 2000-587533/55.

N-PSER: AAC77807

Nevel isolated medicional to enepoising suppressed encoding proptides useful for treating or diagnosing e.g. cancer -

Claim 11; Page 1631-1632; 2352pp; English.

definition of the control of the con harmerial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44248 impresent sequences used in the coemplification of disorders, allergic reactions, graft versus host disease and organ rejection, modulate themselytic artivity modulate inflammation, cancers, cardiovascular disorders, neurological disease and AAC77607 to AAC78448 encode the human cancer associated proteins given in AAR43398 to AAB44239. The proteins can have activities based on the the present inconfirming larned to teat immine disorders by reflea or inhibiting the proliferation, differentiation or mobilisation of immine cells, to treat disorders of basematopoletic cells, autolmmune tissues and cells the genes are expressed in. Example of activities include: expostation, proliferative: vulnerary, immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; the present invention.

343 AA; Sequence 

Gaps .. c 0.7%; score 71; DB 21; Length 343; 37.0%; Pred. No. 4.3; 10; Mismatches 19; Indels Oudry Match
Best Local Similarity 37.0%
Matches 17; Conservative

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## SUMMARIES

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September 4, Application GSZS+692395
Fation No. 440442
GINERAL INPRAMITOR:
APPLICANT: Kartmann, Joseph
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TITLE OF INVENTION: A CRYSTAL OF BACHDRIAL CORE FNA POLYMERASE AND METHODS FITLE OF INVENTIONS: OF USE THEREOF FILE REFERENCE: 600-1-258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; score 66; D8 4; Lonath 1525; 44.3%; Fred. No. 79;
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APPLICANT: Scla-Murlade, Marianne H.
APPLICANT: Vocamits, Alexandra A.
APPLICANT: Wolosbuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Bubertus J.M.
TITLE OF INVENTION: FUNGAL PESISTANT PLANTS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \mbox{Doctation:} (1247) OTHER INFORMATION: Any amino acid can be at this position
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                                                                                                                                                                                                                                                  CURRENT FILLY AND STREET TRY (700, FCIE CURRENT FILLN DATE: 1999-09-15 NUMBER OF SEQ ID NOS: 4 SOFTWARE: Fatentin Ver. 2.0 SEQ ID NO.)
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APPLICANT: Mealenhoff, Elisabeth J.S.
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                    > Sequence 1, Application US/09396651B
> Patent No. 6225076
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// Patent No. 5670706
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755 Page Mill Road
                                                                                APPLICANT: Darst, Seth A
APPLICANT: Zhana, Gongyi
APPLICANT: Campball, Elizabeth
APPLICANT: Minakin, Leonid
APPLICANT: Severinov, Konstant D
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Matches 13; Conservative
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                                                                J GENERAL INFORMATION:
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US-08-047-414-13
US-09-396-651B-1
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PRIOR APPLICATION DATA:

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ADDRESSEE:
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                                                                      TOPOLOGY:
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                                                                                                                                                                                                             Matches
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TITLE OF INVENTION: PUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: ORTALING FURGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNDELECTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 64; DB 1; Length 343; 31.0%; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                           31.0%; Pred. No. 15;
tive 8; Mismatches 21; Indels
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REFERENCIZIOCKET HOMBER: 24,959
REFERENCIZIOCKET HOMBER: 24,959
TELEPHONE: TOTATION INFORMATION:
TELEPHONE: 415-813-5600
TELEPAX: 415-494-0792
                                                                                             REFERENCEZEGRET BUMBIE. 24617 29022 OR
TELECOMMUNICATION INFORMATION:
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Metchers, Leo S.
Meulenhoff, Elisabeth J.S.
Van Rockel, Jerson S.C.
Sela-Buurlage, Marianne B.
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US 07/647,831
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STREET: 755 Page Mill Road
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                                                                            29,959
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 13:
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ATTORNEY/AGENT INFORMATION:
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                FILLING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
                                                            NAME: Murashiqe, Kate H.
REGISTRATION NUMBER: 29,
                                                                                                                                         415-813-5600
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Matches 14; Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                           ToPOLOGY: linear
MOLECULE TYPE: protein
JS:08-047-413-13
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  APPLICATION NUMBER:
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                                                                                                                                             TELEFAX: 4.0. TELEFAX: 706141
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2.1P: 94 +04 -
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FUNGAL RESISTANT PLANTS, PROCESS FOR ORTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT POLYNUCLEOFIDES FOR USE THEREIN
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Meulenhoff, Elisabeth J.S.
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APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
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FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
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KELEKOMMINICATION INFORMATION:
TELEPHONE: 415-4313-5600
TELEFAX: 415-494-0792
TELEX: 704341
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755 Page Mill Road
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INFORMATION FOR SEQ ID NO: 13:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                           31.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 343 amino acids
                                           343 amino acids
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                     SEQUENCE CHARACTERISTICS:
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US-08-229-050-13
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APPLICANT: Shiba, Kiyotaka
APPLICANT: Kranz, Janico E.
ATTLICANT: Schimmel, Paul K.
IIII.E OF INVENTION: Human Isoleogyl TRNA Syntherase
TITLE OF INVENTION: Proteins. Nucleic Acids and Tester Strains Comprising Same
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Best Loral Similarity 28.4%; Stod. No. 1.60-02;
Matches 15; Conservative to: Mismatches 28; Indexs
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CORRESPONDENCE ADDRESS:
ADDRESSEE Hamilton, Brock Smith & Reybolds, E.C.
STEDET, INC. MILLIA DATO:
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                  APPLICANT: OFOZCO, Buddy
APPLICANT: Schwaber, James S.
APPLICANT: Schwaber, James S.
FILE REFERENCE: HR-1193
FILE REFERENCE: HR-1193
                                                                                                                                                                                                                                                                                                                                                                                                    to: Mismatches
                                                                                              CURPELLI ALEL CALLOR RUBBLE: "L. CONTRETE S CURPENT FILLING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CP194-14A
                                                                                                                                      EARLIER AFFLECATION NOMBER: 55,093,530
BEARLIER FILLOS DALE: JULY 21, 1998
NUMBER OF SEC ID NOS: 37
SOFTWARE: Microsoft SITICE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPICATION: 435
PRIOR APPLICATION IMIA:
APPLICATION NUMBER: US 08/250.952
PILING TALE: 27-MAY-1944
ATTORNIY/ACIMIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UMBER: US/OB/A68,557
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08468157
Patent Ro. 5759833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22,592
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APPLICANT: Famodu, Layo o.
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US-08-468-557-4
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MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                              ) PRGANISM: Homo sapiens
US 09-357-251-33
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GENERAL INFORMATION:
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                                                                                                                                                                                                                      SEQ ID NO 33
                                                                                                                                                                                                                                                              TYPE: PRI
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APPLICANT: Famodu, Layo O. APPLICANT: Orozco, Buddy APPLICANT: Falco, S. Carl

GENERAL INFORMATION:

RESULT 11

Ö a ORGANISM: Homo sapiens

US-09-357-251-32

1266

TYPE: PRT LENGTH:

SEQ TO NO 32

GENERAL INFORMATION:

US-09-330-611-14

TYPE: PRT

Onery Match

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US-09-330-611-14

RESULT 12

<u>a</u> 5

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Predicting Folded Structures of Proteins
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 62; DB 4; Length 701; 34.1%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (International) 41 1 632 2830 TELEFAX: (International) 41 1 262 2437
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                                                                                                                                                                                                                CHERENT APPLICATION NUMBER - HS 709/132,028
                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0
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                                  Patent No. 6222014
Patent No. 6222014
Fatent No. 6222014
GENERAL INFORMATION
APPLICANT: Wilding, Edwina Imogen
AFFLICANT: Black, Michael Treyor
APPLICANT: Traini, Offristopher M.
TITLE OF INVENTION: nrde
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT; ORGANISM: Staphylococcus Aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steven A Renner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Benner, Steven A. TITLE OF INVENTION: PredictionIMMREP OF SEQUENCES: 114
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OPERATING SYSTEM: MacIntos
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Quinn, A. M.
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GENERAL INFORMATION:
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CLASSIFICATION:
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US-07-857-224B-56
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                                                                                                                                                                                                                                                                                                                                                LENGTH: 701
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                 US-09-132-028-2
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                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
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APPLICANT: RUZICKA, Frank J.
TITLE OF INVENTION. DNA MOLDCULES ENCEDING BACTERIAL LYSINE 2,3-AMINOMUTASE
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                                                 0
                                                                                          68 PERSQLAKTERRSVQTKAVHROTEPHTSEPTELITERPAGPFTEBWITHP 120
                                                                                                                   295 PLEDYTZECELRGALIVIANIANZELPETISVVÄÄRTYETAFTAFVAVAGENTIR 347
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46.2%; Pred. No. 32;
Live 8; Mismatches 6; Indels
0.6%; Score 63; DB 1; Length 1266;
                                            10, Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Schwaber, James S.
TITLE OF INVENTION: Plant Aminoacyl tRNA Synthetase.
FILE REPERENCE: 88-1193
                      Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCH: 032026/0476
CURRENT APPLICATION NUMBER: US/09/830.bll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/357,251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1999-07-20
EARLIER APPLICATION NUMBER: 60,093,530
EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 37
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                                                                                                                                                                                                                                                        Sequence 32, Application US/09357251
Patent No. 6271441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 1999-06-11
  Ouery Match
Best Local Similarity 28.3%;
Matches 15; Conservative 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Ver. 2.0
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Matches 12; Conservative
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AUTHORS:

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Filla of INVENTION: Kin. Ses
Filla of BEADACHES. 21
FORESPONDENCE ALDRESS:
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WERENI APPLICATION LAIA:
APPLICATION NUMBER: Ps1//Bjor//Scoss
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SUBJECT INDOMAID ON:
APPLICANT: SCHOOL INC.
APPLICANT: SCHOOL INC.
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APPLICANT: GT. ABLYONE ON INTO A APPLICANT: GT. APPLICA
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Computer: 18M PC Computible
OPERATINE SYSTEM: PC (48,7ME (45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wissenschaften E.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pennie & Eunonds
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PEGISTANTO NUMBER: 0.742
PEFERENI STOVINE INVEST: 75
FELEVARIEMENTALL R. REGINATER: 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hetgarten Str. 2
APPLICANT: Munchen 80539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US OB FILLON DATE: LECARPETON TANSTER ALE SMALL NE ALL OF MEY/A BRIT ONE BMALL NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NES (212) 790 3690
1 (212) 854 9741
3 6141 PENNIE
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Horritor, I.
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                                                                                                                                                                           VALUMES 241
PARES 42 52
DATE: DARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.5 or? 857 2.24B-56
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Beset Loans Co
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0.585 Store 612 100 55 Longth 5055 21170; Pred, No. 73

siery Match Best Loral Similarity

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1822 TUPATERTYK FERNWERBINGER MET GERHI GAMEKELE, DERGEGOTALE FRATERAL IF 1827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 20.5%; Pred. No. 44;
Matches 18, Conservative 21 Missatches 49; Indols
                                                                                                                                                                                                                                                              APPLICANT AND Gynheung
TITLE OF HYEH-FON. GYNHEUNG
TITLE OF HYEH-FON. GLBES CONTROLLED FOORTH BYENGERHUN
TITLE OF HYEN-FON. AND AFIGAL FAMINANCE IN PLANIS
TITLE OF HYEN-FOR. 70
zl: Indels
                                           1210 ILLIANIERKERONGALINPTERMISSONELPADIONISSONELLASS
                                                                      ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston, LLP STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Suite 1600
10; Conservative 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1882 SENDLEEVGETENCIIDCLVAMVVELSE 1909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 0.5, 037423,449
FILING DAIE: October 14, 1994
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SR. 4:30 47071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                    Sequence 17, Application US/08H67UH7B
Patent No. 5990386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 248 amino acid residues TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-476-008-64
; Sequence 64, Application US/08476008
; Patent No. 5627664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/2 inch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordforfor 5.1
CURRENT APPLICATION DATA:
APPLICATION NOMBER: US/SOR/9F
FILING DATE: June 2, 1997
CLASSIFICATION: B00
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dow, Alan E.
REGISTRATION NUMBER: 35,123
REPERCHONORY NUMBER: 4, 1
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 0.S. 0
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TELEPHONE: (503) 226-7391 | SELEFAX. (504) 228-9446 | INFORMATION FOR SEQ 1D NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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US-08-867-0878-17
                                                                                                                                                                                                                                                         GENERAL INFORMALION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Portland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U1 2.1P: 97204
                                                                                                                                                                                   US-08-867-087B-17
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Matches
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us-09-603-665-5.rai

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Patent No
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APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Encipyrovpishikimate 3 Phosphate Synthases
CORRESPONDENCE: 69
                             APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Emolpgravylsbikimate-3-Phosphale Synthases
NUMBER OF SEQUENCES: 69
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    Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway

                                                                                                                                                                   ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                    SOFTWAKE: Patentin kejedse #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSICATION DATA:
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/576,537 FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08 07/749,611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: HOERNEY Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6044
TELEFAX: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Barry, Gerard F. APPLICANT: Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                  Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 - AUG - 1991
Barry, Gerard F.
                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   426 amino acids
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                                                                                                                                                                                                                                                                                                      COMPULER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                                                                                                                                                                                        Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                               63198
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                    APPLICANT:
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TITLE OF INVENTION: 5-Enolpyruvylskikimate 3-Phosphato Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
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47.8%; Pred. No 78;
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700 Chesterfield Village Parkway
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                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/AB/306,063
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                                                                                                                                                                                                                  FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE: 07/749,611
APPLICATION NUMBER: 11S 07/749,611
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patent No. 5804425
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APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Cancah M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
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                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: HOETDER Jr., Dennis R.
REGISTAATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30,914
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                                                                                                                    IBM PC compatible
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INFORMATION FOR SEQ ID NO: 63:
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Matches 11; Conserva
                                                                                                                  COMPUTER: IBM PC of OPERATING SYSTEM:
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AFFICANT: KIRCHE, anosh M.
AFFICANT: PROPERTY Stockers William P.
AFFICANT: Stockers William P.
ILLE OF INVENTED N: Chyp.osarto Colerant
ILLE OF INVENTED N: Chyp.osarto Colerant
ILLE OF INVENTED N: Chyp.osarto Synthases
NUMRER OF SPECIENCES: 69
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Best Goral Similarity 47,88; Pred. No. 78;
Marches III, Cacagorities 4; Missiricher 8; 10,5038
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7 o thestorrield Village Furkway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | NAME: | H. & T. & T. & L. | Destricts | R. | P. DESTREEL | NORTHEEL | SECTION | TELEPO-MEINT-SALES | NORTHEEL | SECTION | TELEPO-MEINT-SALES | S. DESTREEL | S. DESTREEL
| TASSELTATION | 45 | APER | PARTICION | ATACA | APER | AP
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PALEN NUMBER OF BESTER OF SERVICE
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PREPER APPLICATION DATA.
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Patent No. (2480)
GENERAL INPORMATION:
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ALLOENEY/AGENT INFORMATION:
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US as as A. C. DASSACA
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FILLS OF INVENTION: Cloned Polphyromonas dinairalis forms
TITLE OF INVENTION: and Probes for the Extention of Meriodontal Disease
NUMBER OF SEQUENCES: 29
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Best Loval Similarity 47,8%; Fred. Ko. 79;
Matches II; Conservative 4; Mismarches 8; Indexs
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57.9%; Fred, No. 97;
ative 3; Mismarches 5; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SEEN, BENALD M.; DICARD, PAUL E. FILLE OF INVENTION: INHIBITIES OF HERBES SIMPLEX VIKUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSED: Fed W. Whitlook
STREET. 2421 R.W. 41at Street, Suite A 1
CITY: Gainesville
PRIOR APPLICATION DATA:
ACTICACE N EXHIBER 52 7/976,547
FILLING TALE: 31-ANO-1959
ATTORNIT/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/07/482,634
FILING DATE: 21-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2028 ENPLOSPEYEOFPVTRPLIPGIA 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Progulske-Fox, Ann APPLICANT: Tumwasorn, Somying APPLICANT: Lepine, Guylaine APPLICANT: Han, Naiming APPLICANT: Lantz, Marilyn APPLICANT: Patti, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 2, Application US/08570311; Patent No. 5824791
                                                                                                   NAME: ROPINGLAIN DENDIS R. REDISTRATION NUMBER: 30-417 REFERENCE AND MEET NUMBER: 34-1ELECOMMUNICATION INVERSALES
                                                                                                                                                                                              | HILEPBONE: (314)737-6099
| HILEPAN: (314)737-6647
| INPORMATION FOR SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 LSPYFLLKPAQKCLEWLIH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 VSAVFLLKPOKICLDWLGH 327
                                                                                                                                                                                                                                                                                       : LENGTH: 426 amino acids
: TYPE: amino acid
:1-E0LONY: innar
: MOLECULE TYPE: protein
US-09-147-440-64
                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rest Local Similarity 57.9
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5223391
; APPLICANE (2013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
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08-08-360-673-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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APPLICANT: Pattl, Joseph
TITLE OF HYPRION. Cloned Diphyromonus quadvalls Concs
TITLE OF HYPRION. and Probes for the Detection of Periodontal Discase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ċ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IAM PC Compatible
OFGRATING JOTHAL PC DOLYMS DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM, 1C-DGZ/MS DGS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1668 QTALYTLKLLCKNPGAENPDPFVPVLXTAVKLIAP 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY, Gainesville
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
                                                                                                                                                                                                                                        APPLICATION NUMBER: 08-08/353,485
FILING DAFE: 09-DEC-1994
                                                                                                                                                                                                                                                                                  CLASSIFICATION, 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,119
                                                                                                                                                    08/08/570,311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPERENCE/DOCKET NUMBER: UF15.C3
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Progulske-Fox, Ann
APPLICANT: Tumwasorn, Somying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPAN: (904) 375 8100
TELEPAN: (904) 372 5800
INFORMATION FOR SED ID 0. 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Han, Naiming
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 FILLING DATE: 25-JAN-1991
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    497 amino acids
                                                                                                                             CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
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                    COMPUTER READABLE FORM:
                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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O; Gaps
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40 0%; Prod. No. 99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patentin Pelease #1 0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1668 OTALYTIKLICKNFGAENPDPFVPVLXTAVKLIAP 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       335 EAANFTIKILEETIGSDKPAPMNLVKSEGVKLPAP 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhone-Poulenc Rorer Inc.
                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/241,640
FILING DATE: 08-SEP-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/08/360,673
                                                                            ng n77647,119
APPLICATION NUMBER - HS/08/353,485
                                                                                                                                                                                                                                                      PEFFFFNOF/ADOCKET NUMBER: UF15.C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PC-DOS/MS-DOS
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; Patent No. 5679544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 Arcola Rd 3C43
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                      36,965
                                                                                                                                                                                                                                                                                            TELEPHONE: (904) 375-8100
TELEPAX: (904) 372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-JUN-1993
PRIOF APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Fleer, Reinnard
APPLICANT: Fourtier, Allain
APPLICANT: Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 25-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                             25-JAN-1991
                FILING DATE: 09-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                               497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rest Local Similarity 40 0
Matches 14; Conservative
                                                                                                                                                                                                                     NAME: Whitlock, Ted W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, Julie K. PPGISTPATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                   HOLPOUR TYPE: protein US-08-353-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER PEADABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                      REGISTRATION NUMBER:
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                                                        PRIOR APPLICATION DATA:
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                                       CLASSIFICATION: 424
                                                                              ICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                               TYPE; amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                                                                                CLASSIFICATION:
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                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWAPF
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Ouery Match
Hest Local Similarity 40.0%;
Matches 14, Conservative
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APPLICANT: Chien, David Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUCCEDINGE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
AFPLICATION RUMBER. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DAIA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : MOLECOLE TYPE: protein
US-08-570-311-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLITATION SUMMER FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPOTER: IRM PC COPERATING SYSTEM: SOFTWAKE: Patentin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amine acid
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US-08-444 818-10
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9.346. Skyter for DB 1: Demath 561;
Bost Local Similarity (7.34) Pred. No. 1.2e-02;
Mittack II: Numerication of Mismarches 19; Edd-1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Parker, Michael I.
1111E -@ INVENTEN. ASTRMCT VIWAL PARTITION AND THITE
1111E -@ INVENTENCE SOE IN A VANCUE E- ROTAVIRAL DISEASE
NUMBER - SEQUENES: 40
1 SREESE NUEWIE AND ASSESS:
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C-MADISE: INM PS compart Blo
S-FIWAFE: Patentic Rejouse #1.0, Versjan #1.25
WEEPST ASSLAND A GAA.
WEEPST ASSLAND A GAA.
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SIEFEL: 945 Middleticid Road, Saite zeo
SIEFE: Memlo Park
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SEQUENCE CHARA TERESTICS:
HEPPINE: (*L*) 154 (R O)
171EAN: (*L*) 154 (R O)
1NF PMALLOR FOR STORY (R O)
SEQUENT: HARATTER (F.)
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TERNYALINI NE 424
NAMES FATES, FARMINE ELISTEATE
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Materials (YPE) protein
a de de electro
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MECTER READABLE FORM:
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Sequence 14, Application US/C0570311
Sequence 14, Application US/C0570311
Forent No. 2824791
Forent No. 2824791
GENERAL INFORMATION:
APPLICANT: Produlske-Fox, Ann
APPLICANT: Lepino, Guylaine
APPLICANT: Hat, Naimina
APPLICANT: Battz, Marilyn
APPLICANT: Pattz, Marilyn
TITLE OF INVENTION: Cloned Pyrphyromenas dingivalis Genes
TITLE OF INVENTION: and Probss for the Detection of Periodental Lisease
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10.0%; Pred, No. 1.4e+03;
19e - 6, Mismatches 15; Edeis
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ADDRESSEE: lod W. Whithork
STREET 4421 N.W. 4181 Street, SOTIE A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/241,540 FILLING DATE: 08-SEP-1988 ATFORNEY/ASENT UNFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NOMBEE. 82 e7.647,119
FILING DATE: 25.40N-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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09-DEC-1994
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MEDIUM IYPE: Floppy disk
COMPOTER: IHM PS COmputible
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KENICKALLOCK NUMBER: 46,965
KEDERENCZ/DOCKET NUMBER: UP
IELECOMMONICALLON INPORMATION
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TELEFAX: (904) 372-5800
INFORMATION FOR SEC 1D NO: 14:
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REGISTRATION NUMBER: 33,207
                                                                        TELEFAX:
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34.5%; Pred. No. 15;
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           NUMBER OF SEQUENCES: 777
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                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/444,818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LESNIEMSKI, RICHARD R. APPLICANT: LEIMS, TAT K. TTITLE OF INVENTION: HEPATITIS C ASSAY NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/0892/07813
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCY, CACKET NUMBER: 0119.002
                                                                                                                                                                                                                                                                                                                                                            08/08/463,590
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                                                                             Chiron Corporation
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COMPUTER: IBM PC compatible
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       Rutter, William J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 10:
                                                                               ADDRESSEE: Chiron Corporat STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (508)359-3876
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Bost Local Similarity 34.55
Matches 10; Conservative
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US-08-444-818-10
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PRIOR APPLICATION DATA:
                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 59; DB 4; Length 128;
04.5%; Pred. No. 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NANBV Diagnostics and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 0.5%; Score 59; DB - Gast Local Similarity 34.5%; Prod No. 17; Best Local Similarity 34.5%; Prod No. 17; Conscrivative 9; Mismatches
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  4767.P3.03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application HS/08444818
Patent No. 6150087
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REFERENCEZDOCKET NUMBER: 476
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANI: Chien, David Y.
APPLICANI: Rutter, William J.
TITLE OF INVENTION: NANBV Diac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4560 Horton Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (508)359-3876
(508)359-3885
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                                                                                                                           117 amino acids
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                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                708-937-9556
                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-444-818-8
                                                                                                                                                                      single
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                  PCT-US92-07813-12
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34.5%; Pred. No. 92;
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTHUALION NUMBER: 03/08/444,818
                                                                                                                                                                                                                                                                                                                                                                                                                                    115/08/403,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 43,895
REFERENCE/DXCKET NUMBER: 01101-002
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COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC:DOS/ME-DOS
                                                                                                                                                                              COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08444818
Patent No. 6150087
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STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34,895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (508) 359-3885
INFORMATION FOR SEQ ID NO: 68:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILLING DATE: 14-MAR-1995
ATESENEY/AGENT (NESEMAFION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (508)359-3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 53, REFERENCE DOCUMER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           382 amino acids
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Hest Local Similarity 34.5%
Matches 10; Conservative
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PRIOR APPLICATION DATA:
AFFLICATION NUMBER: 3
                                                                                                                         COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
CIIY: Emeryville
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                                                                                  94608-2916
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                             STATE: CA
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ARTITYMI: ZHE VIAN
ARTITYMI: WAREL : RWAT
ARTITYMI: BUTTON RWAY A
1772 - FINVINTEN: HENDEN: A TARGET IN CHRONE KREDE FAILURE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHELLESOLFAFLESIEKMEKSLEF LELNETVAL HAAMGESTELEEGLOSV 106
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Front Nr. (1968)
APRIL ANT CLION DIVIL C.
APRILANT CRION DIVIL C.
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APRIL OF SECURIORS: 77
SCHWISS N. RW. ADMIN ST. 77
SCHWISS N. RW. ADMINST T.
SCHWISS N. RW. ADMINST T.
STREET TYOU BOILD ST. 900
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S.FUMARE FISCASE, TOT WILL-OSS VOLSIOL 200
SUPPRINT AFELONIN BARAINE BARAINE
FILLING DATE: 29 MAY-1997
FILLING DATE: 39 MAY-1997
                          AR VIAPAVOINWORDELFWAKEMWNEISTIG BA
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                                                                                                                                Notes: 1. Compared to the SZCH865273. September No. Condition.
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SPEED FO. FOX OF
CHAN MALEY FORE
STATE: FA
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TELEPHONE, 610-407-07(0)
TELEFAX: +10-407-0701
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IELEX: 440150
INTERACTOR FOR SEQUENCE Z:
SEGRENTE OHARATTERISTIOS:
LENSIN: 241 annio acids
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FimeUIDE: IBM Campatible
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SIRANLFUNESS: Sin
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US 077748,561
FILING DATE: 21-AUG-1991
ATTORNEY/ASENT INFORMATION:
                                                                                                                                                                                        512 amino acids
                                                                                                                                                                     SHOURNCE CHARACTERISTICS:
                                                                                                                             708-937-9556
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                            : MOLECULE TYPE: peptide US-08-867-611-58
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TITLE OF INVENTION: HEFATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                          Guery Match 0.5%; Score 59; DB 4; Length 460; Best Local Similarity 34.5%; Pred. No. 1.2e+02; Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
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                                                                                                                                                                                                                                                                                                        1821 VELPATERTYROIEKNWKNHMGPFMSTLO 1849
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
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LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58, Application US/08867511 Patent No. 6172189
       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAILEY, STEPHEN H
DAWSON, GEORGE J
                     TELLEPHONE: (508)359-3876
TELLEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 20:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVARE, SUSHIL G
DESAL, SURESH M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEWART, JAMES L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: UC 07
FILING DATE: 07-NOV-1990
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                                                                                                   460 amino acids
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                       MOLECULE TYPE: protein
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PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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Y: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.5%; Score 59; PR 4; Length 512; Best Local Similarity 34.5%; Pred. No. 1.4e+02; Matches 16; Conservative 9; Mismatches 10; Indels
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APPLICATION NUMBER: US/AB/AR7 611
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ONE ABBOTT PARK ROAD, CHAD377/AP6D2
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07-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 47, Application US/08867611
Patent No. 6172189
NAME: POREMBERT, PRISCILLA E
REGISTRATION NIMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
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APPLICANT: DALLEY, STEPHEN H
APPLICANT: DAWSON, GEORGE J
APPLICANT: CHTTERREZ, ROBIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEWART, JAMES I. APPLICANT: RUPPRECHT, KEVIN R
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APPLICANT: DESAI, SURESH M
APPLICANT: CASEY, JAMES M
                                                                                                                                          TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 58:
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ITICE E INVENTEUR REPATITIS CASSAY UFILIZING REGIMBINAL
ITICE E INVENTEUR AL ANGERRA
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Marches 1 p. Conserty (1900 pr. Mem. 1.90-02)
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UPPERI APPLICATE NITALA:
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TELECHMONITOLI OF NOO-MALIF N:
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                                                                                                    APPLICATE N NUMBER 1 12 77 14, 560. FELLON (ALE: 21-ADS 18.9)
PELON CATE APPLICATION NAMES.
FILLING GATE: 21 ATH 18.9.
ATHER FAREYARD INFORMATION:
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FILING DATE: OZ-39N 1997
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computer: THM PC compatible
oPERATING SYSTEM: PC-DOS/MS-GOS
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JAMES D
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Partent No. 6172189
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DAWSON, RECREES
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PETGINS CATE: 21 ATT 1991
PETS APPLICATION DATA:
APPLICATION WOMBER: 01 CT
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| 2 September 48 A
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STEWART, JAMES I.
FULLEDHI, KIVIN B.
WENTIGH: HEPATITES C. ASSAY UTILITIES FESTAMHINANI.
WENTIGH: AMTIGENS
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ONE ABBOTT PARK POAD, SHADOSZ/APPODZ
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                                                                                                                                                                                                                                                                                                REGISTERATION NUMBER: 33.20°
REPERFUCEZONOSET NUMBER: 40.44 HS.P6
TELECOMMUNICATION INFORMATION
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                           ELLING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
AGLEGATION DATA:
                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
                                                                                                                                                            APPLICATION MUMBER: US 07/748,565 FILLING DAFF: 21-AUG-1991 PRIOR APPLICATION DAIA:
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                                                                                                US 07,748,561
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COMPUTER: IBM PC COMpatible
CPURALING SYSTEM: PC-1978/MS-DOS
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Patent No. 6172189
                                                                                                                                                                                                                                                                                      POREMBSKI, PRISCILLA E
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APPLICANT: DESAT, SURESH M
APPLICANT: CASEY, JAMIES M
APPLICANT: DALLEY, STEPHEN H
APPLICANT: DAWSON, GEORGE J
APPLICANT: GUITEMEZ, ROHIN A
                                                                                                                                                                                                                                                                                                                                                                                     TELLEFAX: 708-937-9556
INFORMALION FOR SEQ ID NO: 48:
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CLASSIFICATION: 435
FILLING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION RUMBER, US 07
                                                                                                                   FILING DATE: 21 AUG-1991
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                  708-947-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                594 amino acids
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LENGIH: 594 amino acid
                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 708-93, ...
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nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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CORRESPONDENCE ADDRESS:
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PRICE APPLICATION DATA:
                                                                                                ALLICATION NUMBER. PILLING DATE: 21 AL
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICANT:
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SUPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 59; DB 4; Length 597;
34.5%; Pred. No. 1.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
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REPERENCY/COCKET NUMBER: 4834.US.PG
TELECOMMUNICATION INFORMATION:
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                                                                           Sequence 21, Application PC/10Sy206965A GENGRAL INFORMATION.
APPLICANT: DEVARE, S. APPLICANT: DESAL, S. APPLICANT: DALIBY, S. TITLE OF INVENTION: BCV STWINIT; PT
                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/748,555
PRING DATE: 21-ANO-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-ANO-1991
ATTORNEY/AGENT INFORMATION:
NAME: POREMHSKI, PRISCILLA E
                                                                                                                                                                      PILING DATE: 07 NOV 1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  US 07/748,565
APPLICATION NUMBER: US/08/646,757
                                    02/08/179,896
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NAME: POREMBSKI, PRISCILLA E.
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                                                                                                                                                      APPLICATION NUMBER: US 07
FILING DATE: 07 NOV 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          597 amino acids
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MOLECULE TYPE: protein
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                                                                         PRIOR APPLICATION DATA:
                                      APPLICATION NUMBER:
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Best Local Similarity
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                                                          FILING DATE:
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APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
NUMBER OF SEQUENCES: 59
                                                                                                                                                                                                                                     Query Match 0.5%; Score 59; DB 5; Length 597; Best Local Similarity 34.5%; Pred. No. 1.8e-02; Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0, Version #1.25
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ONE ABHOTT PARK ROAD, CHAD377/AP6D2
                                                                                                                                                                                                                                                                                                                         1821 VILIPAIRETYKOTEKNWKNHMOPEMSTLO 1849
                                                                                                                                                                                                                                                                                                                                                 4: | | :: :::: | | | | | :| :| | 401 VIAPAVQTNWQKLETFWAKHMWNFISGIQ 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18 Application US/08867611
Patent No. 6172189
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANC: DEVARE, SURHIL G
APPLICANC: DESAT, SURESH M
APPLICANT: CASEY, JAMES M
APPLICANT: DAILEY, STEPHEN H
APPLICANT: PAWSON, GEORGE J
TELECOMMUNICATION INFORMATION:
                                                          INFORMATION FOR SEG ID NO: 21:
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PRIOR APPLICATION DATA:
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                     708-937-6365
                                                                                                    : 597 amino acids
AMINO ACID
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                                                                                 SEQUENCE CHARACTERISTICS:
                                      708-937-9556
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APPLICATION NUMBER:
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APPLICANT: SIEMARI, JAMES I.
APPLICANT: RUPPERPRINE, KEVIN K
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TITLE OF HAVENTENE. ANTIGENS
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ONE ABBOTT PARK BOAD, CHADO77/APCL2
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AIPLICATION NUMBER, 68 07/572,822
FILING DATE: 24-A06-1990
PRIOR APPLICATION DATA:
AFPLICATION NUMBER: 08 07/514,069
FILING DATE: 07-NOV-1990
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FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 08/08/646,757
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                                                                                                             . Sequence 45. Application 03/08867611
; Patent No. 6172189
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REGISTRATION NUMBER, 33,207
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APPLICANT: DAWSON, SEORGE J
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                                                                                                                                                                        APPLICANT: DEVARE, SUSHILL GAPPLICANT: DESAL, SURESH MAPPLICANT: CASEY, JAMES M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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; MOLECULE TYPE: peptide
US-08-867-611-49
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                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
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STREET: OF
                                                                                       US-08-867-611-49
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                                                                  RESULT 40
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APPLICANT: LESNIEWSKI, RICHARD R
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34.5%; Pred. No. 2.5e+02;
ive 4; Mismatches 10: Indels
         0.5%; Score 59; DB 4; Length 613; 34.5%; Pred. No. 1.9e+02; +;yo q; Mismatches 10; Indels
                                                                                                                                                                                                                                                    APPLICANT: Kutter, William J.
TITLE OF INVENTION: HANBY Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTEK: THM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                1821 VILLPATEREVEGIEENWENHMGPFMSTLØ 1849
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APPLICATION NUMBER: 05/08/403,590
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                                                                                                                                                                                                     Sequence 148, Application US/08444818
Patent No. 6150087
GENERAL INFORMATION:
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; Sequence 4, Application US/08867611
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CASEY, JAMES M
DAILEY, STEPHEN H
DAWSON, GEORGE J
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ATTORNEY/AGENT INFORMATION:
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INFORMATION POR SPQ ID NO:
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Matches 10; Conservative
   Query Match
Best Local Similarity 34.5%
Best Local Similarity 34.5%
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APPLICANT:
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STEWART, JAMES L
RUPPRECHT, KIVIN K
VENTION: HERALILIS C ASSAN UTILIZING RECOMBINANT
VENTION: ANTICENS
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34.58; Pred. No. 2.7e+02;
ive 9; Mismatches 10; Indels
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                                                                                                                                ONE ABBOTT PARK ROAD, CHAD377/AP6D2
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APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 38.07/572,822 FILING DATE: 24-{\rm AUG}{-}1990
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21-AUG-1991
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07-NOV-1990
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                                                                                                                                                                                                                                                                                                                                             UMBER: US/U8/867,611
02-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/U8/179,896
                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
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                                                                                                                                                                                                                                                       Floppy disk
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MOLECULE TYPE: protein
US-08-867-611-4
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PRIOR APPLICATION DATA:
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                                                                                                                                    STREET: ONE ABBOIT
CITY: ABBOTT PARK
                                                                             NUMBER OF SEQUENCES:
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                                      TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                    ADDRESSEE:
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TASSED ATE: 19 or
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NAME OF PERSONS
REPERBORATION NUMBER: 4.227
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PELP APPLICATION CALAS
ANTILOATION BURNEL TOTOGOTOLOGY
FILLING DATE: 14-MAR 1995
ATOGNEY/A TENT TRESMATION.
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MAGENEE TYPE: protects.
FT 1892 SOREA A
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APPLICANT TANGER, STATES AND THE STATE OF THVENTEN HE HE NUMBER OF SEQUENCES.
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ZIP; formes 45mm
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Bost Local Si
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VEHITON: HEFATITES C ASSAY UTILIZIES KES MEHAND
VEHITOR: ARTIGERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 59; DB 4; Length 859; 44.5%; 3.4d; Bo. 3.2c+02;
live 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fatentin Release #1.0, Version #1.25
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ADDRESSER: A RROTT LAB RATORTES
CITY: ARBOTT PARK ROAD, CHAEL 77, APR 12, CITY: ARBOTT PARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETLING DATE: 02-JON-1957
CLASSIFICATION: 4.5
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                RUGISTRALICH NUMBER: 33,895
REFERENCE/FOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION EDMBER, 03-07/348/561
FILING LATE, 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NOMBER, 03-07/748/565
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APPLICANT: CASEY, JAMES M
APPLICANT: DAILEY, STEPHEN H
APPLICANT: UNMSON, GEORGE J
APPLICANT: GUILERREZ, ROBIN A
APPLICANT: LESNIEMSKI, RICHARD B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 52, Application 65,08867611
Patent No. 6172189
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OFERATING SYSTEM, PC BAS/MS-
SOFTWARE: Patentin Release #
                                                                                                                                                                                                      TELEFRAX: (508)359-4885
INFORMATION FOR SEQ ID NOT 30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DEVARE, SUSHIL G
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                                                                                                                                                                          (508) 353 3876
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 859 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Bast Local Similarity 44.5%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
NAME: Harbin, Alisa A.
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
ToPoLoGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                               TELEFIE WELL
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APPETCANT:
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TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 59; DB 4; Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                            16, indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.8e+02;
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ONP ARROTT PAPE POAD, CHAD377/APED2

    Mismatches

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                                                                                                              REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
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                                   APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 53, Application US/08867611 Patent No. 6172189
                                                                                            POREMBSKI, PRISCILLA E
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DAILEY, STEPHEN H
DAWSON, GEORGE J
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                                                                                                                                                                                                         INFORMATION FOR SEC ID NO: 52:
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APPLICATION NUMBER. US 07,
PLILING DATE: 24 AUG-1950
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07,
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Best Local Similarity 34.5%;
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FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
                                                     FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     708-937-6365
                                                                                                                                                                                                                                                971 amino acids
                                                                                                                                                         LECOME...
TELEPHONE: 708-20.
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Conservative
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US-08-867-611-52
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CORRESPONDENCE ADDRESS:
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APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HERATITIS C ASSAY UTLITZING RECOMBINANT
TITLE OF INVENTION: ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 0.5%; Score 59; DB 4; Length 973; Best Local Similarity 34.5%; Pred. No. 3.8e.02; Matches 10; Conservative 9; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B: ABBOTT LABORATORIES
ONE ABBOTT PARK ROAD, CHAD377/AP6D2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1821 VILLPAIKE-YKGIEENWENHMGPFMSIIQ 1849
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TELECOMMUNICATION INPORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 118/08/646,757
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                                                           FILING DATE: 21-AUG-1991
PRIOR APPELICATION DATA:
APPLICATION NIMHER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                  US 01/748,566
                                         115 07/748,561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CASEY, JAMES M
APPLICANT: DAILEY, STEPHEN H
APPLICANT: DAWSON, GEORGE J
APPLICANT: GUTTERREZ, ROHIN A
APPLICANT: LESNIEWSKI, RICHARD R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 54, Application US/08867611
Patent No. 6172189
                                                                                                                                                                                                                             NAME: POREMBSKI, PRISCILLA E REGISTRATION NUMBER: 33,207
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APPLICANT: DESAL, SURESH M
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                                                                                                                                                                                      FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
07-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                    973 amino acids
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TELEPHONE: 708-50,
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PRIOR APPLICATION DATA:
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                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TELECOMMUNICATION INFORMATION:
                                                  TELEPHONE:
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ITILE OF INVENTION: Administrations of Hepartitis Civiras (HSV)
ITILE OF INVENTION: Administration uses in immunoussays for Anti-HEV Anti-hadies
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ANGRESSEE: PLIFC Poperation
SIRREL For Box 4007 (Int. Prop. R 440)
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                                                                                 BUT VIAPAVOINWOKLETEWAKEMMNETSHIO HZH
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    Sequence 12, Application 08/o7/10763
    Privat No. Softward

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SIMANDEDNESS: single
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M. LECTOR (YEF) populobe
A. 867 (11 54
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FILLING DATE:
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APPLICANT: Bloodhion, Michael
APPLICANT: Choo, qui-tim
APPLICANT: Kno, George
IITLE OF INVENTION: Combinations of Hepatitis C virus (BCV)
TITLE OF INVENTION: Antiques for Use in Immunoassays for Abti Hey Antibedies
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Hest Local Similarity 34.5%; Prod. No. 4.10+02:
Matches 10, Conservative 9, Mismatches 10: Indels
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APPLICATION NUMBER: US 07/910,260
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FELDCOMMUNICATION INFORMATION
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Patent No. 5712087
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STREET: P.O. Box 8097 (In. P
                    TELEFAX: (510) 655-4542
INFORMATION FOR SEQ 1D NO: 12:
SEQUENCE CHARACTERISTICS:
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N: 530
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TELEFAX: (510) 655-4542
INFORMATION FOR SEQ ID NO: 12:
(510) 601-2702
(510) 655-4542
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ATEONNEY/AGENT INFORMATION:
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                                                                                          1021 amino acids
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                                                                                                                                                      ; MoLEGULE TYPE: protein
US:07-910-760-12
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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US-08-440-519-12
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STREET: P.O. L
CITY: Emeryville
TYATE: CA
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                                                                                              rreE: amino acid
ToPOLoGY: linerra
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5712087
GENERAL INFORMATION:
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CLASSIFICALION:
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132) IMSTELEMOANVMELEGETYSEGVIHELVRHVIFALLGSTSGUSTEVSENVEFTVVKITSV 1382
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                                                                                                                                                                             APPLICANT: Sampson et al.
TITHE OF INVENTION: Theberous Scienosis 2 Gene and Uses
TITHE OF INVENTION: Thereof
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IRM PC compatible
                                                                                                                                                                                                                                                                                    ADDRESSEE: Kathleen M. Williams, Banner & Witcoff,
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best Local Similarity 25.8%; Pred. No. 9.7e+02;
Matches 17; Conservative 17; Mismatches 32;
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713 VIAPAVÇTNWÇKLETEWAKHMANTISGIÇ 741
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FILING DATE: 23-December-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/040,738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: GB9326470.3 FILING DATE: 24-December-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Wordperfect 6.1a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/652,426
                                                                                                    Sequence 2, Application US/09040738 Patent No. 6207374
                                                                                                                                                                                                                                                                                                                                 One Financial Center
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AITORNEY/AGENT INFORMATION:
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                                                                                      US-09 040-738-2
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1323 IMSTETEMGANVMREEDPTVSFQVINKTVKMVIPALIOSDSGDSTEVSRNVEETVVKIISV 1382
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                                                    Tuberous Sclerosis 2 Gene and Uses
Thereof
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APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRESSANI TARGET PROTEINS
                                                                                                                                     ADDRESSEE: Kathleen M Williams, Banner & Witcoff, ADDRESSEE: Ltd
                                                                                                                                                                                                                                                                                                           Diskette, 3.50 inch, 1.44 Mb storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-October-1996
CLASSIFCATION: 435
PRIOR APELICATION DATA:
APPLICATION NUMBER: GB9326470.3
                                                                                                                                                                                                                                                                                                                                                         PC - DOS/MS - DOS
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                                                                                                                                                                                     One Financial Center
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                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
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ATTORNEY/AGENT INFORMATION:
NAME: Williams, Kathleen M.
REGIETRATION NUMBER: 34,380
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TELECOMMUNICATION INFORMATION:
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APPLICANT: Berlin, Vivian
                                         APPLICANT: Sampson et al.
TITLE OF INVENTION: Tuberc
TITLE OF INVENTION: Thereo
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PC
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PPIOP APPLICATION DATA:
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MEDIUM TYPE: Diskett
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: Patent No. 6232452
; GENERAL INFORMATION:
; APPLICANT: Sampson
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REFERENCE/DxTKEI NUMBER: APV-036.62

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3.5%; Share 54; ER 4; Length Leubra
41.4%; Pred. No. 10903;
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ARE PART M. ROMBGE: 317-67-6-144A
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TOWARD EPET DAM PET COMPACT BASE
TO FINAL TAND SYSTEM. BY LOSS/MET DAS
SPETWARDER: LATHORITE PET COSPORATION, VOLSTON #11-95
TOPHENIA AFRICANT NOTALA
AFRICATION NOMBER: 05/07/21.5/55
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APELLYALI N NUMBER:
BILLING DALE: 20 LES 10 04
ATTCHERZYALURI HARREMATERI
NAME: VINCEOLI MOTTECE E, 20 LETISCHERZYALURI HARREMATERI
NAME: VINCEOLI MOTTECE E, 20 LETISCHERZY NUMBER: (5, 20)
REFERENTENIN NUMBER: ALV COLOR
FELECOMMUNICALIN LINEORMATEON:
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OPERATION SYSTEM: POSCOSYMS DOS
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(September 12) Application USzussio(144)
(Fatember 16), 61504 (**)
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Matches II) Conservative
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219: Oglob 2175
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48] TELEGRECHELATIVELLAMBERK MEISEE VOERFELEKEAVLAKE BERHINVISAISA SAF
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                                                                                                                                                                                                                                                                                                                           5,450
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APPLICANT: Tatem, Joanne M.
APPLICANT: Tatem, Joanne M.
APPLICANT: Wecks-Lovy, Carolyn L.
TITLE OF INVENTION: MITHOUS FOR PRODUCING RNA VIRUSES FROM NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.58; Score 59; DH 1; Lonath Z20\epsilon; be at local dimitarity 21.08; Fred. No. 1, \epsilon = \epsilon \epsilon. Matches 17; Conservative 17. Mismatches 47; Indels
                                                                                                                                                                                                                                                                           0.5%; Score 59; DR 4; Lorath 1809; 41.4%; Pred. No. 12+03;
                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUPTWAKE: Patentin Release #1.0, Version #1.29 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                      2070 LLKTRDSSPRVRFAALITVLALAEKLEENYIVLLP 2104
                                                                                                                                                                                                                                                                                                                                                                                                 419 IVETIIOSSPELPSTAMPILSSIVE_01GKKYOTFIP 453
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Best Local Similarity 41.4%; Pred. No. 10403
Matches 11: Congervative 12: Mismatches
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COMFULER: IRM PC COMPATIBLE
OPERATING SYSTEM, PC 1/0/S/MS-1/0/S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application 08/07852260
Patent No. 5525715
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REGISTRATION NUMBERS 28.678
REITHERMOLYS STREET NUMBER: 30.
IELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
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TELEPAX: (212) 664-0525
TELEX: 422523 COOP UI
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                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1809 amino acids
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LENGTH: 2206 amino acids
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                                             617-832-7000
                                                                INPORMATION FOR SEQ ID NO.
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US-07-852-260-2
                                                                                                                                                     TOPOLOGY: linear
MolECULE TYPE: protein
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                                                                                                                         TYPE: amino acid
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CITY: New York
STATE: New York
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                                                TELEFAX:
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Matches
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APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks Levy, Carolyn L.
TITLE OF INVENTION: MEHHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 59; DB 2; Length 2206; 21.0%; Pred. No. 1.3e+03; tive 17; Mismatches 47; indels
                                                                                                                                                                                                          APPLICANT: Racaniello, Viucent
APPLICANT: Tatom, Joanne M.
APPLICANT: Wecks-Lovy, Carolyn L.
TITLE OF INVENTION. METHODS FOR FROIDCING KRA VINCEES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9
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Patentin Release #1.0, Version #1.25
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STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/461,503 FILING DATE: 5-JUN-1995
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; Patent No. 6136570
; GENERAL INFORMATION:
                                                                                                                                              Sequence 2, Application US/06461503
Patent No. 5834302
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC compatible
SYSTEM: PC-DOS/Ms-
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TELECOMMUNICATION INFORMATION:
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541 PELFKEHESSEVLISNILMLF 561
                                        681 FAMWRITYKDIVQLRRKLEFF 701
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TELEFAX: (212) 34-0425
TELEX: 42223 COG UT
TELEX: 42223 COG UT
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NAME: White, John P.
REGISTRATION NUMBER: 28,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2206 amino acids
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Best Local Similarity 21.0%
Matches 17; Conservative
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US-08-461-503-2
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                                                                                                        RESULT
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481 TSLMLSLNHPLAPVRILAMNHLKKIMKTSKFGVDESFIKRAVLARLGDDN1DVVLSA1SA 540
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APPLICANT: Chico, Pavid Y.
APPLICANT: RILET, William J.
TITLE O: INVENTION: NANBV Diagnostics and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
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                                                    1185 Avenue of the Americas
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                                                                                                                                                                E. Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       Patentin Release 1.30
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; Patent No. 6150087
                                  Cooper & Dunham LLP
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681 FAMWRITYKRTVQLRPFLEFF 701
                                                                                                                                                                                                                                                                                                                                                   28,678
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                                                                                                                                                                                                                                                                                                                                                                                                     : (212) 278-0400
(212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2206 amino acids
                                                                                                                                                                                                                                                                       6-JUN-1995
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NUMBER OF SEQUENCES: 9
                                                                                                                                               COMPUTER READARLE FORM:
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                                                                                         New York
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CLASSIFICATION:
                                                                         CITY: New York
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                                    ADDRESSEE:
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Bost Gorda Similarity (4.5%) Prod. No. 1.4e+03;
Marches To. Conservative 9; Mismarches TO. Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NANHY Diagnostins and Vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Earland Beloase #1.0, Vorsion #1.8)
CURRENT APELICALION DATA:
APPLICATION ROMBER, 03/09/011 Ala
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                                                                                                                       NAME: Hittin, Alisa A.
RESISTEATI WINNERS: CC. 8055
REPERINT AND MERCE. COLLEGE
RESPONDENTIAL NUMBER: COLLEGE
RELEPHYNE: (500) 350 4875
RELEPHYNE: (504) 350 4875
RELEPAX: (504) 350 4875
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ATT-PREZAGNI OKESMATESN.
APPLITATION NUMBERS 198 / 1/2000 00
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APPLICANT PARTICLY, WILLIAM I TITLE OF INVENTED WELLIAM I TITLE OF INVENTED WELLIAM I TITLE OF SEQUENCES. 777
PARTICLE OF SEQUE
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CAMEUTER: ISM PC compatible
OPERATING SYSTEM: PCLOS/MS LOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : Sequence 75. Application OS/08444438
: Futest No. 615c 087
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REPERENCE/D. NED MYMER: 3. 3.
RELETAMMONIATION INFORMATION.
IELEPHENE: (5.04) 654 6976
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(NE EMATION ELP SE, III NOT 75)
                                          FILLING CATE: 14 MAR-1995
ATT-ENEX/AGENT INFORMATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 226) unino acids
unino acid
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ON CHARGE TYPE: protects
ON CHARGE AND SAGE
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18 oct-444-819 75
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OMPOTER READARLE FORM:
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PPL & APPLICATION DAIA:
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US 08 444-818-75
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Score 59; 108.4; Tongth 2436; Pred. No. 1,6e+03;

chery Math Pest Local Similarity

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Best Garal Similarity 31.4%; Pred. No. 1.7e+04;
Matches 11; Censervative 12 Mismatches 12; Indels
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                                                                                                                                                                                                                                            Immunosuppressant larget Proteins
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APPLICANT: Chico. David Y.
APPLICANT: Kutter, William J
TITLE OF INVENTION: MANBY Diagnostics and Vaccines
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  J Mismatches
                                          1821 VILLATERTYRQIEKNWKNIIMGPFMSILO 1843
                                                                                1295 VIAPAVQINWQKLETEWAKHMWNF;SGIQ 1323
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APPLICATION BANA:
APPLICATION BANG:
57 BAY:
FILING DATE:
PRIOR APPLICATION DATA:
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: Sequence 12, Application PC/TUS9506722
: GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DGS/MS-DGS
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Patent No. 6150087
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LENGIH: 2549 amino acids
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  10, Concertabilde
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                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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SIKEET: 40cc
TIV: Emeryville
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Materia
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CORPERTYOR STOURAGES.
                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.5%; Score 59; DB 4; Length 2772; Hest Local Similarity 34.5%; Pred, No. 1.9e+03; Matches 10; Conservative 9; Mismatches 10; Indels
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118,708,74 n.2, e.q.n.
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                                                                                                      0110.002
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SYSTEM: PC-FOS/MS-FOS
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Patent No. 5910404
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APPLICANT: VAN HEGVERSWUN, BUGO
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                                                                            33,895
                                                                                                REFERENCE/FOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             TELEPAX: (508)359-3885
INFORMATION FOR SEQ ID NO. 89.
SEQUENCE CHARACTERISTICS:
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APPLICANT: DELEYS, ROBERT J
APPLICANT: POLLET, DIRK
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                 FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION.
                                                                                                                                             (508)359-3876
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                              2772 amino acids
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                                                          NAME: Harbin, Alisa A. REGISTRATION NUMBER: 31
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MOLECULE TYPE: protein
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APPLICATION NUMBERS
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OPERATING SYSTEM:
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3Y. linear
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                                                                                                                                                                                                          0.5%; Score 59; DB 2; Length 2894;
34.5%; Pred. No. 2e+03;
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                                                                                                                                                                                                                                               Mismatches
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FILING DATE: 14-OCT ASS.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT,/PP01,/02409
TWG DATE: 13-DEC-1991
                                                                                                                                                                                                                                                                                                         1821 VILIPATEKTYKÜLEKNWENHIMGPEMSILQ 1849
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// Patent No 5922532
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Best Local Similarity 34,5%; Pro
Sect Local Similarity 34,5%; 9,
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IBM PC compatible
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INPOPMATION BOR SPO ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DELEYS, ROBERT J
POLLET, DIRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 14-DEC-1990 ATTORNEY/AGENT INFORMATION:
              SEQUENCE CHARACTERISTICS:
LENGTH: 2894 amino acids
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                                                                                                     MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                      amino acid
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STPANDEDNESS: Sir
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US 08:466-975A-23
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                                                                   STRANDEDNESS:
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                                                                                         POPOLOGY:
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                                                      TYPE:
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Matches 10; Conservative
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APPLICANT: VAN HERSERBINA, HEGO-
LITLE OF INVINCENCE SYNCHIET C. ARTHURS FOR FIRE BETESTE IN OF
TITLE F. INVENTEON: ANTER GLES TO HERSALITIES C. VIEGS
                                                                                                                                                                4.5%; Gran 59; LW 2, Langth 2854, 44.5%; Prod. No. 2006; E
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C-MOUTE: EM P-Composition
C-PERATING SYSTEM: PCTS/MS 1-38
SPETMARE: Batedin Refease #1.0, Version #1.60
CHREENT APPLICATION DAIN:
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TO TAT VIANAVIONGELER WARRANNERS (77)
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PERSENTATION DATA.
APPLICATION NAMED: 0.708/001.071
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TELETOMMUNITALI ON INFORMATION:
TELETOHONE: 2074/164000
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MacEntre IYer peptade
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NAMPUIER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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PESTSTRATION MUMBER:
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FILENS DATE:
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SIRANIEDNESS: sin
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CANTESENSE: NO
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APPLICANT: VAN HEUVERSWUN, HOAG
TITLE OF INVINCEDEN: SYNTHEILT APPLIERS FOR THE DELECTION OF
TITLE OF INVENTION: ANTIBODIES TO HEPATITIS C VIEUS
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Best Local Similarity 34.5%; Pred, No. 20004;
Matches 10; Conservative 9; Mismatches 10; Indeis
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APPLICATION NUMBER: US/09/275,265
  9: Mismatches
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13-DEC-1991
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                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: EF 50134241.2
FILING DATE: 14-DEC-1950
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AFPLICATION RUMBER: 03/08/301.671
FILLIO DAIE: 21-FEB-1995
ALDIGATION HERRER: 03.07/020.286
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TELEXORMONICATION INFORMATION
                                                                                                                                                             US-U9 275-265-24
: Sequence 23, Application US/09275265
: Patent No. 6287761
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APPLICANT: POLLET, DIRK
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COMPUTER READARLE FORM:
MEDIUM IYPE: Floppy o
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APPLICATION NUMBER: V
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HYPOTHETICAL: NO
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CORRESPONDENCE ADDRESS:
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TELEPHONE: 7048164100
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                                                                                                                                              RESULT 64
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us-09-603-665-5.rai

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/note= "There is a heterogeneity at
this location; Xaa - Asm or Tyr"
                                                                                                                                                                                                              TITLE OF INVENTION: HEPATITIS C VIRUS ASIALOGLYCOPROTEINS NUMBER OF SECIENCES: 3
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this location; Xaa - 11e or Leu"
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17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                    US-08-443-260-4
; Sequence 3, Application US/08443260
; Patent No. 5942234
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
                                                                                                                                                APPLICANT: THUDIUM, KENT B.
APPLICANT: GERVASE, BARBARA A.
APPLICANT: HALL, JOHN A.
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                                                                                GENERAL INFORMATION:
APPLICANT: RALSTON, KOBERT O.
                                                                                                                                                                                                                                                                          ADDRESSER: Chiron .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : (510) 601-2708
(510) 655-3542
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ATTORNET/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
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FILING DATE: 17-MAY
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STATE: California
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44.58; Fred. No. 2.1e+03;
1729 9; Mismatches 10, Indels
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APPLICANI: CHWASE, BARGARA A.
APPLICANI: CHWASE, PABN A.
ICHIE PETERMICHE. HERALITIS C VIROS ACHAISALIZMA FOTEINS
NUMBER OF SEQUENTES: 4
difficiency PMATEN: Zhote "there is a heterogeneity at fifth INF-BMATEN: This focution; Xaa - Art or Gly"
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this location: Xaa Asn or The"
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TREENL APPLICATI N EARLS
PILING DATE: 17-MAY 1095
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computer; IGM PC computible
openATING SYSTEM: POTIOS/MS that
                                                                                                                                                                                                                                                                                                                                         September 3. Application 98/98442897A
Patent No. - 34445
SENERAL INFORMATION:
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ALGRESSEE: Thiron Torporation.
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PELISTALIAN NUMBER, C, 893,
PERIFENTIAN WERE, C, 893,
PELISTAMMONICATION INFRAMETRAL
                                                                                                                                                                                                                                                                                                                                                                                                          PALSION, ROBERTO. MAROUS, FRANK
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MCETTE IYEE TYPE: profesio
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Patent No. 6074852
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APPLICANT: GERVASE, BARBARA A.
APPLICANT: HALL, JOHN A.
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REFERENCEZOCKET NUMBER: 015
TELECOMMUNICATION INFORMATION:
TELEPAX: (510) 601-2768
TELEPAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 4:
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IBM PC compatible
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STREET: 4560 Horton Street
CITY: Emeryville
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NAME/KEY: Modified-site

us-09-603-665-5.rai

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Fost Lords Statistity (4.5%) Prod. No. 2. 1003.

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this Location, Xaa - 31y of Ard"
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this Location; Xan Phe or By:"
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APELICANT: Oliver Javid F.
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ETLE OF INVENTY N. MARRY Liabouring and Vacuiens
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ATTEMPS AND INFERNATIONS
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4ft: Horton Steet
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MPTIBK PEALANIE F PM:
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Xaa which is either He or Har"
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                                              INFORMATION FOR SEQ ID NO: 124: SEQUENCE CHARACTERISTICS:
TELEPHONE: (508) 459-3876
                                                                                                      LENGTH: 2955 amino acids
                           (508)359-3885
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APPLICANT: GERVASE, BARBARA A.
APPLICANT: HALL, JOHN A.
TILLE OF INVENTION: HEPATITIS C VIKUS ASIALOGLYCOPROTEINS
NUMBER OF SROGENESS: 3
CORRESPONDENCE AND KESS:
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OTHER INFORMATION: Xaa which is either Thr or Ser"
                                                                                                                                                                             Znote. "A heterogeneity exists at
Xaa which is either Tyr or Phe"
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Xaa which is cither Ang or 61;"
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OTHER INFORMATION: Xaa which is cither Gly or Val"
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SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Patent No. 6274148
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NAME: HARBIN, ALISA A.
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Best Local Similarity 34.59
Matches 16; Conservative
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LOCATION: 2349
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REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0154 003
TELECCHMUNICATION INFORMATION:
                                                           TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 3:
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APPLICANT: Parton, David Y.
APPLICANT: Perform William J.
LILE OF INVENTION: NANK DIAMOSTICS and Vaccines
NUMBER OF SECTION: NANK DIAMOSTICS and Vaccines
APPESPONICAL ADGRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DMINT
                                                                                                                                                                                                                                                                                               NAMELTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEAT TREE
                                                                                                                         4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PESSIE:
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Objecty Match 0.5%; Score 5%; 108.4; Tendth 29%; Best Local Similarity 44.5%; Fred. No. 2.1er03; Matches 10; Conservative 9; Mismatches 10; Indexis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAMMALIAN EXPRESSION SYSTEMS FOR HOY MITTED OF INVENTION: PROTEINS
                COMPUTER: IRM PC Compatible CARACLES SYSTEM FO POSZES DOS NO SOFTWARE: Patentin Release #1.0, Version #1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: ABBOTT LABORATORIES DA77/APED OBE ABBOTT PARK ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1821 VLLPATRELYROTERNWENEMGPPMSTLQ 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33,207
ER. 5141.US.D1
                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: INSZMYAD3.590
FILING DATE: 14-MAR-1995
ATTORNIY/AGREET INVAMATION:
                                                                                           TS,TP, 444,818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Trey YOR, YTS 4, 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 71
US-08-453-552-2
: Sequence 2, Application US/0845-552
: The No. 5657992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGBNT INFORMATION:
NAME: POREMBSKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
                                                                                                                                                                                                                                                                         REFERENCE ORET NUMBER. 671
TELENOMMUNICATION INFORMATION:
TELEPHONE: (508) 359-3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE TROUGHT NUMBER. 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                         NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
                                                                                                                                                                                                                                                                                                                                                            INPORMATION FOR SEQ ID NO: 138: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: DEVARE, SUSHIL G. TITLE OF INVENTION: MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BODE, SUZANNE L. ZEFK, BILLY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JULIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FRAIL, DONALD E. APPLICANT: DESAI, SURESH M.
                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH. 2995 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
MEDIUM LYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION - APPLICANT: CASEY, JAMES M.
                                                                          CORRENT APPLICATION DATA:
APPLICATE & MOMBER (18)
                                                                                                                                                                                                                                                                                                                                         (508) 359-3885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein US-08 444-818-138
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                                                                                                                                       CLASSIFICATION, 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATION NUMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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                                                                                                                    FILING DAFF:
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1745 VIAPAVQTNWOKLETFWAKHMWNFISGIQ 1773

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APPLICANT: Weiner, Amy J.
TITLE OF INVENTION: Lamuscreative Polypeptide Compositions
NUMBER OF SEQUENCE: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 59; DB 1; Length 3011;
34.5%; Pred. No. 2.2e+03;
ive 9; Mismatches 10; Indels
                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 34.5%, Prod. No. 2.2e+03;
Matches 10; Conservative 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                1745 VIAPAVOTNWQRLETFWAKHMWNF1SG1Q 1773
                                                                                                                                                                                                                                                                                                          1821 VLIPAIEETVEGIEFNWENHMOFFMSTIG 1849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: MCCLang, Barbara G. REGISTRATION NUMBER: 33.113 REFERENCE/DOCKET NIMBER: 0205.001 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US/08/231,368
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COMPUTER: IBM PC compatible
OPEKATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36, Application US/U6440105
Patent No. 5670152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (510) 601-2708
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ 1D NO: 36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Chiron Corporat
STREET: 4560 Horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.5%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3011 amino acids
                                        SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 34.5%
Matches 10: Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-440-103-36
TELEFAX: 708-937-9556
                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-MAY-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                      single
                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-453-552-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emeryville
                                                                                   amino acid
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                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94608
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                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 72
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APPLICANT: Houghton, Michael
APPLICANT: Choo, Qui-Lim
APPLICANT: Choo, Qui-Lim
APPLICANT: Choo, Good-Lim
APPLICANT: Conc. Good-Limaticus of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                             APPLICANT: Weiner, Amy J.
APPLICANT: Houghber, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
UNMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iu; Indels
                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.25
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34.5%; Pred. No. 2 2r+03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/231,368
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                                                                                                                                                                                                                                                                                                                                                                                                             115,408,4410,542
                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 10, Application US/07910760
; Patent No. 5683864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
APPRESEE: Chiron Corporation
STREET: P O ROX 8097 (Int. P
              Sequence 36, Application US/08440542; Patent No. 5670153; GENERAL INFORMATION:
                                                                                                                                                                            ADDRESSEE: Chiron Corporation STREET: 4560 Horton Street.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (510) 601-2708
(510) 655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McClung, Barbara G.
                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-SEP-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3011 amino acids
                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPERENCE, COCKET NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.59 Best Local Similarity 34.5^\circ Matches 10^\circ Conservative
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-440-542-36
                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                               APELICATION NUMBER
                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                       STREET: 4500
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                                                                                                                                                                                                                                                            USA
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US-08-440-542-36
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                                                                                                                                                                                                                                                         COUNTRY:
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1821 VIIPAIRKIYEQIRKNWKNHMGZEMSILQ 1849

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APPLICANI: Horehten, Michael
APPLICANI: Horehten, Michael
APPLICANI: Choo, 2011 tim
APPLICANI: K.D., Sente
1111E PE INVENTENE: National Antidens of Heparitis (TETERS (HTV)
1111E PE INVENTENE: Antidens for Use in Immunoassays for Anti-HCV Antibodies
NUMBER OF INVENTENE: 12
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FILM DAIN: 0.7 TH. 1042
TASSIFFEATION: 4.6
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1911-1992
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PMEDIEF: LAM PC compatible
PEPALINI SYSTEM: ForewS/MS to S
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PUBLISHER ALTON MARKET COURSE. PETERN ROBOTE: COURSE COURSE OF THE NAME 
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PERALIN'S PRITHE P. L. JAME
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HELEPAX: (710) 9 9 642
INPHANTI N F 8 852, 13 No. 100
SEGUENTE HAPATERISTINS:
HANTHE 6011 milios actids
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TASSEPOATEN: 435
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APPLICANT: Hondhion, Michael
ITLLE OF INVENTION: Immunolearlive Folypeptide Compositions
UNIMBER OF SEQUENCE: 45
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                               Lemath will:
                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.5%; Pred. No. 2.2e++++;
Matches 19, Conservative 9, Mismatches 19, Indels
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COMPUTER: 1BM PC COmpatible
OPERATING SYSTEM: PC-1005/MS-1005
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; Sequence 36, Application US/08241368
; Patent No. 5756412
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REGISTRALION NUMBERS 3 4.111
REFERENCY/SCCKET NUMBER: 0.1
TELECOMMUNICATION INFORMATION:
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TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 46:
TELEPHONE: (510) 601-2702
TELEFAX: (510) 655-3542
INEXEMATION FOR SEQ 1D NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
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LENGIH: 4011 amino acids
                                                                                   3011 amino acids
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APPLICATION NUMBER: UNVETLING DATE:
CLASSIFICATION: 435
                                                             SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
9E 08 231-368-36
                                                                                                                                            ; MALECULE TYPE: protein
US-08-440-519-10
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MEDIUM TYPE: Floppy
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                                                                                                    TYPE: amino acid
loPoLoGY: linear
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GENERAL INFORMATION:
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                                                                                             APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
TITLE OF INVENTION: Immunoreactive Polypeptide Compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0205.001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           ИМВБК: US/08/440,210
12-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us 07/759,575
                                                                                                                                                                                                                                                                                                                                    G: Floppy disk
18M PC compatible
SYSTEM: PC-DOS/MS-DOS
                                 Sequence 46, Application 05/08440210 Patent No. 5766845
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Patent No. 5854001
                                                                                                                                                                                               Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33,113
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APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVARE, SUSHIL G.
                                                                                                                                                                                                                SIREEL: 4560 horton Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (510) 601-2708
(510) 655-3542
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APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07 FILING DATE: 13-SEP-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ⊀011 amino acids
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Best Local Similarity 34.5%
Matches 10; Conservative
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MOLECULE TYPE: protein
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION MIMMER C
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                                                                                                                                   TITLE OF INVENTION: INM
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
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                    US-08-440-210-36
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RESHLT 77
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TITLE OF INVENTION: HELICASE ACTIVITY AND IMPROVED SOLUBILITY
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34.5%; Fred. No. 2.2e+03;
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                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
ADDRESSES: ABBOTT (ABORATORIES D377/AP6)
STREET: ONE ABBOTT PARK ROAD
CITY: ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1821 VELPATKETYPÕTFKNWKNHMCPFMSTLÕ 1849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5131.08.01
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/144,099
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: IIS 07/830,024
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/710,637
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                                                                                                                                                                                    PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                             POREMBSKI, PRISCILLA E.
                                                                                                                                                               COMPUTER: IRM PC compatible
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APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, GUI-LIM
APPLICANT: HAN, JANG
APPLICANT: CHOO, JONHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                              Floppy disk
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                                                                                                                           COMPUTER READABLE FORM:
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California
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FEATURE:
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; Patent No. 6150087
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Matches 10; Conservative
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LOCATION: 2386
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Acterogeneity at this position - Xaa = Tyr or
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANEV Diagnostics and Vaccines
                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.30
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FILING DATE: 14-MAR-1695
ATTORNEY/AGENE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 115 718 7144,818
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                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                  Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 177: SEQUENCE CHARACTERISTICS:
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                                                                                              ADDRESSEE: Chiron correct correct.
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APPLICATION NUMBER 11S
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                    ZIP: 94608 2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                CORRESPONDENCE ADDRESS:
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Host Local Similarity (44.9%) Prod. No. 2.2e+0.0

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GENERAL INFORMATION:
APPLICANT: Weiner, Amy J.
APPLICANT: Houghton, Michael
APPLICANT: Houghton, Michael
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34.5%; Pred. No. 2.2e+03;
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TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
TITLE OF INVENTION: TREATING C HEPATITIS
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34.5%; Pred. No. 2.26+03;
Live 9; Mismatches 10;
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SOFTWARE: PastSEQ for Windows Version 3.0
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EARLIER APPLICATION NUMBER: 97/02,887
EARLIER FILING DATE: 1997-03-06
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GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, GOOT-LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: CCMBINATIONS OF HEPATITIS C VIRUS
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02225
                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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545 Middleffeld Road, Suite 200
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FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER - USZONZO46,604
                                                                                                                                                        PREDIUM TYPE: Floppy disk COMPUTER: TBM PC COMPALIBLE OPHRATING SYSTEM: PC DOS/MS-DOS SOFTWARE: Patentra Patentra
              CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 45k0 Horton Street.
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ATION NUMBER: 33,113
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TELEPAX: (510) 655-3542
INFORMATION FOR SRQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 3011 amino acids
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APPLICANT: Tackney, Charles T.
APPLICANT: Snowwest, John N.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Cysteine Depleted IL-6 Muteins
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                                                                                                                                                                                                                                                          ABBOIT LABORATORIES D377,7AP62
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180 Variek Street
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** 5131.PC.01
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                       Sequence 2, Application PC/FUS9300907
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NAME: POREMBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
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; Patent No. 5545537
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TELECOMMUNICATION INFORMATION:
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                                                     APPLICANT: CASEY, JAMES M.
APPLICANT: BODE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
                                                                                                           JULIE
                                                                                                           APPLICANT: YAMAGGCHI, JULIE
APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
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Best Local Similarity 34.55.
Fee 10; Conservative
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United States
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PCT-US93-00907-2
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NUMBER OF SUQUENCES: 2:
COKRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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CITY: New York
STATE: New York
COUNTRY: United
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PC1 - US93 - 00907 - 2
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22.5%; Pred. No. 40;
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APPLICANT: Tackney, Charles T.
APPLICANT: Snowwactt, John N.
APPLICANT: Fowlkes, Dana M.
APPLICANF: Fowlkes, Dana M.
NUMBER OF SEQUENCES: 8
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                                                                       SOFTWAPE. PatentIn Palease #1 0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                            IMBER: US/OB/200,182C
10-MAR-1994
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                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
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                                                                                                                                                                                                                                                                                                          TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
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NAME: FCit, Irving N.
REGISTRATION NUMBER: 28.6
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                                                                                                                                                                                       FILING DATE: 02-THL-1991
ATTORNEY/AGENT INFORMATION:
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                Floppy disk
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Bost Local Similarity 22.5%
Consorvative
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COMPUTER PEADABLE FORM:
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FILLING DAPP: 02-IIII
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                  MEDIUM TYPE:
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APPLICANT: DelVerchio, Altred
APPLICANT: Zhong Weidond
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FILLE SE BWENLION: AFPASE PROTEIN FROM A VIRUS SE THE FLAVIVIETDAE FAMILY
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APELLIALIA NUMBER: 38/20/100.557
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709 Swedeland Road
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NAMES JERNOTA GALA GA
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SOMFUTER: IBM COMPATIBLE
COPERATING SYSTEM: DOS
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LENGTH: 250 amino acids
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18: Conservative
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Agreements (Chasen
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CURRENT APPLICATION DATA:
APPLICATION BURBER, US,08,722,932
1801 VILLEATERTIE, HORMWERSENDER 1849 1849
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APPLICATION NUMBER: US/07/718,572
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CITY: Charlotte
STATE: No. 5468634th Carol na
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CITY: Charlotte
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TELECOMMUNICALLON INFORMATION:
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MEDIUM TYPE: Floppy disk
O'MMITTER: IBM P1 Compatible
O'FEMATING SYSTEM: P2 Des/MS-DOS
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IIILE OF INVENTION: AXL ORCOGENE
OWHER OF SEQUENCES: 6
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TITLE OF INVENTION: AXE Oncodeno
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08372892
Patent No. 5468634
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: NO. 5468634th Carolina CobnTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application 08/08472892
Patent No. 5468644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31,665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           919-881-3140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
PopoloGY: linear
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TELEFAX: 912 ...
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                                                                                                                                                                                                                                               RESULT 89
US-08-372-892-4
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us-09-603-665-5.rai

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1210. TERLIQHERALESIVEL VETERNIA SPOTEPE PORQANMEYTAVETTASOLI NTOVKIAPE 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 58; i6 1; bength 894, 25.0%; Pred. No. 4.7e<sup>(02)</sup>
Live 15; Mismatches 30, Indels
                                                                                                       Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: 5.25 inch, 860 Kb Hoppy disk
IBM PC compatible
SPSTEW. ACT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/08/445,640
                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: 03/08,372,892
                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/718,572
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STREET: 460 Point San Bruno Blvd
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                                                                                       euri MS inus
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FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                             31,665
                                                  i: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKEL NUMBER: 54
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie R.
APPLICANT: Scadden, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                             : 894 amino acids
amino acid
                                                                                                                                                                                                                                                                           Sibley, Kenneth D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 25.0%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                   919-881-3175
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MEDIUM TYPE: 5.25 inc
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                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                           NAME: Sibley, Kennet REGISTRATION NUMBER:
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                                                                                       OPERATING SYSIEM.
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COUNTRY: U.S.A.
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TELEFAX: 91.5
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                                                                                                           SOFTWARE:
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                                                                      COMPUTER:
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1210 ILECLÖHKKKLESPQILVPTLENIJSPCTEPT-PQEQGNMBYTKQLJTSCILATCOKLSPD 1269
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                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                 Length 894;
                                                                                                                                                                                                                                                                                                                                                    30; Indels
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25.0%; Pred No 4 7e+02;
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein Tyrosine Kinases
                                                                                                                                                                                                                                                                                                                                                      15; Mismatches
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20-DEC-1993
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FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
                       fNPCpt...
Janet E.
Jan. 28,616
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                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Godowski, Paul J. APPLICANT: Mark, Melanie R.
                                                                                                                                              TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34:
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APPLICANT: Baker, Kevin P.
APPLICANT: Haron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     South San Francisco
California
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 25.0%;
Matches 15; Conservative
FILLING DATE: 23-NOV-1993
ATTOPNEY AGENT INFORMATION:
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: 415/952-9881
910/371-7168
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                                                                      REFERENCE/POCKET NUMBER:
                                                                                                               415/225-1896
415/952-9881
                                                                                                                                                                                                             LENGTH: 894 amino acids
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                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                      REGISTRATION NUMBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS
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FILING DATE: 20-DEC
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                                                                                                                                                                                                                                              linear
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                                         Hasak
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                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                US-08-445-640-34
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12 by TUBLOHREP PERCHAMENANCE FREE PRESENTANCE OF COLUMN 2007 (1697)
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                                                                                                                                                                                                             O: Gaps
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Scott 98: LB 3: Tength 894; Best Local Similarity 25: Mg Pred. No. 4.76-02; Marthes 15: Answerentive 15: Mismatches 69: Undels
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Ford Similarity 21.0% Prod. No. 1.70002;
os. 17. Conservative 15. Mismatches so. Indols
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AFELL MATER WORRES COMPANY.
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BOMED of DECENTIO, 35
VERESPONDENTE ALCRESS:
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46c Point San Branc Bled
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See period (44) Application US/PR445461
Februari No. 9, 96527
FEREFAL UNERRHALLOW
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APPLICANT: Mark, Meianie k.
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RETISTRATON NUMBERS
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25.0%; Pred. No. 4.7e+02;
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Matches 15, Conservative 15, Mismatches 30, Indels
                                                                                                                TITLE OF INVINCENT: Protein Pyrosine Kinases
HUMBER OF SPOUPWORS: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 36) Kb Hoppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sima Lev
APPLICANT: Joseph Schiessinger
TITLE OF INVENTION: PYKZ REALERS FROMERS
TITLE OF THEORY AND METHODS
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.5" Diskette, 1.44 Mb
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                                                                                                                                                                                                                                                                                    460 Point San Bruno Blvd
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TELEP MARINICATION INFORMATION:
FLICTH 4H: 415,222-1896
FLICTH 4H: 415,925-1896
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STREET: 634 West Fifth Street
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APPLICANT: Scaddon, David T.
APPLICANT: Baker, Kevin P.
APPLICANI: Baron, Will F.
                                                                                                                                                                                                                                                  Genentech, Inc.
                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/15
FILING DATE: 23-NOV-1993
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ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGIH
                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIREET:
                                                                                                                                                                                                                                                                                                                                                                  SIAIE:
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storage

MEDIUM TYPE:

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RESULT 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 58; PM 2; Length lubs;
23.3%; Prod. No. 5.60.02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1203 YWQRVTLILELLOHKKKIRSPOILVPTLPNLLSRCLEPLPQEQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :| :: :(: ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| 
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FORESPONDENCE 25

CORRESPONDENCE 1250 6 Lyon
STREET: 633 West Filth Street
STREET: 613 West Filth Street
STREET: 501te 4700
CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1 CURRENT APPLICATION DATA:
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
                                                                                                                                                                           APPLICATION NUMBER: US/08/357,542A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/460,626
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REPERENCY/OCKET NUMBER: 211/121
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.400,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December 15, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/357,642
                                                                                                                                                                                                               December 15, 1994
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Patent No. 5837815
GENDRAL INFORMATION:
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APPLICANT: JOSEPH SCHLESSINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32,327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (213) 455-0440
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AFFLICATION NUMBER: US/08/
FILING DATE: June 2, 1995
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,3 PEFERENCE,TWORFT NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
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10; Conservative 1
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                                                                                                SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLEGHLE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
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Best Local Similarity
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                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-357-642A-1
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38.5%; Pred. No. 1.3e+03;
tive 6; Mismatches 10; Indels
                                                                                                                                                                                                                                       Length 1009;
                                                                                                                                                                                                                                       0.5%; Sovre 58: DR 2; Londth 1005
23.3%; Pred. No. 5.60:02;
ive 13; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                             1203 YWQRVTLILELLQHKKKLRSPQTTVPTLFNFLSPCTRPTPQEQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Covacci, Antonello
IIII. OF HAVENTION: Helicobacter Priori Carl Region
HUMBER OF SEGURNORS: 46
CORRESTONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0335,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/08477451
Patent No. 5928865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33,113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4560 Horton Street
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: McClunq, Barbara G. REGISTRATION NUMBER: 33,1
                                                       INFORMATION FOR SEQ ID NO: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1781 amino acids
                                                                                                                                                                                                                                                          23.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 510-601-2708
510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE, TOOCKET NIMBER.
                                                                                                                                                                                                                                                          Rest Local Similarity 23.3%
Matches 10, Conservative
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                                                                         SEQUENCE CHAPACTERISFICS.
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                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94608-2916
COMPUTER READABLE FORM:
                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER.
FILING DATE: 07-JIB
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                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Emeryville
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                                                                                              1009
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                                                                                                                                                                                       US-08-460-626-1
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                                                                                            LENGTH:
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                                                                                                                                                                                                                                           Query Match
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613 OTESSEMETATS CHARLES STORED STORES AND ALL CHARLES CHARLES CHARLES AND ALL CLARAST 1972
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Lord Similarity 29,39, Fred. No. 2, Sects.

Prod. No. 2, Sects.

Prod. No. 2, Sects.

Prod. No. 2, Sects.
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                                                                                           BUTON AND ASSESSED FRANCIS D.
APPLICANT: FURBLIDA, FRANCIS D.
APPLICANT: PASTERNA'K, CARY A.
LITLE OF INVENTION: TANEER RELAIED ANTIGEN
NUMBER & SECTEN'ES: 14
'OFFESSED NIENTE ALGERSS:
ACCERSEED NAKER & BOTIS, LILLE.
STREET: LOO PORREYLANDIA APPLICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FASTSED VOTSTOR 1.5
TREEN APPLICATI N GATA:
APPLICATION NUMBER: US. 008 445 0, 008 A
                                             Section 2015 April Continue 1987 (646 of A. Paten). No. 1965 5874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLITATION NUMBER: CB/CPA, FOR FILLING TATE: WITHOUT 1994
APPLITATION NUMBER: CA7/917,715
FILLINGTALE: 24 FOL 1992
ALL ENEX/AGENT TINE SEMALEON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174/148,424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCY SYRET MOMBE. 35. HOLES AMMUNETAL ON THE SEMALE O
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IRM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 JAN 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILLING DATE: 05-00N-1995
CLASSIFICATION: 5.86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2509 amino acids
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SPANHEDNESS: Shorto
Fobolo Incar
M. LEVIGE VPEE: profein
HVP (1851, AL) No.
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COMPUTER REALABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
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Farout No. 6127116
GENERAL INFORMATION:
APPLICANT: FIRE
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935-08-811 566-20
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APPLICANT, Emerson, Susanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION, CLONED GENERES OF INPECTIOUS HEIALITIS C VIPUSES AND
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                                                               MIGRESSEE: Invita A. Jackson, Esq.
STREET: 411 Hackensack Ave. Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.30
TITLE OF INVENTION: VIRUS (HCV) AND USES THERE F
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CORRENT APPLICATION NUMBER: US/09/014,416
CURRENT FILING DATE: 1998-01-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Jackson Esq., David A. BELETATION THREES. 26,742
REFERENCE/LOCKET NUMBER: 1 14-1-006
TELECOMMONICATION INPORMATION
                                                                                                                                                                                                                                                                                                                                                                                 995,018,2801,566
                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DGS/MS DOS
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; Patent No. 6153421
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NUMBER OF SEQ ID NOS: 65
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INFORMATION FOR SEQ ID NO: 20:
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GLASSIFICATION: 435
ATTORNEY/ASERF TREORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : GENERAL INFORMATION:
: APPLICANT: Yanaqi, Masayuki
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                                                CORRESPONDENCE ADDRESS:
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                         NUMBER OF SECUENCES:
                                                                                                                                         CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                          COUNTRY: 07501
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0.5%; score 58; DB 4; Length 3011;

Query Match

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TELEPHONE:
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APPLICANT: Enterit, Kolorit H.
TITLE OF INVENTION: CLANED GENERAL OF INFECTIOUS HEPATITIS C VIRUSES AND TITLE OF INVENTION: USES THERROP
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1 Similarity 34.5%; Score 58; DB 4; Length 3011;
1 Similarity 34.5%; Pred. No. 3e+03;
10; Conservative 9; Mismatches 10; Indels
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TITLE OF INVENTION: FUNCTIONAL DNA CEONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
34.5%; Fred. No. 3e+03;
tive 9; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave. Continental Flaza, 4th
STREET: Ploor
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                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILLING DATE: 1998-01-27
AMELIER APPLICATION NUMBER: US 60/053,062
EARLIER FILLING DATE: 1997-07-18
NUMBER OF SEQ 1D NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1821 VLLPATKKTYKÇIEKNWKNIMGPEMSILG 1849
                                                            1921 VELBATEPTYFETEFNWFNBMCPPMSTLQ 1849
                                                                                  FILE REFERENCE: 20264276
CUMMENT APPLICATION NUMBER: US/09/014,416
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REFERENCE/DOCKET NUMBER: 1113-1-006
TELECOMMONICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scquence 2. Application 08/3881155b
Patent No. 612716
GENERAL INFORMATION:
APPLICANT: RICE, Charles et al.
                                                                                                                                                                                                   Sequence 5, Application US/09014416
Patent No. 6153421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAME, Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Hepatitis C virus
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                                                                                                                                                                                                                                                                  APPLICANT: Yanagi, Masayuki
                       Conservative
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New Jersey
  Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
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US-08-811-556-2
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                   Matches
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1756 YLLSALAALQKVVETLPHFISPYLFGTLSQVIHLEKITSEMGSASQANIRLTSLKKTLAT 1815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 58; DB 4; Length 3012; 34.5%; Pred. No. 3e:03;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Skelly, Susan M.
APPLICANT: Tackney, Charles T.
APPLICANT: Snouwaert, John N.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Cysteine Depleted IL 6 Muteins
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
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Patentin Release #1 0, Version #1 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
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PILLING THE NUMBER N
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Patent No. 5545537
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                                                                          INFORMATION FOR SEQ ID NO: 2:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                         3012 amino acids
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201-487-5800
201-343-1684
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United States
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Best Local Similarity 34.59
Matches 10, Conservative
                                                                                                                   SECUTION CHAPACTERISTICS:
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REGISTRATION NUMBER
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FRACMENT TYPE.
US-08-811-566-2
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1756 YILSALAALERVVETLIIIITTSPYLIITLISLVI OO OO PELMISASAANI HII GI KRTI AT I JA19
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42. YELVESKURBELORESMOESPINGARANDE PRODUCES, O BELLEAMETTE TO
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                                                                                                                                                                                                                                                                                                            APPLICANI: Lackney, charles I.
APPLICANI: Standard John N.
APPLICANI: Standard John N.
APPLICANI: Poslikes, Lond M.
FILL of INVENTION: Cysteine impleted II 6 Matches
NUMBER 9 SECTEMPES, M.
ADDRESSER: INCLOSE Systems Incorporated
ADDRESSER: INCLOSE Systems Incorporated
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AFFLICANT: Nivora D. Wallis
ITILE OF PROFITEN INVENTED IN NOVELTO'S RESPONSE REDUIATOR
PURMBER OF SEQUENCES: 2
PURMBER OF SEQUENCES: 2
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FILMIND DATE: 1992-0702
FILMIND DATE: 1992-0702
ALT-CHEST FORT IND BRACE IN:
NAME: FORT ITELE IN:
REFERENTEZ ON WIMBER: 28,6-01
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FELEPRONTE 212-645 14(5)
FELEPAX: 212-645 14(5)
INF-PMATION F K-SEQ 15 Not 81
SEQUENTE FILMIND SECOND
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Symputer: IMM PS Sampatible
SPERATINESSEEM: PS 105/MS (05)
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GENERAL INFORMATION:
APPELLANT, GASTILL SASSON M.
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I Sequence 2, Application US/08771008
I Sequence Ac. Application
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1055 DEAMVEHLTLGKYNEFSVSLI NFD ÆSLIDTETRAVHTTRFT YAGMPTTOTTALFRITKIPF 1114
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STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
                                                                                                                                                                                         SOFTWARE: FURLESO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/771,098
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TITLE OF INVENTION: No. 6071894el Compounds
NIMMEP OF SECTINGES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
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20-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                               RELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER 9526351.7
FILING IAME: 22-DEC-1995
FILING IAME: 22-DEC-1995
FILING DATE: 22-DEC-1995
ATTORING PATE: 120-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Sequence 4, Application US/09022875
: Patent No. 6071894
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 38,891
                76. Owedeland Road
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IBM Compatible
                                                                                                                                                      IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38
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                    CIEEE, 70, Swedeland
CIIY: King of Prussia
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                                                                                                                                      Diskette
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US-08-771-098-2
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                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskert
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OPERATING SYSTEM:
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1055 DEAAMVLHITIGKYNEISVSLLHEDFKSLDIFIKAVHTTRELVAGMFTIGITALEETIKFF 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                    Guery Match 0.5%; Srore 57; DB 3; Longth 231; Best focal Similarity 28.3%; Pred. NO. 81; Mantches 17; Conservative 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MERAL INFORMATION.
APPLICANT: John B. Hodgson
APPLICANT: Nicola G. Wallis
TITIE OF INVENTION: NOVEL TOTS RESPONSE REGULATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEO for Windows Version 2.0 SURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/354,040
                                                                        REPERENCE/LOCKET NUMBER: GMSGGG9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215 994 2488
TELEPHONE: 215-994-22.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCYLOCKET NUMBER: F31319 TELECOMMUNICATION INFORMATION.
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APPLICATION NUMBER: 08/771,098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09354040
Patent No. 6217862
GENERAL INFORMATION:
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                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4:
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ATTORNEY/AGENT INFORMATION:
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FILLING DATE: 25-FEB-1997
                  ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 3
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                                       NAME: Falk, Stephen T
REGISTRATION NUMBER: 3
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1055 DEAMVLHLFLGKYNEFSVSLLNEDPKSLD1F1KAVHTTKELYAGMPT1Q1TALEKITKPF 1114
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20 A%; Prod No lo+02;
0.54; Score 57; DB 4; Length 231; 28.38; Pred. No. 81; tive 15; Mismatches 28; Indels
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                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CYCLOPHILIN AND RELATED METHODS NUMBER OF SEQUENCES: 16
ADDRESSAW: "
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32 Tozer Road
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                                                                                                                                                                                                                                                                  APPLICANT: CARLOW, CLOTILDE K.S. APPLICANT: HONG, XIQIANG APPLICANT: HONG, TIQIANG TITLE OF THYBOXI TYPOSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                          Sequence 6, Application HS/N9028366
Patent No. 6150501
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TELEPHONE: 978-927-5054
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REGISTRATION NUMBER: 30901
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                                        17; Conservative
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                    Best Local Similarity
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                                                                                                                                                                                          US-09-028-366-6
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  Query Match
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                                          Matches
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APPLICANI: BOLE, JUMITE A.
APPLICANI: FINANCIA, CHARLOS R.
ABELICANI: FILAMORIA, CHARLOS R.
ITILE OF INVENTION: A NITE GENZYLMER AFTOJURINERIBOSIDE
TITLE OF INVENTION: (NAMPR) INSERSITIVE, EGNILSBRATIVE, NATEOSIDE FRANSPORT
TITLE OF INVENTION: FROIEDA, MOCLERY ACTOS ERCHARITHE SAME AND METHODS OF
TITLE OF INVENTIONS HSE
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24.08; Pred. No. 1.4e+02;
Cree To; Mismarches 27; Indels 0; Gaps
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APPLICANT: WILLD, YALLS G.
AFFLICANT: Scilbaner, Jettery J.
ITILE OF INVINCENCE HARDROGAM HACHERAR EXPRESSED IN HOMAN
ITILE OF INVENTION: GMETLEFAL VEHY ENDSCHELAL FILLS
                                                                                                                                                                                                                                     STREET: 411 Harbersons Ave. Parimental Piaza, 4th.
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFEWARE: Forest in Perfects #1.0, Version #1.40
SUPPENT AFFICTATION DAIA:
APPLICATION NUMBER: 05/70/208,000A
FILLION NUMBER: 05/70/208,000A
FILLION NUMBER: 05/70/208,000A
TARSHETAL: 05/70/208
ALL PREZ/ACENT INFORMATION:
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HEITER CONTET WINGES 201
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HINDRAM TON THE STREET WAS CONTET WINGES 201
SEQUENCE CHARACTER STREET
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CAMPHTER: IBM PC COMPATÍBLE
GERALINE SYSTEM: PC-(VS/NS DAS
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14; Pubservative
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SM 649A 4
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Methorite Type: protoft,
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                                                                                                                 TITLE OF INVENTION: PRE-
FITCE OF INVENTION: USE
NUMBER OF PELCENTES: 22
CORRESSONDENTE ADDRESS:
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Best Local a
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TITLE OF INVENTION: HYALURANA REPERSE EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.5%; Score 57; Dk L; Length 551;
Best Local Similarity 22.4%; Pred. No. 1.50-02;
Matches 12; Conservative 19; Mismatches 27; Dafels
COMPUTER KEADABLE FORM:
MEDUUM TYPE: Floppy disk
COMPUTER: IBM PC COmpatible
OPPERATING SYSTEM: PC-DosS/PS-Dos
SOFTWARE. Fatcutin Release #1.0, Version #1.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.45
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC
                                                                                                                                                                                                                                                 FILLING DATE: 10-MAR-1995
CLASSIFICATION: *:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 1F-0028US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBUR, 05/08/700,178
August 20, 1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPERCATION NOMBER: US 08/102,217
FELING DATE: March 10, 1995
ATTORNEY/AGINE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible oPERATING SYSTEM: PC-DOS/MS-10S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application 05/08700178; Patent No. 5788669; Patent No. 5788669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Hawk ins. Phillip K.
APPLICANT: Milds
APPLICANT: Scilhamer, Jettrey.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME. Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-852-0195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-852-0195
INFORMATION FOR SEQ ID NO: 2:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY, AGENT INFORMATION:
NAME: Luther, Barbara J.
                                                                                                                                                                                       SPETWARE, Patentin Rele
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 351 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , MCCDCULE TYPE. protein
US-08-402-217A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-700-178-2
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415-845-4166

TELEFAX

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1479 ETTPKAVSPAKSESQEEMLQVPNVETHTSKQI PHFKPLSVSPMSQLLSSNNFLKKVVE 1536
                                                                                                                                                                                                                                                            APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craid
APPLICANT: Seithamer, Jeffrey
TITLE OF INVENTION: HYDLIROAAN RECEPTOR EXPRESSED IN HUMAN
TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; score 57; DB 3; Length 351; 22.4%; Pred, No. 1.5c+02; tive 18; Mismatches 27; Indels
                                                                                                                                                            0.5%; Score 57; DH 1; Length 351; 22.4%; Pred. No. 1 50+02;
                                                                                                                                                                                                  27. Indols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 2.0 curent Application NUMBER: US/08/995-554 FILLING PATE: December 22, 1997
                                                                                                                                                                                                      19: Wismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Dr.
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FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 2, Application US/08995654
; Patent No. 6025138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: August 20, 1996
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TELECOMMUNICATION INFORMATION:
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                                    351 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
INFORMATION FOR OUGH TO MOT SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: December CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                    MOLECULE TYPE: protein US-08-700-178-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ToPoloGY: linear
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                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                    Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                           US-08-995-654-2
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                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                           RESULT 112
                                                                                                                                                                                                          Matches
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TITLE OF INVENTION: BACILLUS THURINGIENSIS APF AND NPT
LILLE OF INVENTION. FROTEASE CENES AND ALEALINE PROTEASE BEFIGURY AND NEUTRAL
TITLE OF INVENTION: PROTEASE DEFICIENT B.T. STRAINS
                                                                                                                                                                                          APPLICANT: Donovan, William P.
APPLICANT: Tan, Yuping
TITLE OF INVERTION: BACHLUS THURINGIENSIS ADT AND NPT
TITLE OF INVENTION: PROIEASE GENES AND ALMANINE PROIEASE DEFICIENT AND RECTEAL
TITLE OF INVENTION: PROTEASE BENETICIENT B.T. STRAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
0
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46.7%; Pred. No. 1.9e+02;
ive 5; Mismatches 11; Indels
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ADDRESSEE: A.S. Nadel
STRRET: 1601 Market Street, 36th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                    1601 Market Street, 36th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1220 LHNIMSIPTEMMANVMPLDDTYSPOVI 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/415,823
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; Patent No. 5962264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Donovan, William P.
                                                                                                                            ; Sequence 2, Application US/08415823
; Patent No. 5759538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 amino acids
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ADDRESSEE: A.S. Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tan, Yuping
TITLE OF INVENTION: BAC
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                               Philadelphia
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Matches 11, Conserva
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                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
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US-09-086-662-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-415-823-2
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                                                                                                             US-08-415-823-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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COMPITTER:

0; Gaps

1479 ETTPAAVSFNESESGFFMIGVFTVFFFFKQLRHFPFFLSVSFMSQLLSSHHFFPYVVP 1536

Conservative

Local Similarity

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Matches

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US-08-162-462B-8

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ALFELOTANIE PEDIERS N. BERY A.
ALFELOTANIE PARCETA, LAVE D. J.
1111E OF INVENTEUR. As EDALE ALBOMAN MICK FAF
1111E OF INVENTEUR. AS EDALE (BMF) ANTIOCK, FRANCEIG & FUSION PROTEIN
NUMBER OF SELECTIONES. 29
1 APPEROAMETER ALBOMAN.
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Hest Local Similarity 40.7%; Pred. No. 1.9e-02;
Matches 10; Conservative 5; Mismatches 11; Indels
OTHERTING STSTEMS IN LOSSMESTORS SHELD, VOTSTON #11.00
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UBRENT APPLICATION DAIA:
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444 South Flower St., 19th Floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Section of a Application USZ3816_402H
: Parent No. 592(47
                                                                                                                                                                                                                                                            PPD P APPLITATION DATA:
APPLITATION NUMBER: 0.07115.023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEPERAN CONTROL NYMELS TO FELSO MANDER TO STREET THE FELSO MANDER OF THE CASE AND STREET THE FELSO MANDER TO STREET THE CASE AND STREET THE CASE A
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CAMFULER: DAM Compart) (SC
CERALINO SYSTEM: DES
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ATT GENEYZAUTHE INC. SMATTEN:
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                                                                               TURPENT APPLIFALITY DALAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TE.KILLINE
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MolETULE IYPE: protein
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                                                                                                                         APPLICATION NUMBER:
FILING DATE:
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APPLICANT: Hsu, Knang T.
APPLICANT: Padolski, Jaseph S.
TITLE OF INVENTION: Materials and Methods for Immemorphical and Methods.
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Best Local Similarity 27.3%, Fred. No. 4.2e+02;
Matches 12, Conservative II Mismatches 21; Indots
    Length 465;
Out; Match.

0.5%, Scort C2, DB 2; Length 465;
Hest Local Similarity 58.8%; Pred. No. 2.4e+02;
Matches 10; Conservative 3; Mismatches 4; Indels
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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APPLICATION NUMBER, 00/08/184,993H
FILING DATE: 09 NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BOOLSMYSON
                                                                                                                                                                                                                                                  ; Sequence 16, Application US/08484993B ; Patent No. 5837497
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
THILIDHOND: 312/474-6654
TELEFAX: 312/474-0448
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INPERMATION FOR SEG ID NO: 16:
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FILLING LATE: 29 JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02/97
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ATTORNEY/AGENT INFORMATION:
                                                                                          1232 MILSROLDPILPOROGNM 1248
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                                                                                                                                          143 NLASKCVEPLGMENGNI 159
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US-08 484-993B-16
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CLASSIFICATION. 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM. PC
                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
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STREET; box.
Trmv- Chicago
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ZIP: 60606-6402
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                                                                                                                                                                                                            RESULT 116
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                                                                                                                                     D.F.
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CITY: Chicago
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                     STATE:
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27.3%; Pred. No. 3.2e+02;
ive 11; Mismatches 21; Indels
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ADDRESSEE: Marshall, O'Toble, Gerstein, Murray & Borun STREET: 6306 Sears Tower, 233 South Wacker Drive
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                                                                                                        Pharmaceutical Compositions for
                                                                                                                                                                                                                               6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                    ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
                                                                                                                                                                                                                                                                                                                                                                                                           Patentin Release #1.0, Version #1.25
                                                                                                                                 Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,158B
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APPLICANT: Hsu, Knang T.
APPLICANT: Pedelski, Joseph S
                                                                                                                                                                                                                                                                                            COUNTRY: United States of America
                                            Harris Ph.D., Jeffrey D.
Hsu, Kwang T.
Podolski, Joseph S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 16, Application US/U8484596A
; Patent No. 5981228
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 29-JAN-93
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/973,341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/012,990
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                                                                                                                                                                                                                                                                                                                                                      Floppy disk
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N: 514
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Best Local Similarity 27.3%
Matches 12; Conservative
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PRIOR APPLICATION DATA:
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                                                                                                                                                  NUMBER OF SEQUENCES: 61
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                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             60606-6402
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                                                                                                                                                                                                                                                Chicago
      Patent No. 5976545
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                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 570;
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STREET: 6300 Sears Tower, 233 South Wacker Drive
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27.3%; Pred. No. 3 20+02;
ive 11, Mismatches 21; Indels
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                                                                                                                                              Patentin Release #1.0, Version #1.25
                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,596A
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APPLICATION NUMBER: US 08/149,223
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COUNTRY: United States of America
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60606-6402
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Patent No. 5989550
                                                                                                    COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/149,223
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATE: 12
APPLICATION NUMBER: 07/973,341
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TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
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INFORMATION FOR SEQ ID NO: 16:
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ATTORNEY/AGENT INFORMATION:
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                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
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PRIOR APPLICATION DATA:
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                                                              COMPUTER READABLE FORM:
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                                                                                                                                                   SOFTWARE:
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                      COUNTRY:
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SEQUENCE CHARACTERISTICS:
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APPLEANT: Hist. Konno T.
APPLEANT: Pendolski, Joseph S.
ITTLE OF INVENTION: Materials and Method Dr. London Control P. D.
                                                                                                                                                                                                                                                                                                                                                                                                                       6.5%; Score 57; p4 2; Langth 570;
27:3%; Pred. No. 3.20(02;
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STREET: 6 ool Souts Dower 234 South Warker Brigo
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COMPUTER: HWM PC computible
OPERATIN) SYSIEM: PC-LOS/MS LOS
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ATFORNEYZAGENT INFORMATION:
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09 NoV-1992
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FILING DATE: 29-JAN-1994
PRI & APPLICATION DATA:
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ALFORNEY/AGENT INFORMATION:
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PEGISIRATION NUMBER: 6
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                                                                                                                                                                                                                                                                                                                                        ModErouge Type: protein
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NUMBER OF SECHENTES: 59
NORRESPONDENCE ANDRESSE:
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General INF PMALLON:
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FILLIAL DALE
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APPLICANT: Harris Ph.D., Jettrey D.
APPLICANT: Hsu, Kuang 1.
APPLICANT: Podolski, Joseph 3.
TITLE OF INVENTION: Materials and Methods for Immunoconfluception NUMBER OF SEQUENCES: 59
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                                                                                                                                                   0.5%; Score 52; DB 4; Length 57e;
27.39; Fred. Mc, 7.2e+02;
Live 11; Mismatches 21; Indeis
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SIRBET: 6300 Scars Tower, 233 South Wacker Inlive
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COUNTRY: United States of America
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FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IHM PC compatible
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/01
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       570 amino acids
LENGTH: 570 amino acids
                                                                                                                                                     Query Match
Bust Local Similarity 27.3%
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloudh, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JELEPHONE: 312/4...
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                                                           ; Molecule TYPE: protein
US-08-458-731-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-149-223A-16
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                     TYPE: amino acid
ToPoLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                               Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50606-6402
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR IDENTIFYING ANTI-PARASITIC TITLE OF INVENTION: COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guery Match 0.5%, Score 57; DB 1; Length 591; Best Local Similarity 29.8%, Pred. No. 3.46 \pm 0.2; Matches 14; Conservative 10; Mismatches 23; Indels
                                                                                                                                 METHOD FOR IDENTIFYING ANTI-PARASITIC COMPOUNDS
                                                                                                                                                                                                               ADDRESSER: DAVID G. CONLIN: DIKE, BRONSTEIN, ROBERTS & ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1348 KIVKMVIPALIQSDSCDSIEVSRNVEEIVVKIISVFVDALPHVPEHR 1394
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
              US-08-145-995A-21
: Sequence 21, Application US/08145995A
Patient No. 5482850
; GENERAL INFORMATION:
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                                                                                          APPLICANT: CARLOW, CLOTHOE K.S. APPLICANT: PAGE, ANTONY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-5446
TELEFAX: 200291 STRF UR
INFORMATION FOR SEQ 1D NO: 21:
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                                                                                                                                                                                                                                                       130 WATER STREET
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amino acid
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; MOLECULE TYPE: protein
US-08-145-995A-21
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                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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RESULT 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 591;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1348 KTVKMVIPALIQSDSGDSIEVSRNVEEIVVKIISVFVDALPHVPEHR 1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches 23; Indels
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                                                     Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 57; DB 2; 1
29.8%; Pred. No. 3.46+02;
                                                                                                                                                                                                                                                                                                 PEFERFYCE/POCKET NUMBER: NEB-046-DIV TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/145,995
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER. US/09/134,852
                                                                                                                                                                               US 08/145,995
                                                                                                us/08/451,747
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                 COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-134-852-21
Sequence 21, Application US/09134852
Patent No. 6127148
GENERAL INFORMATION:
APPLICANT: CARLOW, CLOTILDE K.S.
APPLICANT: PAGE, ANTONY
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                               WILLIAMS, GREGORY D.
                                                                                                                                                                                                                                                                                30401
                                                                                                                                                                                                                                                                                                                                     (508) 927-5054
(508) 927-1705
                                                                                                                                                                                              29-0CT-1993
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                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                591 amino acids
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Matches 14, Conservative
                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: protein US-08-451-747-21
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                                                                                                                                    CLASSIFICATION: 514
PRIOR APPLICATION UMBER: L
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                               NAME: WILLIAMS, GRECREGISTRATION NUMBER:
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                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                         SOFTWARE:
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                                                                                SEQ 1D NO 2
LENGTH: 684
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HELL ASE ACTIVITY AND MELLEO THEREFOR
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APPLICATION NUMBER: 02/09/2009
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ASPELL ATT IN NUMBER: 135 65/56 6, 042
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SEQUENCE CHARANTERISTINS.
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CAMPOTER: BM El compatible
PERATING SYSTEM: E' LOS/MS-10.S
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Person No. 28 658 (
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HELERAX: (647) 523 5450
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REFERNT: N FOR SEQ. 15 NO. 213
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M. LECTUR (YER): Profession
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                                                                                   Concry Match 0.5%; Score 57; DB 4; Locath 684; Best Local Similarity 35.0%; Pred, No. 4.3e-02; Matches 14; Conservative 7; Mismatches 19; Indels
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APPLICANT: Bronner, C. Eric
ADPLICANT: Refer, Scan M.
APPLICANT: Hollaw, Romi J.
APPLICANT: Rolodner, Richard b.
TILLE OF INVENTION: BANALIAN DAM MISMATCH REFAIR SENES
TITLE OF INVENTION: BAL
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                                                                                                                                                                                   2053 SVAMADDSIJWKFILNYOTILIKI KINSSPRVRFAALLI VIJALA 21192
                                                                                                                                                                                                           207 SLDTVIDELYHTIRQGILKRIHDK SISVEVQAVMGIGRIA 244.
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REFERENCE/DOCKET NUMBER: OHSD 405A
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBTRACTOR FACTOR FATA:
APPLICATION NUMBER: US/08/209,521
FILING DATE: 08-WAE-1994
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1BM PC compatible
ststem. ic L-3/Ms-bes
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: Patent No. 5922855
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TELEFAX: (503) 295-6679
INFORMATION FOR SEQ ID NO: 13:
ORGANISM: Asperqillus nidulans
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy .
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US-08-209-521-13
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CORRESPONDENCE ADDRESS:
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Query Match
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Kolodner, Richard D.
TITLE OF INVENTION: COMFOSITIONS AND METHODS RELATING TO DNA
MISMATCH REPAIR GENES
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                                                                                                                                      Bollaq, Romi J.
Kolodner, Richard D.
VITHTION: COMPOSITIONS AND METHODS RELATING TO DNA
VENTION: MISMATCH RUPAIR GENES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/961,810
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REGISTRATION NUMBER: 33,557
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Patent No. 6191268
GENERAL INFORMATION:
          Sequence 123, Application US/08961810
Patent No. 6165713
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Bronner, C. Bric
Baker, Sean M.
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TELEPHONE: (503) 224 6655
TELEFAX: (503) 295-6679
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INPORMATION FOR SEQ ID NO: 123:
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                                                                          Liskay, Kobert M.
Bronner, C. Eric
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                                                                                                                   Baker, Sean M.
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; MOLECULE TYPE: protein
US-08-961-810-123
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TITLE OF INVENTION.
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Best Local Similarity
                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                  CITY: Portland
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US-08-961-810-123
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32 4%; Pred No 5.1e(02)
Five 7; Mismatches 18; Indels
                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hustad, Carolyn M.
APPLICANT: Ghidyal, Namit
TITLE OF INVENTION: Human E3 Ubiquitin Protein
TITLE OF INVENTION: Ligase
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                                                                                                                                                                                                                                                                                                           NAME: Van Rysselberghe, Pierre C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 123:
                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               RECISTRATION NUMBER: 33,557
                                                                                                                                                                                                                                                                    CLASSIFICATION <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (503) 224-6655
                                                                                                                                                                                                                                                                                                                                                  PEFFERNCE/TOCKET NUMBER TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          FILING DATE: 09-Dec-1994
                                                                                                            MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (503) 295-6679
TELEX: 360619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09070060 Patent No. 5976849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 770 amino acids
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ATTORNEY/AGENT INFORMATION:
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                                                                                     COMPUTER READABLE FORM:
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TITLE OF INVENTION: No. 593778361 Gomes Mapping in the Diagotae and TITLE OF INVENTION. Velicialdiofacial Syndrome Minimal Critical Feation
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                                                                             ADDRESSE: Woodcock Washburn Entr Markiewicz & ADDRESSE. No. 593784is, LLP
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Wersion #1.46
CURRENT APPLICATION DAIA:
APPLICATION NUMMPP - US/08/2775,009
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APPLICANI: Godowski, Paul J.
APPLICANI: Mark, Melanie R.
APPLICANI: Seadden, David I.
APPLICANI: Baker, Kevin F.
TITLE OF INVENTION: Protein Tyrosine Kinases
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1995
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SOFTWARE: patin (Genentect)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 45, Application US/08445640
; Patent No. 5709858
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CLASSIFICATION: 4 >> ATTORNEY/AGENT INFORMATION:
MAME. ITGILLIO, BOTCER Yatko
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                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,719
REFERENCE/DECKET NUMBER: CH
TELECOMMUNICATION INFORMATION:
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(215) 568-3449
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MOLEGULE TYPE: protein
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                                       NUMBER OF SEQUENCES: 4'
                                                                                                                                                                                                ZIP: 19103
COMPUTER READABLE FORM:
                                                                                                                                       Philadelphia
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STRANDEDNESS: sin
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US-08-775-009-34
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LENGTH: 888 amino acids

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RESULT 136
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NUMBER OF SEQUENCES: 35
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Patent No. 6001621
                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 854C2
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 08/157563
                                APPLICATION NUMBER: 08/170558
FILING DATE: 20-DEC-1993
PRIOR APPLICATION DATA:
                                                                                          08/157563
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CURRENT APPLICATION DATA:
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IELECOMMUNICATION INFORMATION:
TELEPHONE: 415.000 1996
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APPLICANT: Mark, Melanie R.
APPLICANI: Scadden, David T.
APPLICANI: Baker, Kevin P.
APPLICANT: Baron, Will F.
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FELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 35:
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ATTORNET/AGENT INFORMATION:
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                                                                                                          FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                  NAME: Hasak, Janet E.
REGISTRATION NUMBER: 2
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                PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                          amino acid
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US-08-445-640-35
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Matches 14, Conserv
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1.1 to 1.1 and 1997 to 1.5 for 1.3 for 1997 to 1998 consistency and the form of the 1.2 for 1.
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                                                                                                                                                                                        0.5%; Score 57; DB 3; Length 888;
23.3%; Pred. No. 6 4 - 402;
                                                                                                                                                                                                                                                                       29; indels
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MEDIUM TYPE: 5.25 inch, 360 Kb tloppy disk
MEDIUM TYPE: 1BM PC compatible
OPPEMATHN: SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Protein Tyrosine Kinases NUMBER OF SEQUENCES: 35 CORPESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                17, Mismatches
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FILING DATE: 22-MAY-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 35, Application US/08447314; Patent No. 6087144; GENERAL INFORMATION:
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FILING PATE: 20-DEC-1993
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Scadden, David T.
APPLICANT: Baker, Kevin P.
APPLICANT: Baron, Will F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genentech, Inc.
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California
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER. G
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US-08-447-314-35
TYPE: amino acid
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US-08-170-558-35
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24.38; Pred, No. 5,16+02;
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APPLIVANT: Scaddenz par a.,
APPLIVANT: Garea, Kevin P.
APPLIVANT: Garea, Kili F.
FILLE OF INVENT: N: Professing Kinasoss
NIMBER OF SEQUENTES: 45
O GREEFS ONLEND A DOGRESS:
AUTHURAN A DOGRESS:
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SIREET: 400 Frant San Kruic Blvd.
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COMPUTER: IRM PC compatible
4-ERALING SYCHEM: PC POCYTE POS
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REFERENCE/POWKET NUMBER: BS401
TELESSEMMONTALLON INFORMALION
                                                            Sequence 35, Application 08/08445461
Fitent No. + 035523

    Sequence 4. Application of larger ends
    Patent No. 6100449

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ARGUTALION NUMBER: 06/170558
FILING DATE: 20 DEY-1-93
PRIOR ARGUTALD NITATA:
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"URKENT AFPLICATEN DATA:
APPLICATEN UNREDE: DECOM OF PRINCES
                                                                                                                                                                                                                                                APPLICANT: Jodowski, Pari J.
APPLICANT: Mark, Molanie R.
APPLICANT: Scadden, Day d.L.
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ATD-FNEY, ASTROL BROSEMATION
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916/271 7168
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APPLICANT: FLORE, Estable
APPLICANT: FSHEA, Yival
APPLICANT: PAPAN, Han
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REMISTRATION NUMBER:
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40.0%; Pred. No. 1.1e+04;
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Hest Local Similarity 40.0%; Pred. No. 1.1e+04;
Pest Local Similarity 40.0%; Pred. No. 1.1e+04;
Pest Local Similarity 40.0%; Pred. No. 1.1e+04;
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TITLE OF INVENTION: Combined Immanadeficiency Disease
NUMBER OF SECHENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.40 CURRENT APPLICATION DATA:
                                               STREET: 419 Seventh Street, N.W., Suite 408 CITY: Washington
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SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA: APPLICATI
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8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC:Dus/MS-Dus
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ADDRESSEE: HROWDY AND NEIMARK
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INFORMATION FOR SEQ ID NO: 29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-APR-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
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LENGTH: 1240 amino acids
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MOLECULE TYPE: protein
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APPLICATION NUMBER: 1
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384 TELELENNI PHILASLI PEPYTSYSSÄPPMDSNKVSLINBOFLPLIRILES 434

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Saps
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                                                                                                                                                                                                                                                                                   0.5%; Score 57; DB 4; Length 2987; 31.4%; Pred. No. 4.1e+03;
                                                                                                                                                                                Ouery Match
Best Local Similarity 31.4%; Pred. No. 4.1e+03;
Matches 16; Consertative f. Mismethes 29, Indeels
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                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. bzaros.
GENERAL INFORMATION:
APPLICANT: Exihery Meck
TITLE OF INVENTION: Genetic Test For Equipe Severe
TITLE OF INVENTION: Combined Immunodeficiency Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/970,269
FILING DATE: No. 6294334ember 14, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft word for Macintosh
CURRENT APPLICATION DATA:
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8011 Candle Lanc
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NAME: Adler Ph.D., Benjamin A.
REGISTRATION NUMBER: 35,423
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09407562 Patent No. 6294334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 29.
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LENGTH: 2987 amino acids
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              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: no
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                                                                        ANTI-SENSE: no
ORIGINAL SOURCE:
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-407-562 29
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                                                                                                                                                                                                                                                                                                                                                                       US-09-407-562-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
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                                                                                                              FEATURE
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GENERAL INFORMATION:
APPLICANT ORAMOTO, HITOAKI
APPLICANT NAKAMORA, TETSUO
APPLICANT NAKAMORA, TETSUO
TITLE OF INVENTION: POLYNGCLEOTIDES, POLYPEPTIDES, ANTIGEN, ANTIBOUY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
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0.5%; Score 57; PR 1; Length 3033; 38.5%; Pred. No. 4.2e+03; ive 8; Mismatches 8; Indels
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APPLICANT: NAKAMURA, Tetsuo
TITLE DE INVESTION NON A. MONER HENATITIS VIEWS GENOME,
                                                                                                                                                                                                                                                                                                                                3: Beveridge, DeGrandi, Weilacher & Young
1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/925,695
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                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DETECTION SYSTEMS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1752 PAIQSSWPKLEQFWAKHMWNFISGIQ 1777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application US/07925695; Patent No. 5428145
                                                                                                                     ; Sequence 8, Application US/07925695
; Patent No. 5428145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 659-2811
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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PRIOR APPLICATION DATA:
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Best Local Similarity 38.55
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WII 64470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLGGY: linear
US-07-925-695-8
                                                                                                                                                                                                                                                                                                                                                                              Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                       US-07-925-695-8
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                                                                                   RESULT 140
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FILLS OF INVENTIONS FORMORDS FIRES FOR FIRETIDES, ANTIQUE, ANTIGOR, ANTIGOR AND LITTLE OF INVENTIONS FOR FILLIN SYSTEMS
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1616. OF INVENTION: Conortic Fest Ent Epither Severio
1616. OF INVENTION: Cambined Emminoder Detency Disease
NUMBER OF SEQUENCES: 42
                                                                  NUMBER # SECTEMPES: 9
PARESE NOEM'E ADDRESS:
ADDRESSEE: Howerlider, Destrands, Weilreher's Young
STREET: 1850 M Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM IYEE: Floppy disk
COMPUTER: THR PY compariable
JEPATIEN: SPETER, PY AGZMS DGS
SPETEMER: Forten'E: Pericase #1.45, Version #1.25
DREENI APPLICATION DAIA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION RUMBERS: 3 - 66441/201
PILINE DATE: 5 DEC 1091
ALI GRAND HE BAND TONE
RAME: WOULD DOT GOOD OF GO
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FILING DATE: 19920407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 3 - 287402/51
FILING DATE: 09-873 [39]
PEC R APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: for Benjam to A. Adler
8:11 Catalle Latte
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> Patent No. 5976803
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(202) 659-14-2
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Matches 19, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 K 11 M 111
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MPULER KEADABLE FERM:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                                   Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77071
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USHUR 970-269A NO
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41.4%, Fred. No. 6.2e+03;
five 6; Mismatches 29; Indels
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TITLE OF INVENTION: Combined Immunodeliciency Disease
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09/407,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    No. 6294334ember 14, 1997
                No. 5976803ember 14, 1997
APPLICATION NUMBER: US, OR, 370, 200A
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STREET: 8011 Candle Lane
CITY: Houston
                                                                          NAME: Adler Ph.D., Benjamin A. REGISTRATION NUMBER: 35,423 REFERENCE/PROCKET NUMBER: 158860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCIZAGERIA NUMBER: D5860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Application US/09467562 Patent No. 6294334
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NAME: Adler Ph.D., Benjamiu A.
REGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple ) COMPUTER: Apple OPERATING SYSTEM: Macintosh
                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                           TELEFAX: 713-777-6908
INFORMATION FOR SEC ID NO: 30:
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                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3959 amino acid
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Bost Local Similarity 11.4%
Matches 16: Conservative
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                                                                                                                                                                         713-777-6908
                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein HYPOTHETICAL: no
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                                                                                                                                                                                                                                                    TYPE: amino acid
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                                                                                                                                                                                                                                                                                               linear
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APPLICANT: Kathery
                                     CLASSIFICATION:
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                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE:
US-08-970-269A-30
                                                                                                                                                         TELEPHONES
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US-09-407-562:30
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TOPOLOGY: linear

Matches

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PRIOR APPLICATION DATA:
APPLICATION NUMBER - P-T/HS94/09943
FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                               EARLIER APPLICATION NUMBER: US 09/36987
EARLIER PILING DATE: 1998-03-09
NUMBER OF SEO ID NOS: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; OKGANISM: Sacchalopolyspora spinosa
US-09-370-700-5
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HELDIN, CARL-HENRIK
US-09-370-700-5; Sequence 5, Application US/09370700
; Patent No. 6274350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GONEZ, LEONEL JORGE APPLICANT: SARAS, JAN
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                                                                                                                                                                                                                                                                     1999-08-09
                                                                             APPLICANT: Baltz, Richard H
APPLICANT: Broughton, Mary C
APPLICANT: Crawford, Kathryn P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                       CURRENT ALTICATION NUMBER CURRENT FILING DATE: 1999-0
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                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02210
                                                                                                                                                                                                                                     FILE PEFERENCE:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
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O
                                                                                                                                                                                                     384 TRISLERBEIGHELASTI PPETTEYSTOBEMPSWKVSLEAMPOPLPLIBELES 434
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                                                                                                                           Ouery Match 0.5%; Score 57; DB 4; Length 3959; Best Local Similarity 31.4%; Pred. No. 6.2e+03;
                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Dow Agrosciences LLC Patent Department 9330 Zionsville Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                     6; Mismatches
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APPLICANT: Merlo, Donald J.
APPLICANT: Treadway, Patti J.
APPLICANT: Treadway, Patti J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application USZU9Ú3698/A Patent No. 6143526
                                                                                                                                                                                                                                                                                                                                                                                             Baltz, Richard H.
Broughton, Mary C.
Grawford, Kathryn P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NIMBER: 56, TELECOMMUNICATION INFORMATION: TELEPHONE: (317)337-4816 THEREAR (317)337-4847 INFORMATION FOR SEG 1D NO: 5:
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REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                       16, Conservative
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US-09-036-987A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                 MOLECULE 1YPE: protein HYPOTHETICAL: no
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FILING DATE: 09-MAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                       ; ANTI-SENSE: no
US-09-407-562-30
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                                                                                                                                                                                                                                                                                                                     US-09-036-987A-5
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STATE:

RESULT 145

CITY:

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TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN TITLE OF INVENTION: TYROSINE PHOSPHATASES NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: Madduri, Krishnamurthy
APPLICANT: Treadway, Patti J
APPLICANT: Trrner, Jan R
APPLICANT: Maldron, Clive
TITLE OF INVENTION: BLOSYNLHELE Genes For Spinosyn Insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 57; DB 4; 27.8%; Pred. No. 8.6e+03;
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St Caps
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Furent No. 675074
SEMERAL INFORMATION:
APPLICANI: Rotter, David Y.
APPLICANI: Rotter, William J.
FILLE OF INVENTI'N: RANKO Graduostics and Vaccines
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OPERATING SYSTEM: POSTOS/MS-DOS
SOFTWARE: Patentif Release #1.0, Version #1.40
UDPERITARED ASTORIES.
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          PECELSIANI NUMBER 1.546
PERERUNGGENER NUMBER 1.547
PELENAMUNI NIFA INCERNIT. N.
PELENAMUNI NIFA NE SEMITEN
PELENAMUNI NIFA NI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAMUNI NIFANAM
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APPLICATION REMBER: DECOZ/403, Com-
FILING GAIE: 14 MART 1905
ATTORNEYZAGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADJRESSEE: Thirth Corporation STREEL: 4550 Horton Street
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                                                                                                                                     INF-PMATTON FOR SEQ 15 NOT 2013 SEQUENCE CHARACTERISTICS: LENGTH: 75 amino acids
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THE PRAIL A FIG. 15 B. 14.
SEUTENTE TRAPATIENTSLICS:
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                                                                                                                                                                                                      247 amino acids
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amino acid
NAMES SATES, REWARD B.
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COMPUTER READABLE FORM:
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US - 8 444 - 818 14
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0.5%; Score 56; DB 4; Length 257;

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AFFLICANT. Modes Molammadi. Joseph Schlessinger.
AFFLICANT. and Stevan R. Hubbard
TITLE OF INVENTION: CRYSTALS OF THE TYPOSINE KINASE DEMAIN
TITLE OF HAURITHAN. OF ROW INSULIN RESIDERS TYPOSINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.5%; Ecore 56; DB 2; Lemath 295; Best Loral Similarity 33.3%; Fred. No. 1.60-02; Matches 12; Conservative 9; Mismatches 15; Indels
    ored, No. 1.2e+02;
9. Mismatches (0) Indels
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                                                                       1821 VILPALKKTYRUTEKNWKNHMGPFMSILU 1849
                                                                                                  COMPUTER READAHLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: 1BM Compatible OPERATING SYSTEM: 1BM P.C. DGS 5.0 SOFTWARE: PESTSED TOWNINGWS 2.0 CURRENT PAPLICATION DATA: US/OB/701,191A APPLICATION NUMBER: US/OB/701,191A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,327
REFERENCE/CFORT NUMBER: 2,77/088
IELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 63 West Fitth Street
STREET: Los Angeles
STREET: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
                                                                                                                                                                                                                              Sequence 21, Application 05/08701191A
Patent No. 5942428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Sequence 3, Application US/08989478
; Patent No. 5986082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 21, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NE: (213) 489-1600
: (213) 955-0440
67-3510
34.5%;
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APPLICANT: Hunt, Michelle
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                               10, Conservative
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CLASSIFICATION: 530
PKIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: sin
TopoloGY: linear
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    Rest Local Similarity
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                                                                                                                                                                                      RESULT 148
US-08-701-191A-21
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                               Matches
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Molina, Antonio

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445 EEHLKETADLKKOPLPHOPVSLSTSGGKYOFLADSDTSLMLSLNHFLAFVRILAMNHLK 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 Match 0.5%; Score 56; DB 2; Length 314; Local Dimitarity 25.1%; Pred. No. 1.8e.92; es 15; Conservative 14; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                             Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PE/45-21214/PI/47571971
                                                                                                                     No. 5986082artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER, US 60/034,382 FILLING DATE: 27-DEC-1996 PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60,535,621
FILING DATE: 10 JAN 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60,035,622
FILING DATE: 10 JAN 1997
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/989,478
                                                                                                                                                                                                                                                                                                                                                                                                                               PRICE APPLICATION DATA: APPLICATION NUMBER: US 60/033,177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 60/034,379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 50/034,730
                                                                                                                                                                                                                                                                                                         PC DOS/MS DOS
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                                                                                                                                                            Research Triangle Park
No. 5986082th Carolina
                                                                                                                                         3054 Cornwallis Road
APPLICANT. Steiner, Henry York
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM, PC DOSZME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE TWATER NUMBER OF TELECOMMUNICATION INFORMATION. TELECOMMONICATION (919) 541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38,241
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APPLICANT: Friedrich, Leslie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SS: not relevant
not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 13-DEC-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JAN-1997
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                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACLERISIUS:
LENGTH: 314 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO. 3
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TOPOLOGY, not relevan
MOLECULE TYPE: protein
                 APPLICANT: Ryals, John TITLE OF INVENTION: ALT TITLE OF INVENTION: DIS
                                                                                                                                                                                                                      ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                  CORRESPONDENCE ADDRESS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                             NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                       USA
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                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE
                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 150
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Ouery Match 0.5%; Score 56; DB 3; Length 314; Best Local Similarity 25.4%; Pred. No. 1.8e+02;
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                                                                                                                                                  Oostendorp, Michael
VENTION: METHOD FOR PROTECTING PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                 ADDRESSEE: No. 6031153artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/875,015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 607034,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 60,034,379
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10-JAN-1997
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Ruess, Wilhelm
Knauf-Reiter, Gertrude
                                                                                                                                                                                                                                                                                                                                                                                                                 No. 6031153th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         उक्रे, 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 18:60, 98:108 APPLICATION NUMBER: 18:60, 98:108 APPLICATION NUMBER: 10-11APPLICATION NUMBER: 10-1APPLICATION NUMBER: 10-1A
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                                                                                                            Kessmann, Helmut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 27-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
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PRIOR APPLICATION DATA:
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FRICE APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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                                                                             Kung, Ruth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER
                                                                                                                                                                                                                               NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPFPATING SYSTEM:
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                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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       APPLICANT:
                                              APPI, I CANT.
                                                                                 APPI ICANT
                                                                                                                   APPLICANT .
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CHAIRMINE, SOCIETY OF THE MISSON STOCKA CHAIRMINE, THE PMATERN. THOUGHT A. APPLITANT. HEALT N. THOUTHY A. APPLITANT. HEALT N. THOUTHY A. APPLITANT. HEALT N. THOUTHY A. THE OF THIRD OF THE SOCIETY SECTIONS THE PORE THREE OF THE OF THE STOCKE. THE NUMBER OF THE STOCKE STOCKE NUMBER OF SECTIONS SOCIETY SOCIETY SOCIETY SECTIONS SOCIETY SOCIETY SOCIETY SOCIETY STOCKE STOCKE THE STOCKE TH
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99. 5; Mismatches 8; Indels
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APPLICATI NUMBER: T. CONTOURS ETTING DATE: LZ MAR 195
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TELET-MMUNICATION INFERMALLIAN:
TELETH NE: (5/15/74.2.4.4.4
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INFORMATION FOR SEQ ID NOT: 8:
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                                         GENERAL INFORMATION: Straft N. APPLETANT: Seatton, Straft N.
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                                                                Patentin Release #1.0, Version #1.25
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                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER 13,08,330,000A
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MEDIUM TYPE: Floppy disk
COMFGTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-1908/MS-DOS
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805 Third Avenue
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INPORMATION FOR SEQ ID NOT 11:
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                                                                                                                                                                                                                                                                                                                                           INPORMATION FOR SEC ID NO: 8:
                                                                                                                           FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
ATTORROYZAGINT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Uhl, George K.
APPLICANT: Eppler, C. Mark
APPLICANT: Wand, Jai-Bel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 05/98
FILING DATE: 28-APP-1995
CLASSIFICATION: 536
                                                                                                                                                                                           NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,8
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LENGTH: 348 amino acids
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Ehrlichia canis 120-kDa Immunodominant Antigenic TITLE OF INVENTION: Protein Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.5%; Score 56; DB 3; Length 406;
37.5%; Pred. No. 2.7e(02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA ENCODING ATP-SENSITIVE POTASSIUM TITLE OF INVENTION: CHANNEL PROTEINS AND USES THEREDE
                                                                                                                                                                                       0.5%; Score 56; DB 4; Length 348;
55.0%; Pred. No. 2.16:02;
Ecc. 3; Mismatches 6: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE: Immunodominant 120 kba Surface Exposed Adhesion
ITTLE: Protein Genes of Ehrlichia chaffeensis
PATENT COCCMENT NUMBER: US 08/656,034
PATENT FILING DATE: 1996-05-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Townsend and Townsend Khourie and Crew
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San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/141,047A CURRENT FILING DATE: 1998-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application 03/05141047A Patent No. 6043085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08385186
; Patent No. 5744594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Adelman, John P
APPLICANT: Ashford, Michael J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Ehrlichia chafteensis
                                                                                                                                                                                                                                                                               1405 TLGAEKFLWILLILLFEQYV 1424
                                                                                                                                                                                                                                                                                                        55.0%;
                                      ORIGINAL SOURCE:
ORGANISM: Rattus rattus
IMMEDIATE SOURCE:
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Best Local Similarity 77.5%
Marches 15, Conservative
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
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                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Walker, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS: Walker, David H. AUTHORS: Yu, Xue-Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yu, Xue-Jie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      California
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                                                                                                                                                                                                               Rest Local Similarity
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                                                                                                          KHODOP
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                                                                                                                            US-08-430-286A-11
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CITY: Se
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TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSTS USING
TITLE OF INVENTION: FUBIFIED SUPFACE ANTICENS OF BARFSIA HIGEMINA AND SIMILAR
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APPLICANT: WILLIAM C. DAVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 NDPKKIDRQAPDYVPIATPPTPILABGGKPPQDPYMEKSGKCNVHGNVQETYRYLSDLET 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 419;
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19; Mismatches 43; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/07/803,636A
                                                                                               SYSTEM: PC-DOS/MS-DOS
PatentIn Pelease #1 0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 56; DB 1; 1
21.5%; Pred. Wh 2 Re+02;
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GAINESVILLE
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                 5744594man J.
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                                                                              1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                               35,235
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                                                                                                                                                                                                                                                                                                                                                                                                                                           (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 YCSSLSNPINCSVKTVLQT 891
                                                                                                                                                                                                                                                                                                                      FILING DATE: 08-FEB-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                            07-FEB-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            419 amino arids
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                                                                                                                                 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              NAME: Kruse, No. 574
REGISTPATTON NUMBERO
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                                                                                                                                                             APPLICATION NUMBER:
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                                                                                                   OPERATING SYSTEM:
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                                                                                COMPUTER:
                                                                                                                         SOFTWARE:
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COUNTRY:
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Caps
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APPLICANT: WALKET, DEFEICH.
APPLICANT: VOL. XV. 1. XV. 16
TILLE OF INVENTE OF THE CONTRACT OF ENABLED BY SENIOR OF ENABLED BY SENIOR OF THE CONTRACT OF T
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host Lord Similarity 22,5% Pred. No. 4,40:02;
Matches 14; Conservative II; Mismatches 26: redore
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"MEUTER: 1BM PC Sumpartible
"PERATING SYSTEM" PC PC SYMSTEMS
S FUNDAMEN: POTENTIN RECOGNORY #1.0, VOTSTOR #1.40,
THRENI AFFLICATION LAIAN. #7.0, 77.1.1.1

FILLING LAIR M. PERBER. #7.5, 74.1

FILLING LAIR: ACROSS FLOOR FLOOR #1.40,
TASSIFITATION FOR FLOOR F
                                                                                                                                                                                                                   PREPROMEZOWKET MINNEE: WAA-050,01
IELECOMMONDIACEN INFORMACEON:
IELEPHONE: 704 475,010
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TELECCAMMONICATION INFORMATION:
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ALTERITZA BALTARE HALLER.
NAME: SALIWANTHIR, DAVID R
POTESTRALLON NUMBER: 11,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | FELEPHONE: ($12) 414-4000
| FELEPAX: ($12) 4.1, 257
| INF-PMAIL N POP SEQ 12 N STORM
| SEQUENCE HARANTEERSTINS:
| CENTHE: (44 ABLICO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SECULO SECTION 1. 2. SECUENCE CHARACTERISTICS:
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NAME: Sector Finesthy S.
PESISIFALE NORMER: (8),4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 A38.4 808
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APPLICANT: Siminszky, Kalph E. APPLICANT: Dowey, Ralph E. APPLICANT: Dowey, Ralph E. APPLICANT: Corbin, Prederick I. TITLE OF INVENTION: No. 6121512el Cytochrome P-4fm Constructs and TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Transacente Plants NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sidery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Croteau, Rodney B
APPLICANT: Wise, Mitchell L
APPLICANT: Savage, Thomas J
APPLICANT: Ratabira, Evs J
ITHE GE INVENTION: Monoterprise Synthases from Common Sage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guery Match 0.5%; Score 96; 148 9; Lonath 597;
Best Local Similarity 56.2%; Pred. No. 4.6e+02;
Matches 9, Jonetaliec 4, Mismatches 9, Loneis
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STREET: 1420 FIFTH AVENUE
2006 KINTIVILIPESTPFLARIMEDECE (VEHQ/QKTTQQLETV 21.49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,564
                            REGISTRATION NUMBER: 47,092
REPERENCE/TVOCKET NUMBER: 5051-409
THILECOMMUNICATION THORMATION
TELEPHONE: 919-854-1400
TELEPAX: 919-854-1401
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC:DOS/MS-DGS
                                                                                                                                                              Sequence 16, Application 08/08943564
Patent No. 6121512
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Virginia C. Bennett.
STREET: PO ROX 37428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application BS/08947540
Petent No. 5891697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. Elileleth Carolina
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bennett, Virginia C. REGISTRATION NUMBER: 37,09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         576 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1907 LSEVIFRPLFFKLFDW 1922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: protein
US-08-548-564:16
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Raleigh
SIAIE: NO. 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DAFE:
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                                                                                                                                                 US-(IR-948-564-16
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SEATTLE

CITY:

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15; Conservative

Martinhers

word Similarity

: 628 amino acids amino acid

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SEQUENCE CHARACTERISTICS:
                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
                                                              TOPOLOGY:
                                                                                                         US-08-656-034-2
                          I.ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                   RESULT 161
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GENERAL INFORMATION:
APPLICANT: Walker, Barid H.
APPLICANT: Ya. Xue Jie
TITLE OF INVENTION: IMMUNCOMINANT 120 KDA SURFACE-EXFOSED
TITLE OF INVENTION: ADHESION PROTEIN GENES OF EHRLICHIA
TITLE OF INVENTION: CHAFFEENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 56; DB 2; Length 591;
34.6%; Pred. No. 4.7e+02;
Live 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWAKE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                       ATTORNEY AGENT TRECHMALION.
NAME: Shelton, Dennis K
REGISTRATION NUMBER: 26,997
REFERENCE/DOCKET NUMBER: 26,997
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEC 1718
TELEPRAX: 206 224 0779
INFORMATION FOR SEQ 10 NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/98/656,034
FILLING DATE: CONCULTENCLY Herewith
CLASSIFFCATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               United States of America
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                                                                                                                                                                                               APPLICATION NUMBER: US/08/937,540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 LVDKDINLLSSIERALELFTHWRVQM 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08656034
Patent No. 6015691
Patent No. 6015691 5786172
                                        ZIP: 98101-2347
CMPUTER REALABLE FORM:
MEDIUM TYPE: Elappy disk
COMPUTER: HW PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Corder, Timothy S.
REGISTRATION NUMBER: 38,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPERENTL/IAACKEI NOMBER: 3TE
TELECOMMUNICATION INPOKAATION:
TELEPHONE: (512) 418-3000
TELEPEAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        591 amino acids
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Best Local Similarity 34.55
Feet Local Similarity 54.55
Conservative
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                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MonECULE TYPE: protein
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      WASHINGFON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                         CLASSIFICATION:
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                             SA
                                                                                                                                                                                                                   FILING DATE:
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US-08-656-034-2
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                          COUNTRY:
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Query Match 0.5%; score 56; DB 3; Length 628; Best Local Similarity 37.5%; Pred. No. 5.2e^+02; Matches 15; Conservative 7; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Indels
                                                                                                                                                                                                                                                                                               GENERAL TIPORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit, Dorit, Dorit TiTLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1159 BOVPIPLEPPPKAKPLGTVOOKPPOKKKOODLESVOE 1198
                                                                                            2006 KERYTVELPESTPPLAPTMEDROTPWINGORFFCOT PTV 2135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 KHLKLGLEQPDHQTASTJVQQQQQQQQQQQQQQQHLQQQQQQQQQQ
                                                                                                                         210 KEDETVSQPSSEPFVAESEVSKVEQEETNPEVLIKDLQDV 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/190,802A
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US-08-190-802A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: P O Rox 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                    Sequence 63, Application BS/08190802A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fabian, Gary R.
PEGISTPATION NUMBER: 33.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 63:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        713 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94306-0850
COMPUTER PEADABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                            Patent No. 5519003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA
                                                                                                                                                                                                                                      HS-08-190-802A-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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42. 9; Pred. Mg. 6, 60:02;
Tyo 11: Mismatches 16; Indels
                                                                                                                                                         APPLICANT: Mochly-Rosen Darla
APPLICANT: Fol. Lorit
III.E F INVENTIA: WE 4. - Fortrod Poptidos and Uses
III.E F INVENTIA: Dereof
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUPTIWAPE: Foreign to reserve at 3. Version #1.25 CUPPENT APPLICATION DAIA.
APPLICATION NUMBER: US/CH2/177, 416
FILLIN ANDRES: US/CH2/177, 416
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RETERRATION NUMBER: 79,959
PEFFERENCE/GOORS AND THE AMOUNTAIN INCOMMENTED.
                                                                                                                                                                                                                                                                                                                                                                                                                                         kashington
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EARLIER APPLICATION NUMBER: 08/608,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MELTOM TYPE: Fisppy disk
* MEUTER: IMM P* compatible
OPERATING SYSTEM: PC DOS/MS-LOS
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US confloy 1837-6
; September 6, Applikantion US/10132993A
; Parent No. 6.442244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/487,872
FILLER BATE: 07 JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                           ALAPESSEE: Morrison & Foerster
                                          Sequence 53. April or bar 08/34479 de
Potent No. 3 decemb
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MolECULE TYPE: profein
HYPOTHEFICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: ZORRESS:
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                                                                                                                           SENERAL INFORMALION:
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18 477 146 E.S.
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Best Lorai S
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0.5%; Score 56; DB 4; Length 744;
31.7%; Pred. No. 6.6e+02;
ative 9; Mismatches 19; Indeis
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                                                                                                                                                                                                                                                                                                   1779 FETTLAVIHTER ITSEMISASQANIRLISHERTLATTLAP 1819
                                                                                                                                                                                                                                                                                                                                            423 VEGILGALLDISKLESGRAAVSTUPVELDRIMEELSDEFAP 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUDRESSER: Curtis, Morris & Safford, P.C.
STREET: 530 Fifth Avenue, 25th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 454310-2570 TELECOMMUNICATION INFORMATION
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FILING DATE: 20-MAR-1991
ALFORNYZASENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-1008/M3-DGS
                                                                                                                          ) okganism: whodobacter sphaerolides
0S-09-192-983-6
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// Paicat Mc. 578597
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APPLICANT: de Taisne, Charles
APPLICANT: Tine, John A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
EARLIER FILLING DATE: 1996-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212) 840-3333
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425066 CURIMS
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Hest Local Similarity 31.7%
Matches 13, Conservative
                    NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
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                                                                                   LENGTH: 734
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TITLE OF INVENTION: CDNA OF DOCKIRO GENE AND DOCKIRO PROTEIN
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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            Length 740;
                                                      7; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                      APPLICANF: Lindquist, Susan
TITLE OF INVENTION: Methods and Compositions of Genetic
TITLE OF INVENTION: Stress Response Systems
NIMMER OF SECURNCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
G.5%; Score 56; DB 1; i
Hest Local Similarity 36.7%; Pred. No. 6.7e+02;
Matches 11; Conservative 7; Mismatchee 17
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                                                                                                                      385 KISLKNNIDHLLASLLPEFYISYSSQEEMD 414
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                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Arnold, White & Durkee STREET: P. O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/710,187
FILING DATE: 31-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,165
REFERENCE, DOCKET NUMBER: APCD:024
TELECOMMUNICATION INFORMATION:
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; Patent No. 5777094
                                                                                                                                                                                                                                       Sequence 2, Application US/08249380
Patent No. 5827685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 1BM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 713-787-1400
TELEFAX: 713-789-2679
INFORMATION FOR SEQ ID NO: 2:
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MOLECULE TYPE: protein
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ZIP: 77210
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TITLE OF INVENTION: CENA OF DOCK180 GENE AND DOCK180 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 56; DB 1; Length 1865; 37.5%; Pred. No. 2.7e+03; Live 5; Mismatches 15; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; FRAGMENT TYPE:
; ORICHNAL SOURCE: spleen cell of homo sapiens
US-08-588-985-2
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805 Fifteenth Street, N.W., #700
                                                                                                         Diskette, 5.25 inch, 500 kb
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; Patent No. 5786461
; GENERAL INFORMATION:
                                                                                                                                                                                                                 January 19, 1996
                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                        TELECOMMINICATION INFORMATION:
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Wordperfect 5.1
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N: 536
                                                                                                                                                            SOFTWARE: Wordperfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1865 amino acids
                                                                                                                          IBM Compatible
                                                                                                                                           MS-DOS
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            202-371-8850
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APPLICATION NUMBER: US.
                                                                                                                                                                                                                                                                                                                        Warren M. Cheek,
                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Conservative
                                                                                                                                                                             CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                          COMPUTER READARLE FORM:
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                                                                                                                                                                                                  APPLICATION NUMBER
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                                                                                                                                             OPERATING SYSTEM:
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Best Local Similarity
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                                                                                                                                                                                                                 FILING DATE:
                                                                                                           MEDIUM TYPE:
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                                                                       20005
                                                                                                                              COMPUTER:
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                                                      COUNTRY:
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TOPOLOGY:
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APPLICANT: ONLSHI, Jangt, - SHEI, GAB-JD
TITLE OF INVENTION: TAX ENCOUND 1,3 BELA D GLECAN
HUMBER OF INVENTION: SYNHASE SHGHNIFS
CORPESPONDENCES: 8
CORPESPONDENCE ADDRESS:
ADDRESS:
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APPLICATION NUMBER: 38708/F19, 554
TANSSELIAN DATE: 01-806
TANSSELIAN (AIA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELLY, FOSCHOLIE, 'PAPENT, S.A. MARRINAN, JOHN. FRAMADAN, N.M. M.R.KIN, ROLLA, RESTSIER, ELA
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APPLICANT: CHERREL Sury L.
APPLICANT: TEMAS. JOSEPh
APPLICANT: EL-SHEPREINT: Mchammed
APPLICANT: RAIN, JOSEPH PRINCAL
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US od 619 554-4
7 September 4. Application OS/38619554
7 Fatent No. 6421455
AND DEPARTMENT NUMBER OF COMMENT AND
                                                                                                                                                                                         18, 41,7
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LEWITH: 1865 amino acids
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COMFUTER: TBM Compatible
OPERATING SYSTEM: DOS
                                                                                     ALLOPHIN/A-BRITTRE-FMATTER.
NAME: WILLOR M. Book B.
PESTSTFALL on NUMBER: (5)
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ModECHE TYPE: protein
HYPOTHETTAL:
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APPLICANT: GARE, LEGNEL JORGE
APPLICANT: SAKAS, JAN
APPLICANT: CLAESSON-WELSH, LENA
APPLICANT: CLAESSON-WELSH, LENA
TITLE OF INVENTION: FRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NOTLEGATION SEQUENCIES FOR MAND. FROM FINA
TITLE OF INVENTION: TYROSINE PHOSPHAIASES
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                              Ouery Match 0.5%; Score 56; DB 2; Length 1895; Best Local Similarity 24.2%; Pred. No. 2.8e+04; Matches 16; Conservative 10; Mismatches 40; Indels
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FILING DATE: 01-SEP-1993
ATTOKNEY/AGENT INFORMATION:
NAME: GATES: BEWARD R.
REGISHATION NUMBER: 31,616
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рч-Апс-1496
REFERENCE, TOTKET NUMBER: 19104PI
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MEDITM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
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; Patent No. 5821075
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                      TELECOMMUNICATION INFORMATION:
TELEPHONE, 742-594-6734
FELHYAX: 732-594-4720
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TELEX: 92.1742 ESEKIEL
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                    INFORMATION FOR SECTIONO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1895 amino acids
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LECULE TVDF
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                                                                                                                                                                                              FYPE: amino acid
STRANDHDNESS: unk
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MOLECULE TYPE: protein

1907 LLDVIHYVNGVSTQGMTLEEVNRALDMSLPSLVLK 1941

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Bost Local Similarity
Matches 12; Conserv
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                                              HS-09-080-855-12
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                                RESULT 171
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APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLECTIBE SEQUENCES FOR MOVEL PROTFIN
TITLE OF INVENTION: TYROSINE PHOSPHATASES
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                                                Query Match 0.5%, Score 56; DB 2; Length 2465; Best Local Similarity 34.3%; Pred. No. 4.2e+03; Matches 12; Conservative 8; Mismatches 15; Indels
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                                                                                                                                                                  1907 LLDVIHYVNGVSTQGMTLEEVNRALDMSLPSLVLK 1941
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                                                                                                                            355 VVSIIHHVTGEETEGMDGQIYKRHLEALLTKISLK 389
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                                                                                                                                                                                                                                                            Sequence 3, Application US/09100864 Patent No. 6066472
                                                                                                                                                                                                                                                                                                                    APPLICANT: GONEZ, LEONEL JORGE APPLICANT: SARAS, JAN
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REFERENCE/OGCRET NUMBER: LOA
FELECOMMINICATION INFORMATION:
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APPLICATION NUMBER: US 08
FILING DATE: 09-AUG-1996
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ATTORNEY/AGENT INFORMATION:
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US-09-100-804-3
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FILING DATE:
CLASSIFICATION:
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Matches 12; Conserv
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US-08-596-291-3
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APPLICANT: Franzn, Petra
APPLICANT: Aspenstrm, Pontus
APPLICANT: Hellman, Ulf
APPLICANT: Gonez, Leonel Jorge
APPLICANT: Heldin, Carl-Henrik
TITLE OF INVENTION: PARG, A GTPASE ACTIVATING PROTEIN WHICH INTERACTS WITH PIPLL
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34,3%; Pred, No. 4.2e+03;
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CUBRENT APPLICATION NUMBRE: US/AB/ABB55A
CURRENT FILING DATE: 1998-05-18
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SOFTWARE: FastSEC for Windows Version 3.0
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Sequence 12, Application US/09080855A
Patent No. 6083721
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STREET: 600 ATLANTIC AVENUE
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ATTORNEY/AGENT INFORMATION:
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                                                               GENERAL INFORMATION:
APPLICANT: Saras, Jan
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APPLICANC: Marcheson, Eric 3.
HILL of INVENTION: Artisonse Compound Modulation of Fas Mediated Signaling FILE WEFERENCE: ISPH-0451
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Post Decad Similarity (4.2%) Prod. No. 4.2003;
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T. TIMER BRY LILE OF INVENTOR. MARMALLAR BYSERY, N. T. TIMER BRY NIMBER OF SECRET SECTIONS. BY MARKET OF SECRET SECTION SECURITION. BY THE SECTION SECT
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SOMPULE: IAM P. Compatible
OPERALING SYSTEM: P. LOSZWS DOS
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Application USZURIBBERIB Fateur No. Schooler
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INFORMATION FOR SKO ID NOT 2:
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SOFTWARE: Patentin Release #1.0, Version #1.25
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REFERENCE, COURT OF THE STATE OF THE STATE
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                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/UB/188,281H
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DGS/MS-DGS
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Patent No. 5667992
                                                                                                                                                                                                               AFTORNEY/AGENT INFORMATION:
NAME: POREMESKI, PRISCILLA E.
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,207
REPERENCE/INCRET NUMBER: 552
TELECOMMUNICATION INFORMATION:
TELECHONE: 708-437-636
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APPLICANT: YAMAGUCHI, JULLE
APPLICANT: FRAIL, DONALD E.
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34.6%; Pred. No. 5.7e+03;
ative 8; Mismatches 9; Indels
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0.5%: Score 56: DR 1; Length 3011;
Best Local Similarity 34.6%; Pred. No. 5.7e:03;
Matches 9; Conservative 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMMALIAN EXPRESSION SYSTEMS FOR HCV PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D377/AP6D
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                                                                                                                                                                                                                      1821 VLLPAIKKTYKQIEKNWKNHMGPFMS 1846
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STREET: ONE ABBOTT PARK KÖAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1008/MS DOS
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                                                                                                                                                                                                                                                                                                                                    Sequence L, Application US/U8/10637
Patent No. 5854001
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: 80DE, SUZANNE L.
APPLICANT: ZECK, BILLY J.
APPLICANT: YAMAGUGHI, JULIE
APPLICANT: PRAIL, BONALD E.
APPLICANT: DESAI, SURESH N.
APPLICANT: DESAI, SURESH N.
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TELECOMMUNICATION INFORMATION.
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ATTORNDY/AGENT INFORMATION.
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US-08-710-637-1
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                                     MOLECULE TYPE: protein
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CLASSIFICATION: 435
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TITLE OF INVENTION:
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STRANDEDNESS:
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                     TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                          US-08-453-552-1
                                                                                                                                                                                                                                                                                                                     US-08-710-637-1
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TILLE OF INVENTION: RAMMALIAN EXPERSION SYSTEMS FOR HCV
TITLE OF INVENTION: ENVELOPE GENES
                                                                                                                                                                                                                                                                                             MAMMALIAN EXPRESSION SYSTEMS FOR HCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Indels
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APPLICATION NUMBER: POT/US94/Annon2
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                                                                                                                                                                                                                                                                                                                                                                             APROTT LAROPATORIES D377/AP6D
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1745 VITPAVQTNWQKLEAFWAKHMWNFIS 1770
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GENERAL INFORMATION:
                                                                                                                    ; Sequence 1, Application FC/TUS9300907; GFNEPAL INPOPMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: POREMBSKI, PRISCILLA E.
EEGISTRATION NUMRER: 33,207
REFERENCE/DOCKET NUMBER: 5131.
                                                                                                                                                                                                                                                                                                                                                                                                   : ONE ABBOTT PARK ROAD ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WATANABE, SHINICHI APPLICANT: YAMAGUCHI, JULIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM PC compatible
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                                                                                                                                                                                                                                                                              APPLICANT: DEVARE, SUSHIL, G. TITLE OF INVENTION: MAMMALIAN TITLE OF INVENTION: PROTEINS
                                                                                                                                             FNFPAL INC. CASEV, JAMES M. APPLICANT. CASEV, JAMES M. APPLICANT: SDCK, BILLY J. APPLICANT: SECK, BILLY J. ANAMAGUCHI, JULIE
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APPLICANT: FRAIL, DONALD E.
APPLICANT: DESAI, SURESH M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
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TELEFAX: 708-937-9556
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Best Local Similarity 34.v.
Best 1009 9; Conservative
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Qy 1821 VELPATKETYNÇIERNWKWIMGPFMS 1846

Conservative

Best Local Similarity Matches 9: Conserv

Query Match

Gaps

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TITLE OF INVENTION: NON-A, NON-B HEPATITIS VIRUS GENOME.

TITLE OF INVENTION: POLYNUCLECTIDES, POLYPEPTIDES, ANTIGEN, ANTIBOLY AND
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1850 M Street, N.W., Suite 809
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SOFTWARE: Patentin Release #1.0, Version #1.25
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Best Local Similarity 34.6%; Pred. No. 5.7e+03;
Matches 9, Conservative 8, Mismatches 9,
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FILING DATE: 19920807
CLASSIFICATION: 435
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FILING DATE: 09-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NOMER: JF 460141/91
FILING DATE: 05-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5, Application US/07925695
Patent No. 5428145
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IBM PC compatibly
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                                     INFORMATION FOR SECTIONS: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3011 amino acids
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APPLICANT: NAKAMUKA, Tetsuo
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TELEFAX: (202) 659-1462
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Matches 9: Conservative
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linear
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708-938-2623
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MOLECULE 1YPE: protein
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COMPUTER READABLE FORM:
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NUMBER OF SEQUENCES:
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STRANDEDNESS: unk
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                                                                                                                                                                                                                STRANDEDNESS:
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    TELEFAX:
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gg 87 925-695-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF TRYENDERS, MANAMALLAN EXCEDSOF A STOTEMY FOR BOY ITLE OF TRYENDERS BRYEND PROPERTY.
                                                                                                                                                                                                  COMPUTER PERMANEE FORM:
MEDION TYPE: Frappy disk
"MEDION TYPE: Frappy disk
"PARTIEN: HAM FOLORIDATIBLE
"PERMITEN: TAND SYSTEM: FOLORIAN FOL
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Computer: TBM PC computeble
TPEPALINE SYSTEM: PC LOS/MEDEG
SPTWARE Flood for Reloase #1.0, Version #1.25
TPPEN APPLICATE NOARD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEDISTRATION NUMBER: 33,207
REFERENCE/POWER NUMBER: 55,21 to 01
FELECOMMUNICATION INFORMATION:
FEREPHONE: 708-937-5365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATE N NUMBER: POLYMENT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1821 VLLPATERITEQLEANWANHMGPFMS 1845
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TANK ABBURT PARK BUAD
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Aftorney/American (Mrth. R.
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[ESLEPHONE] 708-55.
(TAXY 708-948-2524
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                                              ARBOTT PARK
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                                                                                                                                 VS.
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FOT US95 01087 1
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1007 Market Street
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COMPUTER: Macintosh
OPERATING SYSTEM: Macintosh System, 6.0
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                                                      OF THE SEEDS OF PLANTS
METHODS FOR INCREASING
                   INCREASING THE LYSINE AND THRECOLINE CONTENT
                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
MICPOSOFT WORD VERSION 2.0C
                                                                                                        ADDRESSEE: E. I. DU PONT DE NEMOURS
ADDRESSEE: AND COMPANY
                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,633A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB-1037-C
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APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
                                                                                                                                                                                                                                                                             TEM PC COMPATIBLE
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                                                                                                                                               1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BARBARA C. SIEGELL
REGISTRATION NUMBER: 30,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                            FLOPPY DISK
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                                                                       107
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                                                                                               CORRESPONDENCE ADDRESS:
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                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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   TITLE OF INVENTION:
                                                                                                                                                                    WILMINGTON
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                                    TITLE OF INVENTION:
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                       TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                               COMPUTER:
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21.9%; Pred. No. 48;
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                                                                                                                                                                                                                                                                                                                        ADDRESSEE: E.I. du Pont de Nemours and Company
STREET: 1007 Market Street
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                               1924 PATRETYRQIERNWKNHMGPEMSILO 1849
                                                                1752 PAVOASWPKVEQFWAKHMWNF1SG10 1777
                                                                                                                                                 sequence 105, Application US/08182175A Patent No. 5559223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: BB-1031
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Patent No 5773691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07/743,006
                                                                                                                                                                                                             APPLICANT: Saverio Carl Falco
APPLICANT: Sharon J. Keeler
APPLICANT: Janet A. Rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Linda Axamethy Floyd REGISTRATION NUMBER: 33,692
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy Disk COMPUTER: Macintosh
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Matches 16; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                     TITLE OF INVENTION: STANDMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
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APPLICANT: B. I. DI
APPLICANT: COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                               Wilmington
                                                                                                                                                                                                                                                                                                                                                                                    Delaware
                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-182-175A-105
                                                                                                                                                                                                                                                                                                                                                                                                                   19898
                                                                                                                                           DS-08-182-175A-105
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                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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TITLE OF INVENTION: Synthetic Storage Proteins with Defined Structure Containin NUMBER OF SEQUENCES: 113
                                                              742 LAQKKIRKLESVITAVEIPSEWHIELMLDRGIPVELWAHYVEELNSTQRVAVEDSVFLVF 791
Gaps
                                                                                                                                         35 VMEEKMKKLBEKMKAMEDKMKWLEEKMKKLEEKMKVMEEKMKKLEEKMKAMEDKWKWLEE 94
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LENGTH

Corry Mutch Bost Local

Matches

5 15 5 2

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GENERAL INFORMATION:
APPLICANT: Alland, David
APPLICANT: Bloom, Barry R.
APPLICANT: Jacobs Jr., William R.
APPLICANT: Jacobs Jr., William R.
APPLICANT: Jacobs Jr., William R.
TITLE OF INVENTION: OF USE
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                COLL OF INVENTION. CLAHING BY COMPLEMENTION AND RELATED DITLE OF INVENTION: PROCESSES NUMBER OF SEQUENCES: 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 55; DB 2; Length 446; Pred; No. 2.8e+62;
                                                                                                           ADDRESSEE: Marshall, 0'Toole, Gerstein. Murray & Burun
STREET: 233 South Wacker brive/6400 Sous lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the desire
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CURRENT ADPLICATION NUMBER: US/09/177,349
CURRENT FILIN DATE: 1998-10-23
NUMBER OF SEC TO NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27866,32771
                                                                                                                                                                                                                                                                                                                                               CLASSIETCATION: 435
4108 APPLICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
                                                                                                                                                                                                   United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/588,352
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                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 3, Application US/09177449; Patent No. 6268201
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                                                                                                                                                                                                                                                                  E: Floppy disk
IBM PC compatible
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  Colicelli, John J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SECTIONO: 88:
SEQUENCE CHARACTERISTICS:
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(312) 474-0448
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Rest Local Similarity 40.0%;
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ATTORNEY/AGENT INFORMATION:
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US-08-474-379C-88
                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                       Chicago
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  APPLICANT:
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APPLICANT: LEE, Young Hun
ITHE OF INVENTION: Braiscription Factor Sene Induced by Water Delicit and Abscisic
ITHE OF INVENTION: Acid Isolated from Arabidopsis thalland
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(1.6%; Prod. No. 1.6c+02;
17e | 11; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o.5%; Seore 55; L8 5; Length 107; Similarity 21:9%; Pred. No. 48;
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CHERENIT FILMG DAFFE, 1998-68-27
NUMBER OF SPO. IN NOSC. S. SPINARE, WOLGPELFOFT, A. J. WINDERS
                  APPLITATION NOMBOR: POL/TEDL/OCATO
FILING DATE: 19920807
                                                                                                                                                                       NAME: Linda Axamethy Floyd
RESTSINATION NUMBER: 35,502
REFERENTATION THERES 160-1041
TELESTAMBURYALON INFEMALENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 195
1. Scope 4.4 (7507 BB
1. Sequence 86, Application US/08474.8793
1. Patent No. 5977.805
1. GENERAL INFORMATION
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Fitent No. 5981729
GENERAL INPORMATION:
                                                                 CASSILLATION.
PPLOF ARELICATION IAIA:
AFELLATION NAMES: 077343,
FULING FARE: 0 ARENST [99]
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                                                                                                                                                                                                                                                                (302) 392-4929
(302) 832-7943
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Host Godal Similarity (1.6%)
Matches (2: Conservative 1
                                                                                                                           FILING CATE: A AGOIST 1995 ALTONEY AGOINT INCOMMALION:
                                                                                                                                                                                                                                                                                                                                                                           : 107 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16; Conservative
TERRENI APPLICATION DATA:
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                                                            "LASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
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US - o 141 - 145 2
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RESULT 188
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Kinases
                                          Length 479;
                                                                        9, Indels
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                                                                                                                                                                                                                                                   Sugen, Inc.
515 Galveston Drive
Redwood City, California 94063-4720
United States of America
                                          0.5%; Score 55; DB 4; 1
35.7%; Fred, No. 4.8c+02;
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rtive 16; Mismatches
                                                    35.7%; Fred. wo.
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                                                                                                          910 HQLASISSPVVTSLLINLGSPVKEVRRA 937
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                                                                                                                                         40 HQISSVAANVVPGLINLGAGDEMSGLEQA 67
                                                                                                                                                                                                                     Sequence 12, Application PC/FUS9505008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPPRATING SYSTEM: PC-DGS/MS-DGS
                                                                                                                                                                                                                                                                                                                      Wissenschaften E.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 768
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12:
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Munchen 80539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-APR-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
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Best Local Similarity 21.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      536 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Cornzzi, Laura A.
REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                            Best Local Similarity
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US-09-177-349-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
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                                               Query Match
                                                                             Matches
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APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
                                                            APPLICANT: Wigher, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 638;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marshall, O'Thule, Gerstein, Marray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                  STREET: Two First National Plaza, 20 South Clark
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        S,07,688,352C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPIOR APPLICATION DATA:
APPLICATION NIMBER: US 07/511,715
FILING DATE: 20-APK-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 85, Application US/09146249A patent No 6069240
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-LOSZMS-DOS
           Sequence 22, Application US/07688352C Patent No. 5527896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25447
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INFORMATION FOR SEQ ID NO: 22:
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(312) 984-9740
                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 254. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            638 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 40.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borun, Michael F
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 18.
ETILING DATE: 19910419
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 638 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-07-688-352C-22
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                                                                                                                                                                                                                                                                                                                                 COMPUTER READARLE FORM: MEDIUM TYPE: Floppy o
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMINO ACID
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                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                 60603
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US-07-688-352C-22
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                                                                                                                                                                                                                                                                                                COUNTRY:
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1210 ILELLQHKKKLRSPQILVPTLFNLLSPCLEPLPQEQGNMEYTKQLI 1255

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us-09-603-665-5.rai

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FILING DATE: 20-APR-1990
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CITY: Trumbull
STATE: Connecti
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                                                                                                        tepphology:
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                                                                                                                                                                                                                                               TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: ACIDS 152-885 of SEC ID NG:22 which begins immediately after OTHER INFORMATION: codon. Stop codon may be in an intron."
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APPLICANT: Colicell, John J.
ITILE OF INVENTION: Cloning by Complementation and Related
ITILE OF INVENTION: Processes
ITILE OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
OTHER INFORMATION: /note "Sequence corresponds to perion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \gamma Match 0.5%; Score 55; 18 %; Length 734; Fowal Similarity 40.0%; Pred. 65, 9.2c+0.2, thes 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, o'foole, Gerstein, Murray & Borun
STREET: 6300 Sours Fower, 223 South Wagber Daile
                                   **MPTHER READABLE FORM:
MEDUM IYPE: Floppy d sk
***OMPHER: HWM PO COMpatible
OFBALES, CLAIM, FO COMPATIBLE
OFBALES, CLAIM, FO COMPATIBLE
SOFBARE: Patentin Release #1.0. Version #1.25
**UMPENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Floppy disk
LBM Po compatible
SYSIEM: POTOSE MS-1908
Parentin Release #1.0, Version #1.25
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                                                                                                                                                             APPLICATION NUMBER: US; *** (0.15, 210A FILE) PATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 03,708,7204,1888
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United States of America
                                                                                                                                                                                                                           ERIOR APPLICATION DATA:
APPLICATION WINNERS, 08-07/511,715
FILING DATE: 200-AFR-1090
ALCENISZAGERI, DRESMATION
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                                                                                                                                                                                                                                                                                                             NAME: Cloudh, bayid W
REDISTRATIN ROBBER. 50,107
FELEVEMENTATIN 1998BARTERN
FELEFENE. 312,471 0.02
FELEFAX: 012,474 0448
                                                                                                                                                                                                                                                                                                                                                                                                                     FELEX: 25-8856
INPORMATEN FOR SEQ 10 NO: 85:
SEQUENCE CHARACHERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILLING DATE: 01-MAR-1394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      744 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linear
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                      20th 70309
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                                                                                                                                                                                                         CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : Patent No. 6059240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITON LYPE:
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CHINIER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PEATURE:
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CTHER INFORMATION: 152 985 of SEQ 18 WHOLE Weight included attention of HER INFORMATION: Stop codon. Stop codon may be in an intron."
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                                                                                                                                                                                                                                                                                                                                                                      /note "Sequence coresponds to amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A Receptor Protein Kinase Gene
TITLE OF INVENTION: Encoded At the Self Incomparability Lowus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Obery Match 0.5%; Score 55; DB 3; Length 734; Best Local Similarity 40.0%; Pred. No. 9.2e-02; Matches 12; Conservative 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
GENERAL INFORMATION:
AFFILCANT: June Mascallah, Michael Masrallah, and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2022 PLVDÇLENRIGGERKFQERVTEHLIPCIAÇ 2051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFFCATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s: Yahwak & Associates
25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07717331F
Patent No. 5484905
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                                                                        TELECOMMUNICATION INFORMATION:
                                                      36107
                                                                                                                    TELERA: 312-474-0448
TELEX: 25-3856
NHORMATION FOR STY IT NO: 85: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEG ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 857 amino acids IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (203)268-1951
(203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPEKATING SYSTEM: MS-DOS
SOFTWARE: MICROSOft Word
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy Disk COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
                                                                                                       474-6300
                                                                                                                                                                                                                             LENGTH: 734 amino acids
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
OTHER INFORMATION: /not
Fatent No. £109025
                         NAME: Clough, David W. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-07-717-331F-2
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                    amino acid
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Omery Match Best Local Similarity

Matches

Patent No. 5977305 GENERAL INFORMATION:

US-08-474-3790-65

RESULT 192

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60606-6402

MEDIUM TYPE:

Chicago

ADDRESSEE:

SIKEET: STATE:

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GENERAL INFORMATION:
AFFLICANT: Wigler, Michael H.
AFFLICANT: Colicelli, John J.
TITLE OF INVENTION: Clinelly by Complementation and Related
TITLE OF INVENTION: Plucesses
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APPLICANT: Colicell, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%, Score 55; DB 3; Length 886;
10.0%; Pted. No. 1.2e+03;
                                                                                                                                                   8: Marshall, O'Toole, Gerstein, Murray & Borun
6300 Sears Tower, 233 South Warker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE. Marshall, O'Toole, Gerstein, Murray & Borun
STREET: (300 Soars Tower, 232 South Warter Price
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE. Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
AFFLICATION NUMBER: US/03/146,249A
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SOFTWARP: Patent[B Pricase #1 0, Version #1 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: IIS 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         United States of America
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                                                                                                                                                                                                                                                                                                   E: Floppy disk
IBM PC compatible
SYSTEM: PC+POS/AB+DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 65, Application US/08206188B; Patent No. 6100025; GENERAL INFORMATION:
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Clough, David W. REGISTRATION NUMBER: 36,107 TELECOMMUNICATION INFORMATION:
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                                                                                                                                   CORRESPONDENCE ADDRESS:
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COPPESPONDENCE ADDPESS:
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                                                                                                             NUMBER OF SEQUENCES:
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Bust Local Similarity
                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC
OPERATING SYSTEM.
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                                                                                                                                                                                               Chicago
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                                                                                                                                                                           STREET
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                                              0; Gaps
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                                                                                                                                                                                                                                                                                               APPLICANT: Wigher, Michael H.
APPLICANT: Colicell, John J.
THILL OF INVENTION: CLOHING BY COMPLEMENTATION AND RELATED
TITLE OF INVENTION: PROCESSES
Score 55, DH 1, Length 857, Pred. No. 1.2e+03, 8; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.5%; Score 55; DB 2; Length 886; 40.0%; Pred No. 1 28+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                233 South Warker Drive/6300 Sears Tower
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555 VKRLSKTSVQGTDEFMNEVTLIARLQHINLVQVL 588
                                                                                    502 LKKIMKTSKEGVDESTIKEAVLARLGDDNIDVVL 535
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19-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Illinois
COUNTRY: United States of America
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FILING DATE: 20-APR-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     Sequence 65, Application US/08474379C
Patent No. 5977305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 65, Application US/200746249A; Patent No. 6069240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPERBUTE CHAPTER MUMBER | 273
TELECOMMUNICATION INFORMATION:
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(312) 474-0448
  0.5%;
                      38.2%;
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N: 435
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                                        13; Conservative
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; MOLECULE TYPE: protein
US-08-474-3790-65
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CLASSIFICATION:

FILING DATE:

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Best Local Similarity

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Query Match

US-09-146-249A-65

RESULT 193

Gaps

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RESULT 197
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APPLICANT: Colicell, John J.
IIILE OF INVENTION: CLOCKING BY CONTEMENTATION AND KELATED
LITLE OF INVENTION: PROCESSES
CORRESPONDENCY AND ADDRESS.
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Hest Lacal Similarity 40.6%; Pred. No. 1.2ev03;
Matches 12; Conservation 6; Mismatches 12; Indels
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"OMFULEM: IMM POR COMPATIBLE
SPETMANE: PATOTIL EF (1952M2 1933
SPETMANE: PATOTIL Release #1.0, Version #1.30
THERENI ACCUCATION BAIN: 15/08/ACM, GTOT
FILING DATE: 07.5HN-1995
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CoONTRY: United States of America
ZIP: 60606-6402
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: Patent No. 9977405
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BELEPHONE: (12/174-6-80)
FELENAX: (12/174-6-80)
FELENX: 25-6856
INP-PARTITION FOL. 380, 10. 80, 65, 800, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 10. 80, 1
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PRIOR APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
                                        01-MAR-1994
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REGISTRATION NUMBER: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 MolECULE IYPE: protein
US os-205-1888 65
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                                                             FILLING DATE: 01 CLASSIFICATION:
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US or 474-479712
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APPLICANT: Colicelli, John J
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
CORRESPONDENCE: 85
CORRESPONDENCE: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Overy Match 0.5%; Score 55; DB 4; Length 898; Rest Lengt Similarity 40.0%; Pred. No. 1.20+03; Matches 12; Conservative 6: Mismatches 12; indels
                                                                                                                                                                                   Ouery Match 6.5%; Score 55; DB 2; Lkngth 898; Best Local Similarity 40.0%; Pred, No. 1.2e-03; Matches 12; Conservative 6, Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marshall, O'Too.e, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6300 Sears Tower, 233 South Warker Drive
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                                                                                                                                                                                                                                                                                              US/09/146,249A
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COUNTRY: United States of America
ZIP: 60606-6402
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COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/U9144,249A Patent No. 6069240 GENERAL INFORMATION:
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TELEBRAY: 312,474-6300
TELEFAX: 312-474-0448
INPURMATION FOR STO ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
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                                           898 amino acids
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                                                                                                    , MOLECULE TYPE: protein US-08 474-379C 12
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TREERMATION FOR SEC-
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COUNTRY:
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                                                                         APPLICANT: Wigler, Michael H.
APPLICANT: Colicell, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
NIMBER OF SEQUENCES: 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF HYPERTICH: Clening by Complementation and helated
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40.0%; Pred. No. 1.2e+03;
tive 5; Mismatches 12; Indels
                                                                                                                                                                                                 Marshall, O'Toolo, Gerstein, Murray & Borun
                                                                                                                                                                                                                6300 Sears Tower, 233 South Wacker Drive
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STREET: Street
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01-MAR-1994
                                                                                                                                                                                                                                                                               COUNTRY: United States of America ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPIGE APPLICATION DAFA: APPLICATION NUMBER: US 07/511,715
              Sequence 12, Application US/UR206188B
Patent No. 6100025
GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5527896
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INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                          Floppy disk
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Matches 12, Conservative
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US-08-206-1888-12
                                                                                                                                                         NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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                                                                                                                                                                                                                                         CITY: Chicago
STATE: Illinois
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US-08-206-188B-12
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No. 6043073cl Phospholipase D Polypeptide and DNA Sequences
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MEDIUM TYPE, Floppy disk
COMPUTER: IRM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWAVE: Patentin Polesso #1 0, Version #1 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 27805/30197 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                          1991<u>04</u>19
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APPLICATION NUMBER: US/08/968,7528
FILING DATE: 13-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
AFFORNEY/AGENE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US 50/025,469
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x: (312) 984-9740
25-3856
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ATTORNEY/AGENT INFORMATION:
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TYPE: AMINO ACID
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TELEPAX: 510-222-9758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Boron, Michael F.
REGISTRATION NUMBER: 25
                                                                                                                                                                     CURRENT APPLICATION DATA:
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CLASSIFICATION. 435
PRIOR APPLICATION DATA:
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2014 FRANAGMMPLNOGLENRIGGEREGEGEGEGEGEGEGEGEGEGEGENMPLNEGEGET 2073
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                                                                                                                                                                                                                                                                                                                                                                                               1594 TEPPETPEPPEPPPPOLIVONNEPSVPPPALDEENNPFIQQNESWPPTTVTPFFPPPFALVO 1654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1654. PKKKEGEEFGATNPQTALYTIKLI CKNFGAFNPDPFVPVLXTAVKI TAPFPKEEKNVLGS. 1713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1714 ALLCIAEVTSTLEALATPQLPSLMPSLLITMKNTSELVSSEVYLLSALAALQKVVETLPH 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1774 FESPYLEGII SQVIHLEKTITSEMSSASQANIBLITSI KKTI ATTI AFPVILPALKKTYKQI. 1833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1834 FKNWKNHMGPPMSTLOEHTGXMKKFFTTSHOSOLTAFPTFALDFFAQHSENDLEEVGKTE 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (894 N) IIDCLVAMVVKLSEVTFRPLFFFILFDWAKTEDAPKDRILITFYNLAD II AEKLKOLFII. 1954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1954 FAGHLVKPPADTLXQVNISKTDEAFFDSENDPERGGLLLQFILUNTLYRIFLFDIGHFISK 2013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ALLCIAEVISTLEALAIPQUPSLMPSLLTTMKNTSELVSSEVYLLSALAALQKVVETLPH 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 FISPYLEGII.SQVIHLEKTISEMSASQANIRLISLEKHALITARITARIKANAAARKIYKOI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 NCTIDCLVAMVVKLSEVTFFPLFFELFDWAKTEDAPKDRLLTFYNLADCTAEKLKGLFTL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.8.1. EPAEALMMPLVIQLENPLGGEERFGEPVTKHLIPCTAGESVAMATOSTWKPTNYQTILLKT 54.0
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                                                                                                                                                                                                                                                                                                                                          1 VVESGSPETLKGLEEPLLETVL3Y SAVAGSMERNALKLTVKFWFALLSKAYDLLDKVNA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoqai T., Ota T., Hayashi K., Smilyana T., etsuki I., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cherdata: Craniata: Vertebrata: Putelenstomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.4%; Score 3051; DB 4; Longth 611; 99.3%; Pred. No. 6;
                                                                                                                                                                                                                                              4: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                    Cobley V.;
Submitted (eff 2000) to the BHBL/Combank/DASJ databases
EMBL/ALISTED (20015848.1) -.
NON_TER
                                                                                                                      611 AA; 69032 MW: A9P374DA7977EA71 CR3643
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01-0CT-2000 (TTEMBLEEL 15, Last sequence update)
01-0CT-2000 (TTEMBLEEL 15, Last unnotation update)
CDNA FLI10359 FIS, CLONE NIZRM2001243.
                                                                                                                                                                                                                                              0 Mismatches
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                                                                                                                                                                                                               Best Loral similarity 99.3%
Matches 607; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2134 TVLGEPLUSYF 2144
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Eukaryota: Metazea; Cl
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                                                                                                                   SEQUENCE
                                                                                                                                                                                               Query Match
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요즘 물론 보증
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Addams M.D., Celliker S.E., Holf R.A., Evens C.A., Gocayne J.D.,
Addams M.D., Celliker S.E., Holf R.A., Evens C.A., Gocayne J.D.,
Addams M.D., Celliker S.E., Holf R.A., Evens R.A., Galle R.F.,
Addams M.D., Celliker S.E., Holf R.C., Ghange R.A., Galle R.F.,
Addered R.A., Lewis S.E., Krichards S.N., Shang O., Chen L.X.,
A brandon R.C., Mortham J.R., Yandell M.D., Zhang O., Chen L.X.,
A brandon R.C., Haxter E.C., Hall G., Ghange M., Pfeiffer B.D.,
A brill J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Radlen B.D.,
Abrill J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Radleu B.D.,
Abrill J.F., Bason R.Y., Berman B.P., Bhandari D., Boshakov S.,
A Borkova D., Botchan M.R., Boock J., Brokstein F., Brotticr P.,
A Borkova D., Botchan M.R., Bluck C., Pavengert R.R., Cander A., Chandra I.,
Cherry J.M., Cawitey S., Dahlke C., Pavengert R.R., Dietz S.M.,
A Gedson K., Doup L.E., Downes M., Diqan-Pocha S., Dunkov R.C., Dunn P.,
A borkin K.J., Evangeliska C.C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                               1796 MCSASQANIPLITSLEKITLATITLAPPVILPAIRRIYAQIEKNWRNHMGPFMSILQEHIGXM 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2026. PEQERVIFILIECTAQESVAMADISIMPLINYQILI PTPISSPYVPEAALITVLALAEKL. 2095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1916 FFKLEDWAKTEDAPKDRILTEYNLADCIAEKIKGIPTIFAGHIVKPFADTLXOVNISKTD 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1856 KKEELTSHQSÇITAFFLEAFÞFPAGHSENDJEFVGKTFNCTIDGLVAMVVKLSFVTFRPL 1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prerydota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
Magaisuma M., Hosciri T., Paki Y., Podaira H., Pondo H., Sudawara M., Takabashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiqudii S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yawaineto J., Wakamara Y., Ishii S., Kawai Y., Saito K., Ninomiya K., Mayanagi T., Rakamura Y., Nagahari K., Masuho Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 KEERLYSHQSQLYAPPLARIDPRAQHSENDLEFVORTENCTIDCLVAMVVKLSEVTFRPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24] KFQERVIKHETPCTAQPSVAMADDSTWKPLNYQILLKTPPSSPKVRFAALITVLALAFKE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MGSASOANIPETELPRETATELAPPULLPAIKETYPOLEKNWKNHWGPFWSILQEHIGVM 60
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                                                                                                                                                                                                                                                                                                  16.5%; Score 1778; DB 4; Length 349; 99 18; Pred No 2 90-221; Live 0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2006 FENYIVLI PESTPPLAFLMEDFOPEVEHOOOKTIOOLETVIGEPLOSYF 2144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "NEDO human cDNA sequencinq project.";
Submitted (PER-2660) to the EMBL/GedBank/DDBJ databases.
EMBL: AKO0121; BAA99564 1;
SINGURHER: AFO AA, 40020 MM; CAPALWEGAREFETS THE04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
030805 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                       Matches 346; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               Local Similarity
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NCBI_TaxID-7227;
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                                                                                                                                                                                                                                                                                                       Query Match
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RA Foster C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K., KA Glock A., Gorg P., Gorrell J.E., Gu. Z., Gabriellan P., Harris M., Harris M.L., Hauvey D., Heiman T.J., Heimander J.E., Horre J., Hottin D., Hallim, Kalush F., Karpen G.H., Ne Z., Kemison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ne Z., Kemison J.A., Ketchum K.A., Raimmel B.E., Kodira C.D., Krafi C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., R., Lai X., Mattei B., Morlosh T.C., McLeod M.P., McPherson D., RA Lasko P., Levitsky, A.A., Li J., Liz J., Liang Y., Lin X., RA Mount S.M., Moy M., Murby D.M., Nelson D.L., RA Mount S.M., Moy M., Murby D.M., Nelson D.L., RA Mount S.M., Moy M., Murby D.M., Nelson D.L., RA Mount S.M., Moy M., Murby D.M., Nelson D.L., Randero M., Pittman G.S., Pan S., Pollard J., Puri V., Reose M.G., Reiniglou R., Saundero R.D.G., Scheler F., Shen H., Reiniglou R., Saundero R.D.G., Scheler F., Shen H., Rhie R.C., Sidelling A.C., Stapleton M., Strong R., Sun R., San R., Rang Z.-Y., Wassarman D.A., Weinstock G.M., Waissenbach J., Mang Z.-Y., Wassarman D.A., Weilse K.C., Wu D., Yang S., Yao Q.A., R. Weilse R.W., Rubin G.M., Venter J.C.; Shor S., Zhon S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 FEQFEAPLESQLAKTLEPSVQTKAVNKQLDENISLFLIHLSPYFLLKPAQKCLEWLIHRF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 UJELYNQUSTIACVLPYHFTRIFVRVIGILKINNSKERWFWLLPVKQSGVPLAKGTLITH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z TSLAQQLQELALADASOASOLSKDEVASLLFDFKEAALIDKDIAFAIGCIGLEELLJIDFS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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01-MAR-2001 (TTEMBLEEL 16, Last annotation update)
HYPOTHETICAL 186.4 KDA PROTEIN 02385.045 IN CHROMOSOME II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         es; indels
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Submitted (MAY-1998) to the EMBL/GenBunk/DDBJ databases.
-!- SIMTI,ARITY: TO YEAST YJL109C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTTE: PRODUCT, ALDOKETO PEDUCTASE_3; UNKNOWN_1.
PROSTTE; PS00402; BPD_TKANSP_INN_MEMBR; UNKNOWN_1.
SEQUEN'S 2096 AA, 237217 MN, 3E7P3CG7FEDP620 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schiposaccharomyces pombe (Fission yeast).
Fukatyota, Fungi: Ascomycota, Schiposaccharomycetes;
Schiposaccharomycetales; Schiposaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.7%; Score 511; DB 5,
48.0%; Pred. No. 6.3e-56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FlyBase; FBgnon3l864; CGl0805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 AASNPAFLGFTCQSTQKAVK 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 287:2185-2195(2000)
RMBL; AE003615; AAF52447.2;
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Matches 96; Conservative
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InterPro, IPR001395;
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MILLINE 941-075 PubMed 7905-098;

MILLINE 941-075 PubMed 97, MILLINE 12, Just M., Johnston E., Johnston E., Johnston E., Johnston E., Johnston E., Johnston E., Marking T., Hiller E., Jahrellle P., Lichtting J., Eloyd 7., Mentrimore B., C'Calladhan M., Auridon M., Smith A., Soundamer E., Staden R., Shilston J., Shownkeen P., A. Millerty Mire 1., Thomas K., Vardin M., Vardhan M., Smith A., Soundamer E., Staden R., Shilston J., Malicity Mire 1., Thomas K., Vardin M., Vardhan P., Materston P., Mariana M., Milkinson Spreat J., Molidaen P., C'Calladhan P., Mariana M., Milkinson Spreat J., Molidaen P., C'Calladhan P., Mariana M., Mariana M
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                                                                                                                                                                                                                                                                                                                                                                                             24 SELETPEREAATTI RELAFA SOTOTILEELLI STEPEPERERESQUANTERSVQTKAVN 87
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Rhabditidnes Peloderinaes Gaenorhabditis.
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(5.198) Pred, No. 1.5e-15;
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                         InterProp IERocott?; ...
PROSTER ISSONT: URAL_PEDRAL: 1
PROSTER ISSONT: URAL_PEDRAL: 1
PROSTREM _24 _24 __PEDRALIA.
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PROSTE; PSOUN 49; PHINT_PROSTEASP_HTS; UNKNOWN_1.
SEQUENTE 1550 AA; 185.226 MW; A4146208F739F029 CR364;
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01-NoV-1996 (TrEMHITEL 61, Last sequence update)
01-NoV-2090 (TrEMHITEL 13, Lest arrectition applate)
04DED POR BY C. ELEGANS COMA YKRBH3.5.
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EMBL: AGUZ 4287; (TAAT8872.1)
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                                                                                                                                                                                                                                                                                                                                    Mathhes 44: Conservative
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InterProj IPRODUSZ4;
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Rest Local Similarity
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023495;
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1.54; Score 164; DR 5; Longth 1650; 45,28; Prod. No. 7.16:11;

guery Match Best Lecal Similarity

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                                 64. QEPADLESQI AKTI PESQUKAVNIKQI DENISI ELTHI SPYELLIKPAQIKOLEWILIHKEHI. 123
                                                   Whalen W.A., Yoon J.H., Shen R., Dhar R.;
"Regulation of mRNA export by putritional status in tission yeast.";
Genetics 152:827-838(1999).
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Submitted (FEB-2000) to the EMBL/SenBank/DDEJ databases.
EMBL, AL157917; CAB76031.1; -.
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1.9%; prod. No. 13;
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**; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schizosaccharomyces pombe (Fincion yeast).
Eukaryota, Fundi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                      Enkaryota, Fungi, Ascompcofa, Schizosaccharomycetes;
Schizosaccharomycetales: Schizosaccharomycetaceae;
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01-NºV-1999 (TrEMBLrel, 12, Last sequence update)
01-NAY-2000 (TrEMBLrel, 13, Last annetation update)
                                                                                                                                                                                                                                                     01 GCT 2000 (TrEMBLREL, 15, Greated)
01-GCT-2000 (TrEMBLREL, 15, Last sequence update)
cl-sct-2000 (TrEMBLREL, 15, Last annotation update)
                                                                                                                                                                                                                     PRT: 1564 AA
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24; Mismatches
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                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
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                                                                                                 124 HLYNQDSLIACVLPYHETRIFVRVIQLL 151
                                                                                                                                 125 YSFNAETLILTFLPFHETKVYSKILKIL 152
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 31; Conservative
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Matches 18; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                      NUCLEOPORIN.
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1819 PRVILLPAIKKTYKQIEKNWKNHMGPFMSTLQEHICXMKKEELTSHQSQLTAFFLEAIDFR 1878
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Pterygota; Necptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosids 1;
Gucurbitalos; Queurbitaeoae: Curumis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAP-1999) to the EMBL/GenBank/DubJ databases.
-:- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-:- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.7%; Score 75; DB 10; Length 246;
20.0%; Pred. No. 2.2;
15c - 27; Mismatches 49; Indels
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DNA-binding; Nuclear protein; Transcription Legulation.
SEOGENICE 246 AA; 28217 MW; 1366494903330776 CMC64;
1709 NVLGSALLCTAEVTSTLEALATPQLPSLMPSLLTTMKNESELV 1751
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JON-2000 (TrEMBLrel. 14, Last annotation update)
                      886 NCLPHILCCIAPILGITSALITAPWPSFTPSLLAVMINSTDIV 928
                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 15, Last sequence update)
01-MAR-2001 (TrEMBLrel, 15, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-CHANGGHUNMICL; TISSUE-FLORAL BUD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liu F.O., Chen M., Hai S.N., Xu Z.H.; "An AGL2 like gene in cucumber.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prosophila melanodaster (Fruit fly).
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PROSITE; PS50066; MADS_BOX_2; 1.
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                                                                                                                                                                                                                                                                                                              Cucumis sativus (Cucumber)
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PF01486; K-box: 1
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Host Local Similarity 20.09
Matches 19; Conservative
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                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR002100; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P11746; 1MNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-3659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CG6043 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                         09SEG4
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                                                                                                                  RESULT 9
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Adams M.E., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.E., Scherer S.E., 11 P.W., Howkins P.A., Gocayne J.D.,
RA Garder B.A., Towis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sitton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Berlandon K.G., Hogers Y.-H.G., Blazel K.G., Change M., Pelifer B.D.,
RA Mari J.F., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abri J.F., Boules P. V., Bernan B.P., Bayrakeroglu I., Beasley E.M.,
RA Buckosa D., Batchan M.E., Bayrakeroglu I., Relsahecy S.,
RA Buckosa D., Batchan M.E., Bayrakeroglu I., Relsahecy S.,
RA Buckosa D., Batchan M.E., Bayrakeroglu I., Relsahecy S.,
RA Buckosa D., Batchan M.E., Bayrakeroglu I., Relsahecy S.,
RA Buckis K.C., Busan D.A., Battler H., Caddeu E., Center A., Chandra I.,
RA Burkis K.C., Busan D.A., Edulpati H., Caddeu E., Center A., Chandra I.,
RA Gerry J.M., Caralog S., Duhlkov B.C., Dunkov B.C., Dunin P.,
Activosa D., Boldich A., Dong S., Mays A.D., Ivw I., Nortz S.M.,
Activosa D., Boldich A., Dong S., Mays A.D., Ivw I., Nortz S.M.,
Activosa D., Boldich A., Bowland T.J., Weil M., Classer K.,
RA Burkis K.J., Evangelista C.C., Ferrac C., Ferrac C., Ferrac C., Ferrac C.,
RA Harris N.L., Harvey D., Helman T. J., Weil M., Classer K.,
Adalai M., Adush F., Katrell J.H., Gu Z., Kraft C., Kraft 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murphy L., Quali M., Hariis L., kajandreda M., Ivens A., Barrell B.; Submitted (JOL-2000) to the EMBL/Geubank/EDBJ databases. EMBL; AL160493; CAB97623.1; -. NON_TER 198 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euglenozoa, Kinetoplastidā, Trypanosomatidae; Loishmania.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.7%; Score 75, 16 5, Length 930; 35.0%; Pred No 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DD99C0057CDA5E44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-001-2000 (TrEMBLrel. 15, Created)
01-001-2000 (TrEMBLrel. 15, Last Sequence update)
01-001-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1159 EQVRIEDEPPDKAKPLGTVQQKREQAAMQQKKSQOLESVQE 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98948 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     900 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leishmania major.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=5664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-2000
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SEQUENCE
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Estargotas Metazoas (Toodutas Chamiatas Vertebratas Enteleostomis
Archosaumus Avess Neoquathaes Galliformes; Phaslanidae; Phaslaninae;
                                                               O: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                     Edwarpela, Viridiplantae, Embryephyta, Tracheophyta, Spermatophyta,
Memod bepäyta: edanc tylodens: edre endrests, Rosidae: edrosids II;
Brassicies: Brassicacea; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peters S.A., Van Stazoron M., Dirbso W., Stjobomi W., Mowes H.W.,
Lemeke K., Mayer K.E.X.;
Schmitted (MAP-2000) 15 Plo EMEL/Coentre/Applited Jatabases.
                                                                                                                                                                                                                                                                                                                                              Borda M., Poters S.A., Par Stronen, M., Dirkso W., Stjaboma W.,
Bordo et J., Mowes H.W., Mayor K.E.X., Lemenke K., Schneller C.,
Supmitted (AER 1993) 15 (146) FMH, Absolab / HBBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.7%; Store 74; DB 10; laungth 408; 42.6%; Pred, No. 5.2;
                                    0.2%; Score 74, (48.5, Laughh 198; $5.3%; Pred, No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15; indels
                                                           10) Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis septencing project;
Submitted (ATD-1993) no the PMEL/Control/Sizzi databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencina project;
sadmitted (MAR-Salo) to the EMBL/GenBuck/AddR databases
EMBL ALOAD (MAR 128.1)
EMBL: ALDA MOS CARGESTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART: SMOOZOG, FECK; ].
Hypotheticai protein.
SEQUENTE: 408 AA; 46744 MW; PRD4F4FAEOLF63P ORO64;
21951 MW: 7067993888360P59 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.24 EPEALEVESTALKETESVITAVETPSEWHIELMIJORSTPV 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171 TPYFVKVESIKENSWEELESVASSIGILFYFYFHILYBROYOV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      woo room (Fremminel, 67) Last sequence update) desmark zool (Fremminel, 16, Last annotation update) besmin (Fremminel).
                                                                                                                                                                                               PRI: 448 AA.
                                                                                     124 THUYNGOSULA VEPTHELPTPVRVLULLKINNS 156
                                                                                                                                                                         PRI: 408 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        corry Match.

Hest Local Similarity (2.6%) Prod. No. 5.25
Marches 14: Conservative 14: Mismatches
                                                                                                      4 VHIYEVASVERAFLPYHOHNIFARALLILOLEDT 37
                                                                                                                                                                                                                                                           Atabidopsis thaliana (Mouserear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of AGS Leas (ItEMMErel, 07, Greated)
                                                                                                                                                                                                                                  HYPOTHETTO'AL 46.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTIEC PSTOTAL, FROX. 1.
                                               Rest Local Similarity (4.3%
Matches 12: Unservative
                                                                                                                                                                         PPELIMINARY;
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                                                                                                                                                                                                                         Zeed (ITEMBLEED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Integration (PROGRAM)
1 +8 AA:
                                                                                                                                                                                                                                                                                                                                  SECUENCE FFOM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUSION REPORTS
                                                                                                                                                                                                                                                                                                         N'BI_TaxID (702;
                                                            : 7 :
SQ SEQUENCE
                                                                                                                                                                                               CHELLY MATERIA
                                                                                                                                                                       34 ERS4.5
                                                                                                                                              3 (4 ) 4 )
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2005 LINYQILLEYPISSPKVPFAALITV "ALAEKLEENYIVLLEESTPFLAELMEDECEEVEHU 2124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 IQEETQIMEFAENNLAAFRADVAAATARTDIERRITESTQEETAFURKVHDEETREGAQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SdPS 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata: Cramiata: Verrebrata: Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-99359868; PubMed-10440757;
Li D.X., Tapsott T., Gonzalez D., Hurch P.E., Quinours M.A.,
Zoqubi W.A., Hill R., Hachisk L.L., Mann D.L., Koherts R.:
Toesmin Mutation Responsible for Dilated Cardiomyopathy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amatch 0.78; Score 73; Das 13; Longth 448; Local Similarity 30.78; Pred. No. 7.8; Personal Similarity 12; Mismatches 40; Endels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia: Euthoria: Primates: Catarrhini: Hominidae: Homo.
NCRL raxip 4606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 30.7%; Score 73; DB 4; Loudth 470; Best Local Similarity 30.7%; Fred. No. 8.2; Matches 23; Conservative 12; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coiled coil; Heptad repeat pattern; Intermediate filament.
VARIANI 451 451 M - 1.
                                                                                                                                                                                                                                                                                                                                                                        Coiled coil; Heptad repeat pattern; Intermediate filament
                                                                                                                                                       Submitted (MAR 1998) to the PMPL/General/PJGES databases.
-!- SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY.
EMHL; AB011672; BAA25132.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18509EAE51FBB319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       448 AA; 51663 MW; 198EBC377DH94B40 CRC64;
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- F. SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY
EMBL; AF137053: AAF15400.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (FrEMBLrel, 13, Greated)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, 19st angetation update)
                                                                                               STRAIN-WHITE LEGHORN: TISSUE-MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 470 AA; 53553 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                 Ptam: PF00038: filament: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2125 COKTICOLETVIGEP 2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2125 COKTIQUERTVEGEP 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 LOFQHIGVEMDISKP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 LQEGOVQVEMDMSKP 268
                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00226; IF: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00226; IF; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                     InterPro; IPR001664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPRU01664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                   SECTENCE FROM N.A.
NCB1_Tax1D=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                           448
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Pred. No

33.3%

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Best Local Similarity
                                                                                                                                                                                                                                                                        09YVT6;
                                                                                                                                                                                                                                                     9TVY90
                                                                                                                                                                                                                   RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
               Matches
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                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Cwinn M., Hickey B.K., Clayton P., Ketchum K.A., Sodergren E., Hardham J.M., McLood M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2065 LNYQTTLETRESSPKVEFAALITVLALAERIKENYTVLEPRATPFLAFIMEDECRRVEHO 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                      Park K.-V., Dalakas M.C., Semino-Mora C., Lee H.-S., Litvak S., Goldbarb L.G.,
Goldbarb L.G.,
Submitted (LHL-1999) to the EMMLAGenHank Zibbl databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 0.7%; Scote 73; DB 4, Length 470; Best Local Similarity 30.7%; Prod. No. 8.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  490 AA; 52809 MW; 7289A98AFGED4CF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                VARIANT 406 406 W -> R.
SEQUENCE 470 AA; 53565 MW; 1C2AEFAB4BB319 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria: Spirochartales: Spirochaetaceae: Trepodema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-N/V-1998 (TrEMBLrel. 08, Created)
01-N/V-1998 (TrEMBLrel. 08, Last sequence update)
01-6CT-2000 (TrEMBLrel. 15, Last annotation update)
SERINE-TYPE D-ALA-D-ALA CARBOXYPEPTIDASE (DACC).
                                                                                          01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 490 AA.
                                                        470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
                                                          PKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-98332770; PubMed-9665875;
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Pfam; PF00768; Peptidase_S11; 1.
PRINTS; PR00725; DADACBPTASE1.
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                                                                                                                                                                                                                                                                                                                             EMBL; AF167579; AAG41217.1; -
VARIANT 406 406 v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2125 CONTIDULATVIORP 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 LOPOQUOVEMPMSKP 268
                                                          PRELIMINARY;
                                                                                                                                                                      Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                         NCB1_Tax1D=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN NICHOLS;
                                                                                                                                               MUTANT DESMIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TICK: TP0800:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spirochete.
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                                                          Q9H319
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                      RESULT 15
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                                           C9H + 1.9
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0.7%; Score 73, DB 2, Length 490,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 ELLEGLERKLEKLYSSPERKATTERTRURKETERTRODDVAKETREKATETTER 223
                                                                                    | : : | | | | : | : | | | 370 TDVRTAISDALPCAIPVLGSKRPGALRPILHPSCTSCPVLNTPGTRISITFALPPLLRAP 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o: Gaps
                                                  291 TKIPSLIKDGLSCLIVLLØRQKPESLGKKPFPHLCNVPDLITILHGISETYDVSPLLRYM 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryola, Metazoa, Chordata; Craniata; Vertebrata; Chondrichthyes; Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Melanoplus sanguinipes entomopoxvirus (MSEPV).
Viruses: dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFUBARBA; AAF97677.1; -.
SEQUENCE 1127 AA; 134265 MW; F185DA1D5A3FE7D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Afonso C.L., Tulman E.R., Lu Z., Oma E., Kutish G.F., Rock D.L., "The genome of Melanoplus sanguinipes entomopoxvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schultess J., Toebbecke A., Schaffeld M., Lieb B., Markl J.; Submitted (SEP-1998) to the EMRL/CenBank/DDBJ databases.
-!- SIMILAPITY: TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 0.7%; Score 73; DB 14; Length 1127; Local Similarity 21.3%; Pred. No. 22; htsmatches 48; Indole to Conservative 22; Mismatches 48; Indole to
41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (FFEMBLEEL: 08, Last sequence update)
01-MAR-2001 (TrEMBLEEL: 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLTel 10, Last sequence update)
01-MAR-2001 (TrEMBLTCL. 10, Last annotation update)
ORF MSV156 HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                    PRT; 1127 AA.
     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1521 MSQLLSSNNFLKKVVESGGPFILKGLRER 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 KKELLERGEBLAMTIDERGEBLIKKUNDR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07, Created)
                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99102612; PubMed-9847359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scyliorhinidae; Scyliorhinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virol. 73:533-552(1999).
     25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINAPY;
                                                                                                                                                         351 LPHLVVSIIHHVTGE 365
                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                        430 LOETDVIGFAHVLDE 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scyllorhinus stellaris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Entomopoxvirus B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STPAIN=THOSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Lin S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
Comway A.R., Dewar K., Fent J., Kim C., Kurtz D., Li Y., Palm C.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 LOOBIC EKEEAENITAAPRI EVDAATIARITERETEALQEETAFIKKVHEEFILRIIQAQ 237
                                                                                                                                                                                                                                                                                                                                 (i) Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eskarysia: Viridipi natas, Embryaphyta, Tracheophyta: Spermatophyta;
Magnoi Saphyta; endivotyledous; vore endicots; Rosidae; enrosids II;
Brassicales; Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIP Finding Calebon binding Sering ^{\rm O}({\rm Li}) wine protein Klauner Pansterase.
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                                                                                                                                                                                                                                                        0.18; Score 72; DH 14; Length 455; 01.78; Pred. No. 11;
                    Infertros (Péroloca; ).

Prant Provides ilament: 1.

Prestito Psiodzen (F. 1.

Politod coil: Replad repeat pattern: Intermediate filament.

SEQUENCE 455 AA: 52230 MMS 845A2ECF895BCE9 CRC64;
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                                                                                                                                                                                                                                                                                                                          li: Mismatches 41: Indels
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"Theologis A.;

"Theologis A.;

"SMILAPHIY: 10 THE SERZIUD FAMILY OF CHOIFIN KINASI'S

"SIMILAPHIY: 10 THE SERZIUD FAMILY."

EMBEL APOND VOZE AN 28510.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 AA: 33175 MW; 71F96A3A5975B607 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The View (TEMMisse), exploited;
et NeV Lew (TEMMisse), exploits seperate update)
et MAK perl (TEMMisse), l6, Last amonation update)
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                                                                                                                                                                                                                                                                                    40.7%;
EMBIL: Y15064; 'AA75.447.1,
                                                                                                                                                                                                                                                                                                                          24: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           212" "CKIIJOLETIVLOEP 213-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prime PForcests enhands 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECLIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 COROHVOVEMBUSKP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plane Procedery pkinaser
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                                                                                                                                                                                                                                                           poery Match
Best Local Similarity
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FBK4.11.
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"Structural analysis of Arabicopsis thaliana chromosome 5. 111.
Sequence features of the regions of 1,791,918 bp covered by seventeen physicially assigned PP clones.";
DNA Res. 4:401-414(1997).
EMBL: AB008268: BAB09858.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sdr() ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pubercycla: Viridiplantae: Embryophyta: Trachecybyta: Spermutophyta:
Magnoliophyta; endicotyledons; core endicots; Kosidae; eurosids II;
Brassicales; Brassicaceae; Archidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, alpha subdivision, Rhizobiaceae group,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2008 OHFISKERAXALMMFLVBQLENKLAGEEKFQERVIKHLIPCIALFSVAMADOSLWKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; score 71; DB 10; Length 1269; 37.0%; Fred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.7%: Score 72: DB 2: Loudth ilB9;
Rest Local Similarity 29.4%: Pred. No. 32;
Matches 17; Conservative 11 Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                             Matthysse A.G., White S., Liquitoot R.;
"Genes required for cellulose synthesis in Agrobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1913 LATTLAPPVILPATKKTYKQTEKNWRNI9MOPEMSTLOEHIGXMKKE 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1269 AA; 141450 MW; F63E4614B8DE1069 CRC64;
                                                                                                                                                                                       01-NoV-1996 (TYEMBLEEL: 01, Last sequence update)
01-MAE-2001 (TYEMBLEEL: 16, List intolation update)
CELA, CELB, CELC, CELE, CELE GENES, COMPLETE CDSS; FIXE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA270C4PS2D2ADSD CRC64:
2100 IVLLPBSIPFLABLMEDETEEVEHTYTIGSFFFVIGFPFG 2141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last amnotation update)
                    51 1VVQPHKLPLPLPQPQEKQKLINH2KOSTLQQPEFTLARPPE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1269 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LILLE (Mailine eact oftess).
                                                                                                                                                                         01-NOV-1996 (IrEMBLrel, 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Bacteriol, 177:1069-1075(1995).
EMBL; L38609; AAC41432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 95164506; PubMed-7860585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98162728; PubMed 9501997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01546; Peptidase_M20; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 1189 AA: 129616 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 37.0%;
                                                                                                                                                                                                                                                                        Agrobacterium radiobacter.
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                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                               Rhizobiaceae; Rhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN COLUMBIA;
                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabid paid that
                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumefaciens.";
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Q44415;
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sest Local Similarity Matches 14; Pomsermi

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Ptergata, Neaptera, Eudiphoryandu, fishodu. Brachgessu, Musemmempha;
Ephydroidea; Drosophilidae; Drosophila.
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                                      Schmidt-Zachmann M.S., Knecht S., Kraemer A.; "Molecular characterization of a nove; widespread nuclear protein that calocalizes with spliceoscome components."; Mol. Biol. Cell 9:143-160(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metamoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                             0.7%; Score 71; DB 13; Length 1307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.7%; Score 71; DB 5, Length 1322; 37.0%; Pred. No. 48;
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                                                                                                                                                                                                                                                                      19: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1522 AA; 147323 MW; BA4EESEL6757FF84 7R364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1813 LATTLAPRVLLPAIKKTYKQIEKNWKNAMGPFMSTLQEHIGXMKKE 1858
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Submitted (THT-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U64951; AAB06728.1; -.
                                                                                                                                                                                                                                                                                                              1813 LATTLAPRVLI.PAIKKTYKQIEKNWKNHMGPFMSTLQEHIGXMKKE 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ainsrough R.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 250874, CA490775.1; -
EMBL; 250874, CA490775.1; -
EMBL; 250875, CA490777.1; -
EMBL; 250875, CA490777.1; -
EMBL; 250874; CA490777.1; -
                                                                                                                                                                 1307 AA, 146213 MW; 6B226D5F036C69B3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1997 (TremBirel. 02, Created)
01-FEB-1997 (TremBirel. 02, Last sequence update)
01-MAR-2001 (TremBirel. 16, Last annotation update)
NON-LTE EFFFOTFANSPOSABLE FLEMENT R2 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10, Last sequence update)
10, Last annotation update)
                                                                                                                                                                                                                       Query Match
0.00
Best Local Similarity 37.0%; Pred. No. 48;
Matches 17, Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 1322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      021909; 022332;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila bipectinata (Fruit fly).
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SEQUENCE FROM N.A.
MEDITAR-GRAGGES, PUDMEG-9436997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPOSON=PFTPOTPANSPOSON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 37.0%
Matches 17; Conservative
                                                                                                                    EMBL; Y08997; CAA70201.1;
Nuclear protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1999 (TEFMELED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCRI_TAXID=6239;
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Eukaryota; Metazoa; Chondata; Cramiata, Vertebrata; Estelmostomi;
                                                                                                                                                                                                                                                                            Enkaryota, Metazoa, Chordata, Cianiata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andersson B., Wentland M.A., Ricafrente J.F., tim W., Sibbs E.A. "A 'double adaptor' method for improved shotgun library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-57264341, PubMcJ 9110174, Muzny D.M., Dinq Y., Liu W., Yu W., Andersson B., Worley K.C., Muzny D.M., Dinq Y., Liu W., Ricafrente J.Y., Mentland M.A., Lennon G., Gibbs R.A.; "Larqe-scale concatenation cDNA sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amphibia; Batrachia; Anuta; Mesobatrachia, Fipeidea, Fipidae,
Xenopodinae; Xenopus.
NEBI_TaxID 8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.7%; Score 71; DB 4; Length 1304;
37.0%; Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98252826; PubMed~9585501;
Wang C., Chua K., Seqhezzi W., Loes B., Gorani O., Peed R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1813 LATTLAPRVLLPAIKKTYKQIEKNWKNHMGPFMSILOFHIGXMKKE 1858
        01-Nov-1998 (TFEMBLEEL 08, Created)
01-AuG-1999 (TFEMBLEEL 11, Last sequence update)
01-Any-2000 (TFEMBLEEL 13, Last annotation update)
SPLICE/SOME PROTEIN SAP 155 (PUTATIVE NUCLEAR PEGIEIN).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yu W., Glbbs R.A.;
Submitted (JUN-1948) to the EMBL/GenBank/DDBJ databases.
EMBL: AF054294 AAC97189.1; -.
EMBL: AF070540; AAC28033.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1304 AA; 145814 MW; 400821A5209155A7 CRC64;
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Last annotation update)
    PRELIMINARY; PRT; 1304 AA.
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Anal. Biochem. 236:107-113(1996).

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SEQUENCE OF 1011-1304 FROM N.A.

TISSUE=BRAIN;

SEQUENCE OF 1011-1304 FROM N.A.

TISSUE-BRAIN;

Best Local Similarity 37.0% Matches 17; Conservative

Query Match

Nuclear protein.

SEQUENCE

01-JUN-1998 (ItEMBLIEL, 06, 01-JUN-1998 (TrEMBLIEL, 06,

PRELIMINARY;

057683; 057683

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RESULT 23

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146 KDA NUCLEAR PROTEIN.

Genome Res. 7:353-358(1997).

MEDITINE 96207227, FubMed 8619471,

SEQUENCE OF 1011-1304 FROM N.A.

TISSUE BRAIN,

RARRAR

Genes Dev. 12:1409 1414(1998).

catalysis.

SEQUENCE FROM N.A.

NCB1\_Tax1D=9606;

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075533; 075533

RESULT 22

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Gaps

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Kitada K.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukiryota, Farali Asconiyota, Sarcharonyotin, Sachharonyotes,
Saccharonyotiales, altosporio Saccharonyetiales, Candida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ^{\circ}A verteofable acno express) a system for the pathorenic functor and out table t_{\rm s}(\varepsilon)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 7 t; Les 4; Length Lo45; 42,7%; Pred. No. 5c;
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                                                                                                                                                                                    0.6%: Score 70; 68 5; Length 305; 41.7%: Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toy Mismatches 23; Indels
                                                                                                                                                                                                                    The Mismathelias 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1045 AA; 116(10 MW; BCMBK41170BCA5BC CRC64;
                                                                                                                                    TOO AAS TOTOL MWS B44APSEDAETCESAB CROS4;
                                                                                                                                                                                                                                                      1810 BRILALILARBANLEZATER REJERNMENBROPERSILOP 1850
                                                                                                                                                                                                                                                                                                                                                                                                   of MAY From (FEMMILTE), For Treated)
of MAY-From (FEMMILTE), For List sequence update)
of MAK-2001 (FEMMILTE), For List animitation update)
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of MAXY-2001 (TrEMBLie), (S. Last September update)
of MAX-2001 (TrEMBLie), (S. Last annotation update)
                                                                                                                                                                                                                                                                        25.4 PRILITIER PREPARE (2007) A VINCENTAL | 1 | 1 | 1 | 1 | 1 | 1 | 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sundida alabitata (Yeust) (forulopsis alabitata)
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Fram: PF000.05; ABC (Lenn: Z.)
PP0.8THE: PS00.2TH: ABC (RANSE STER; UNKN.WH_Z.)
PP0.8THE: PS00.077; HEAL; REPEAT: Z.)
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                                                                                                                                                                                                                                                                                                                                                                          1045 AA
                                                                                PNA birdings Motal binding; Zinc-Tinger
              Information IPROGRAZZ:
Petran Programmer of Carry II.
Petran Carry Company Zimi I.
SMAARI: SMY ON SE VARZ I.
Elybases FB460016158; Obip\Rz element.
                                                                                                                                                                                                                                                                                                                                                                          PPELIMINARY: PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STEATN APPROBLE
MEDITINE 98455898; PubMed 9782488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mirrobischoup (44:24 / 24)5(1998).
EMBE: AROLESHIE BAASSUSSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSLATION ELONGATION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches log Conservative
                                                                                                                                                                                                                      ity Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1FP0001687;
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Rest Local Similarity
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SEQUENTE 1045 AZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBL Laxib 5478;
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MEDILINE-2016 60045 PubMed-10741142;

Adams M. D. Celniker S. E., Holt R.A., Esaus C.A., Gocarne J.D.,

RA Administrates S. E., Holt R.A., Esaus C.A., Gocarne J.D.,

RA Administrates S. E., Holt R.A., Hoskius R.A., Galle R.F.,

Ballawa K.D., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Amanaitdes P.G., Schoers Y.-H.C., Hlazel R.G., Champe M., Prelifer B.D.,

Randon P.G., Mortana J.R., Yandell M. L., Zhang O., Chen L.A.,

Randon P.G., Mortana E.S., Helt G., Champe M., Prelifer B.D.,

RA Hensen R.M., Hasu A., Razendale J., Bayraktaroqlu L., Heasley E.M.,

Roberson R.Y., Hengs P.V., Rerman P.P., Hendert D., Freitfer B.D.,

RA Hensen R.M., Hasu A., Barandle J., Bayraktaroqlu L., Heasley E.M.,

Roberson R.Y., Henge P.V., Rerman P.P., Hendert D., Freitfer B.D.,

RA Henris R.C., Busmam D.A., Butlin H., Cadros E., Center A., Chandra E.,

RA Cherry J.M., Campey S., Dablike C., Davengour L.M., Daviers P.,

RA Cherry J.M., Campel S., Dablike C., Davengour L.M., Daviers P.,

RA Cherry J.M., Campel S., Dablike C., Perriora S., Fleischmann W.,

RA Cherry J.M., Campel S., Gabriellan A.E., Ghia N.S., Gelbart W.M., Glasser R.,

RA Glodde A., Gond P., Gorrell J.H., Go Z., Gulbart W.M., Glasser R.,

RA Harris N.L., Harvey D., Heiman T.J., Hernders J.A., Forchman C.,

Jaiali M., Kalush E., Marpin S.H., Chun S., Pulp D., Hai Z.,

Lasker F., Lei T., Levi T., Levi Revilland T.J., Mei M. H., Liberwan C.,

Jaiali M., Kalush E., Marpin S.H., Marny D.M., Nelson D.J.,

Merkulov G., Milshina N.V., Mabarry C., Morris J., Moshreli A.,

Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.J.,

Spier E., Spradling A.C., Stalleton M., Strong K., Sun E.,

Syler E., Spradling A.C., Stalleton M., Strong K., Sun E.,

Syler E., Spradling A.C., Stalleton M., Strong K., Sun E.,

Syler E., Shradling S., Zhan W., Wolskern D.J.,

Milliams S.M., Woys R., Whyer R. W., Wolley R., Marny S., Short H.,

Shire R.C., Short E. Daver C., Daver C., Chan S., Short S., Short
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        960 TERAFETTSINAAVIQUIAFILEEL QREEKLIKSHQKLSETTENITSCVYSCVSTIAKIIM 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 VSILEEIRQHYRHILEQHITTLMN LHDFMREKNMIVSDPAKSSYSILFKIFNSIQKNIL 413
Drosophila meianogaster (Fruit 11y).
Eukryota: Medazoa: Arthropoda: Tracheata: Hoxapoda: Insecta:
Picryota: Neoptera: Endopteroa: Diptera: Krachyeera: Museomorpha:
Ephydroidea: Drosophilidae: Drosophila.
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Flybase, Franco38827; cc17269.
Slycence - 1269 Aa; 143662 hb; 74A217cafedo3eac crc54;
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01-MAY-1999 (TrEMBLrei, 10, Last sequence apolito)
01-MAY-1999 (TrEMBLRei, 10, Last annotation apolito)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRT;
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Best Local Similarity [19.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                             SECURIOR PROMINIA.
                                                                         Ephydroidea; 5ros
NCBI_TaxID 7227;
                                                                                                                                                                        STRATN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92T24:
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IFA-BINDING PROTEIN.

SEQUENCE FROM N.A.

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2049 IAQPSVAMADDSLWKPLNYQILLKTHDSSPKVRFAALITVLALAEKLKENYIVLLPESIP 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."; Submitted (JUL-1999) to the EMHL/Genhank/DDBJ databases.
EMBL; AJ248285; CAB49776.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mclanoplus sanguinipes entomopoxvirus (MSEPV).
Vituses, dsDNA Vituses, no KHA stage, Fox:iridue; Entomopoxvirinae;
Entomopoxvirus B.
                                                                                                                                                                                                                                                                                                                                                 Archaea, Euryarchaeeta, Thermococalos, Thermococcaceae, Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Afeas C. L. Tulman E.F. Lu ? . Oma P. Putish G.P. . Brok D.L.;
"The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73-533-552(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 0.6%; Score 68; DB 1; Length 286; Best Local SImilarity 27.3%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1998) to the EMBL/Genbank/DDBJ databases.
EMBL; AF063866; AAC97765.1; -.
InterPro; IPPROA447; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF02498; BRO; 1.
SEQUENCE 409 AA; 48676 MW; A062DEF999B47D57 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 286 AA; 31430 MW; 54375F278B46DACF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-2001 (TrEMBLrel. 16, Last annotation update) ORF MSV194 ALI MOTIF GENE FAMILY PROTEIN.
                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 31.4 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1999 (TrEMBLrel, lu, Created)
                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99102612; PubMed-9847359;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR000707; ...
InterPro, IPR001450; ...
Pfam; PF00037; fer4; 2.
Pfam; PF00991; ParA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q45560; 1BWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHOUENCE FROM N. A.
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                                                                                                                                                                                                                                                                                                                        Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax1D-29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-TUCSON;
Afonso C.I T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ORSAY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Heilig R.;
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                                                                                                                 Q9V0C8:
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                                                                              09V0C8
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                     RESULT 30
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                                                 9V0C8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1217 KERLIRSPOTI VPTLENI I SPOLEPI POGROCNMEVTKOLJI,SOLLANI COKI,SPINGCKIPKD 1276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       739 KLESVITAVELPSEWHIELMEDRGIPVELWAHYVEELNSTORVAVEDSVELVFSLKKFIY 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 FAREPELLYAAVVARSHCPLRRRPVISVNGWTYPPETLRVGT&VLIVUDIEDSGATINXIA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 EFTLEFKTVTIETKMPVLNINEERILEAQCSMESSHISSLHNAMFHLEQRVSVDGIECPEG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Caps
              Bukaryota; Viridiplantae; Embryophyta; Trachcophyta: Spermatophyta;
Magnoliophyta; eudicotyledoms; core eudicots; Kosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 69; DB 10; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%, Scene bs, 148 2, Langth 262; 27.4%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 23.9%; Pred. No. 15;
Matches 17; Conservative 21; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 41, indels
                                                                                                                                                                                                                                                                  Coller M.E., Saunders M.J.;
Submitted (MAY-1997) to the EMBL/GeuBank/FDDBJ databases.
EMBL: AF004554-189012424.1:
SIGGURGE 275 AA, 32273 MW; ED09e58458EF59AF FR064;
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
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                                                                                                                                                                                                                               STRAIN-LANDSBERG ERECTA; TISSUE-FLOWER;
Arabidopsis thaliana (Mouse-ear cress).
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STRAIN=NICHOLS; MEDLINE-98332770; PubMed-9665876;

SECUENCE FROM N.A.

NCBI\_TaxID-160;

Treponema pallidum

InterPro; IPR000836; -. Pfam; PF00156; Pribosyltran; 1. Transferase.

SEQUENCE

Science 281:375-388(1998). EMBL; AE001190: AACh504h i;

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                                                                                                                      14° CESV, BUTOSI MNI GOVICE AL PERRELLI PERANSENES ESQUERMAÇANA DEL SEGO 1509
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Submitted (NOV 1997) to the EMBL/Genhank/DBF1 databases.
-!- SIMILAMITY: FO OTHER PROKARYOTIC SENSORY TRANSBUSTON HISTIBINE
                                                                                                                                                                               114. EYK I AKKILALI OLI ONEONILLI JAKOOKKEUJOONI NOEKARIJ MISTOLIALI KARILAKO 170
Scorp 68; (B.14; Length 4.9);
Fred, No. 31;
                                                               200 Mismatches 240 Indels
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Bacillus/Staphylococous croup; Bacillus.
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                                       1 Similarity = 22.84;
14; Conservative = 2
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Swkaryota: Metacoa: Chordata: Craniato: Vertebrata; Eureleostomi:
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Local Similarity 21.3%; Pred, No. 55;
es 13, Conservative on the conservative of the conservative 
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submitted (NoV-1999) to the EMBL/Genbank/SEED databases.
EMBL; AFOZZISE; AAFI2952.1;
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Plam: PF01226; MMK-HSR1, 1.
Hypotherical Protein: Chicrop ast.
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09N3M2
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                                                                                                                                                                                                                                                                  Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.K., Matero A., Shah K., O'Shaughnessy A., Bodriguez M., Shckher M., Schutz K., See L.H., Swaby I., Habermann K., Podhia N.N., Mewes H.W., Lemcke K., Mayer K.P.X., Submitted (MAR-2000) to the EMRI/GenHank/ChiH. databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2082 FAALLTVIALAEKLKENYIVLEPESIPFLAEIMFDEGEBVEHOOOKTIQQIFTVIGEP 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 FPADVDAATLAPLDLEPPTFGLHEBIAFLARIHGERIRELONQMORSSUVQLUMDMSKP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).

Eukaryota: Viridiplantue, Emblyodaytu, Truchcophytu, Spermutophytu,
Magnol jophyta: eudicotyledons; core eudicots; Rosidae; eurosids 11;
Massicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horwath M., Hilpert M., Kunze R.; "AtMHH, an Arabidopsis homologue of the F. coli mutL DNA mismatch repair gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                Overy Match 0.6%; Score 68; DB 13; Length 473; Best Local Similarity 31.0%; Pred. No. 37; Matches 18; Conservative 13, Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                    Coiled coil; Heptad repeat pattern; Intermediate filament.
SEQUENCE 473 AA: 54050 MW; D687C4670e74FAE5 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted (NOV-1998) to the EMBL/GenBank/DDRI databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMRL/Genkank/DDRJ databases.
EMBL; AJ012747; CAA10163.1; -.
EMBL; AL161514; CAB78038.1; -.
                                                                             Lim T.M., Chan W.T., Gong Z., Chua K.L.;
Submitted (JAN-1990) to the EMBL/Genbank/hess databases.
                                                                                                                                                                                                          Submitted (SEP-1944) to the EMBL/OPERARE/ORBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLE). 16, Last annotation update) MLH) PROTEIN (FRAGMENT). MLH] OR AT4G09140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PS00058; DNA_MISMATCH_REPAIR_1; UNKNOWN_1.
                                                                                                                                                                                                                            SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01119; DNA_mis_repair; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00387; HATPase_c; 1.
                                                                                                                                                                                                                                                                                               PF00038; filament; 1.
                                                                                                                                                                                                                                                       EMBL; U47113; AAB03217.2; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PREILIMINARY;
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                                                                                                                                                                                                                                                                                                                   PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                             1PR001664;
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                                          SECUENCE FROM N.A.
                                                                                                                                                SEQUENCE FROM N.A.
NCBI_TaxID: 7955;
                                                                FISSUE-EMBRYO;
                                                                                                                                                                      I'I SSUE-EMBRYO;
                                                                                                                                                                                          Chua K.L.;
                                                                                                                                                                                                                                                                               InterPro;
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0.6%; Score oß; DB 13, Length 737,

Query Match

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1109 KIJEPFRANISHEKVOJKIJEMLEHIJAVNTKUSUCAGTVSSVFKOISVNAEQVRIELEPP 1168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 ASLREARTLLAANQYSQAANVAHSLFCTCHKFNLQ1ERASVLLLLAEHHKSGNAVLGLP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khan S., Kim C., Shinn P., Brooks S., Buehler E., Chao O., Dunn P., Walker M., Altafi H., Arauj. R., Conn L., Conway A.B., Consaler A., Hansen N.F., Huizar F., Kremenerskala L., Lonz C., Li J., Liu S., Larcas S., Rowley D., Schwartz T., Tortumi M., Vysorskala V., Yu G., Davis R.W., Pederspel N.A., Theologis A. Feker J. R., "Genomic sequence for Arabidopsis thaliana BAC F12K11 (rom chromosome
                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Khabditoidea;
                                                                                                                                                                                                                                                                                                                                                                               Eukarjota, Viridiplantue, Embryephyta; Trachoophyta: Spermatophyta; Magrolicphyta; eudicotyledens; environtyledens; enrosids II;
Brassicales; Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 6%; Score 68; DB 10; Length 819;
19.4%; Pred. No. 69;
Live 29; Mismat~hes 75; Indels
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2000) to the EMBL/GenBank/EDBJ databases.
EMBL, AC007592; AAF24811.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7592; AAF24811.1; -.
819 AA; 90584 MW; 523118F5F8D77CBA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07T-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                   13;
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                                                                                                                                                                                                                              819 AA
                   5; Mismatches
                                                              1168 PPKAKPLGTVQQKPRQKMQQKKSQPLESVQEV 1199
43.8%; Pred. No. 61;
                                                                                                     429 PDKVSSLSVVPSSVPQPNDKETAD1 SSVQEL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Khabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLirel, 13, Created)
                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BRISTOL N2;
MEDLINE=99069613, PubMed=9851916;
                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                  PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
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Matches 25; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1229 TLFNLLSRC 1237
  Rest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
                        14;
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                                                                                                                                                                                                                                                        Q9SHK3;
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                                                                                                                                                                                                                                OGSHK3
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                                                                                                                                                                                     RESULT 36
                          Matches
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SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LUEDOVQVE 69
                                                                                                                                                                                                                                                                                                   NCBI_TaxIP-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_Tax1D=3750;
                                                    2946 APL 2948
                  492 APV 494
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NON_TER
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                                                                                                                                         USGZR6
USGZR6;
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                                                                                                       RESULT 39
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                                                                                                                                                                            2069 ILLECTROSSPRINDALLINIALAEELEENYIVI OESTOELAELMEDECEEVERINGEL 2124
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                                                                                                                                                                                                                                                                                    4.42 TESKYPPTLIOVILLERILKETAGLARGELLERGEVSLSTSOFFLETAGGET MISTARPT 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic Res. B.185-145(1998).
-11-741ATT - ACTIVITY: N. DECXINCLEOSIDE TRIBHUSPHATE - N. PYROPDESSERATE - LOA(N.) (BY SIMILARITY).
-11-MISCELLANEOUS: IN EURAPPOTES THERE ARE FIVE DNA POLYMERASES:
ALPHA, BETA, JAMANA, DELLAA, ARD (15) TOJA WINTOH ARE RESCORDED FOR PROPERRY REACTIONS OF DNA SYNTHESIS (BY SIMILARITY).
-11-SIMILARITY: BELOWIS TO UNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukatyeta: Bedeussas Elneteplastida; Trypanonsmatidae; Leishmania.
N'NG Laxie 9664:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purnelle B., Galteau A., Ivens A.C., Lawson D., Quail M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lowis S.M., Bagherzadeh A., Zhang L., Chan H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.68; Score 58; DR 5; Length 3095;
                                                                                                                                                                                           Match 0.6%; Score 68; DB 5; Longth 1942; Local Similarity 23.9%; Pred. No. 1.8e-92; est 17; Conservative 17; Mismatches 37; Eddels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHA Figlication CMA Eledina, CHA directed CHA polymetaser.
SEQUENCE - KON-AA; - 4291-88 MW; - ABLZBEZOKEED4940 CRC44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith D.F.:
"A physical map of the Leishmania major Friedlin genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 8.10+02;
8; Mismarches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rajandream M.A., Barrell B.G.;
Submitted (DPC)eee, to the EMBE Zecometek/2004 databases.
                                                                                                                                           3EC970F3FDC34BED 3RC64,
                                                                   Submitted (MAR-2000) to the PMR Abelian Applied by aleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF MAY 2000 (TERMELOS, 16, Created)
MAY 2000 (TERMELOS, 16, LAST SEQUENCE update)
OF MAE 2001 (TERMELOS, 16, LAST INDUSTED OPDATE)
PECHANIE DNA POLYMERASE ZELA CAFALLIG COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI: 4096 AA.
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                                                                                EMBL: AND 44798; AAP 60721 1; Interpreted PRO00 87; PRO00 87; PROSEITE: PSS00077; HEAL ROPEAL; Z. SEQUENTE 1942 AA; Z14425 MK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FRIEDLIN;
MEDLINE: 98146435; Pubmod 9477411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primar PF(oil 65; DNA poil_B; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best foral Shallarity (1.7)
Matches Zo; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFINISC PROCESS, DNAPSLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      2129 TOQUETVISSEP 2149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1PR002064;
                                                                                                                                                                                                                                                                                                                                                                          68% LQQTARVVRNP 69%
12]
SEGUENTE FROM N.A.
STPAIN BRISTOL NZ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN FRIEDLIN;
                                                  Waterston R.:
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                                                                                                                                                                                           CHALLY MATCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Overy Mateh
                                                                                                                                                                                                                                                                                                                                                                                                                                                               230.07
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                                                                                                                                                                                                                               Matches
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2065 INVOLLERENSEPEVBEVALITV.ALAEKLEENYIVLLESSIPFLAELMEDECEEVEHU 2124
                                                                                                                                                                                                                                                                                                                                                                                             Park K.-Y., Dalakas M.C., Gocoel H.H., Ferrans V.J., Semino Mora C.,
Lityak S., Takeda K., Goldfar, L.G.;
Submitted (SEP-1997) to the Eddd,/GenEank/PDFcl Astabases.
EMBL: AF189281; AAGA 4460.1;
EMBL: AF189280; AAGA 4469.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LOPETOLKERAENNLAAFPADVPAATLARITOLEKETESLNEETAFT KKVHERETRELOAU 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mains domestica (Apple) (Mains sylvestris).
Edsaryita, Vitificiantue, Ethyra, Teather Phyra, Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Kosidae; enrosids I:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular who has and characterization of a NAGS teasuRAA clone of the Paji apple.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sung S.-K., An G.;
Subwitted (THE 1958) to the Preformise CDRF databases.
- Subwitting Localion: NOTIENE (EN SIMILARILY).
- The Subwitting Localion: NOTIENE (EN SIMILARILY).
- THE SUBWITTING TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                              Pukaryota, Metaroa, Chordata, Cromiata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.68; Score 67; DB 4; Length 73; 31.98; Pred. No. 5.9;
                                                               01-MAR-2001 (TrEMBLre). 16, created)
01-MAR-2001 (TrEMBLrel, 16, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
MOTANT DESMIN CSM-7 (MOTANT DESMIN CSM-6) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQÜENCE 73 AA: 8537 MW; RO62E7ZE455FE95C CRO64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel, 08, Created)
01-NOV-1998 (TrEMBLrel, 08, Last Sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ted. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Cell Physiol, 48:484-48' (1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN CV. FULL: TISSUE FLORAL BUD:
MEDLINE 97320151; PubMed-9177035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : KT
   PRT;
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31.98; ....
18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2125 COKTIQQLE 2133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MADS-BOX PROTEIN 1.
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HSSP; P11746; 1MNM

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InterPro;
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                                                                                                                                                                                                                                                                 OdlFU6;
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                                                                                                                                                                RESULT 42
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                                                                                                                                                                                                    Q9LFU6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1819 PRVILPAIKKTYKOTFKNWKNHMOPFMSTLØEHTGXMKKFRITSHQSQLTAFFLEALDFR 1878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 PAKELESSYREYMKLKGRYESLQRTQPNLLGEDLØPLNTKELEQLERQLEGSLKQVRSTK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   edeb (o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryofdyta; Trocho-quyta; Spermatopdytu,
Magnoliopdyta; endicotyledons, core endicots, Rosidae, enrosids I,
Rosales, Rosaceae, Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
--- SUBCELLULAR LOCATION, NUCLEAR (BY SIMILARITY).
--- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIFTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yao J., Dong Y., Kvarnheden A., Morris B.,
"Seven apple MADS-box genes are expressed in different parts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 67, DB 10, Length 240; 18.9%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%, Scote 67, 58 10; Length 246, 18.9%; Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20, Mismatches 51, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probom: PDUUZD/); ....PDUUZD/); PROSTIE; PS00350; MADS_HOX_1; 1. PROSTIE; PS0046; MADS_HOX_2; 1. SWART; SW0432; MADS; 1. DNA-binding; Nuclear protein; Transcription regulation.
                                                                                                                                                                                             PROSITE: PSS0350; MADS_BOX_1: 1.
PROSITE: PSS0066 MADS_BOX_1: 1.
SMART: SMO0432; MADS: 1.
SMART: SMO0432; MADS: 1.
SMART: Nuclear protein, Transcription regulation.
SEQUENCE 246 AA, 28278 MW, 641F35E21C887FA1 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (ItEMBLrel, 15, mast Sequence update)
01-MAR-2001 (TrEMBLrel, 16, mast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1879 AQHSENDLEEVGKTENCIIDGLVAMVVKLSEVIFR 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144 TOYMLEGLSELQNKEQLETEANNELTMKLDEISSR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maius domestica (Apple) (Maius sylvestris).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
Mendel; 32687; Maldo;MADS;32687.
InterPro; IPR002100; -.
InterPro; IPR002487; -.
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ProDom; PD002673; -; 1.
                                                                                            Pfam; PF00319; SRF-TF; 1.
Pfam; PF01486; K-box; 1.
PRINTS; PR00404; MADSDOMAIN.
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HSSP; P11746; 1MNM.
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Best Local Similarity 18.9%.
Matches 18; Conservative
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Pfam; PF01486; K-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 18.99
Matches 18; Couservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. GRANNY SMITH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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1828 KIYKQI-EKNWKNHMGPEMSTLQPHTGXMKKERLTSHQSQLTAFFLEALDFRAQHSENDLE 1887
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
02-Marbidopsis thaliana (Mouse-ear cress)
03-Marbidopsis 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P14F8_180
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantie, Embryodyla: Troche-phyto. Spermotophyta;
Magnoliophyta; eudicotyledous, core eudicots. Kosidae; curosids 11;
Brassicales, Brassicaceae: Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the FMRL Gradonk PDRT databases.
--- SURGPLIATAR LOCATION: NUCLEAR (BY SIMILARITY).
--- SIMILARITY: TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION FACTORS.
EMBL: AL3911444; CAC01779-1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato S., Nakamura Y., Kaneko T., Kato T., Ashmizu E., Kotani H., Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (AUG-2000) to the EMRL/GenBank/DDBJ databases.
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Bost Local Similarity 18 18, Prod No. 25,
Matches 15, Conservative 25, Mismatches 43, Endele
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DNA-binding, Nuclear protein; Transcription regulation.
SEGUENCE 262 AA, 23314 MW, EUGHRECE 262 AA, 23314 MW, EUGHRECE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-027-2000 (TEMRLEE), 15, Last sequence update)
01-MAR-2001 (TEMRLEE), 16, Last annotation update)
1879 AQHSENDLEEVGKTENCI!DCT.VAMVVKLSEVTFR 1913
                                                                                                           144 TQYMLDQLSDLONKEQLLIEANRDLTMKLDEISSR 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                262 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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PROSITE: PSGOUSO; MADS_BOX_1: 1
PROSITE: ESTGOUS, MADS_BOX_1: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADS BOX PROTEIN AGLZ.
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2061 CMERCINY/CLIER FRONTSPRANCIAL INTALALAR AND TALLAR AND THE STATISMEDISCUED STORT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A CLIPERIQUE MIQUE PARSITUS PROTOVINASTARTOTE PRAVESTORE AND PARTICLE ELECTOR. 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative 17; Mismatches 41; Indels 0; Gaps
                                                                          Sequence testures of the regions of 1,455,315 bp covered by nineteen physically assumed Pland FAC ciones."; nAR Res. 5:41:54(1998).
                       Miyajima N.,
                                                                                                                                                                                                                                                                                 1475 BEKEETTPKAVSENKSESQEEMLQVENVETHTSKOLPHPKFLSVSPMSOLLSSSNNF 1530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota: Metakas, Oberlata, Oraniata, Vertebrata, Enteleostemii
Mammalia: Entberia: Primites: Catarriini: Hominidae, Homo.
                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromesome 5, IV.
                                                                                                                                                                                                         Querry March 0.6%; Score 67; DB 10; Length 349; Best Local Similarity 33.9%; Pred, No. 35; Marches 19; Conservative 9; Mismatches 28; Indebs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 67; 148.4; Tength 354;
28,5%; Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  biled coil: Heptad repeat pattern; Intermediate filament.
                                                                                                                                                                                                                                                28. Indels
MEGLINE CHECKET PERMOG SKZB582;
Sator S. Karokovili, Kofeni H., Nakhmera M., Asmita B.,
                                                                                                                             EMBL: ABOUGOS6, BABOBŽ2B.1; -.
SPUTENCE - 449 AA: 49783 MW: 34FS9B698FB41C09 OBC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of N.V. 1996 (ITEMBLE), 01, Cheated)
of N.V. 1999 (ITEMBLE), 12, Last sequence update)
of MAK-2001 (ITEMBLE), 15, Last annotat on update)
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EMBL: MIRBY: AAA/1281.2: JOUNED.
EMBL: MIRBY: AAA/1281.2: JOUNED.
EMBL: MIRBY: AAA/1281.2: JOUNED.
EMBL: MIRBY: AAA61281.2: JOUNED.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo Sapiens (Human).
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EMBL: MIRRBS;
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                     Sato K. R.
Tabata S.,
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110 011
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Coombs J.M., Brenchley J.E.; "Blochemical and phylogenetic analysis of a cold-active beta-
quiactosidase from the lactic acid bacterium carnebacterium piscicola
strain BA.";
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                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA-binding: Nuclear protein: Receptor: Transcription requisition;

    -!- SUNCELLUIAR LOCATION: NUCLEAR (BY SIMILARITY).
    -!- SIMILARITY, TO C4 IYPE SIEROID RESERVER ZINC FINGER FAMILY.
    EMBL: ALOZI472; CAA16299.1; -.

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23:8%, Fred. No. 51;
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01-MAR-2001 (TrEMBLrel, 16, Last amotation update)
BETA-GALACTOSIDASE BGAB.
                        01-JUN-1998 (TrEMBLEG!, 06, Greated)
01-JUN-1998 (TrEMBLEG!, 06, Jast sequence update)
01-MAR-2001 (TrEMBLEG!, 16, Jast annotation update)
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hes 10; Conservative 14; Mismatches
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                                                                                                                                                                            Caenorhabditis elegans.
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                                                                                                                 Y17D7B.1 PROTEIN.
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045910;
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TISSUE-EMBRYO;
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01-JUL-1997 (TrEMBLrel 04, Last sequence update)
01-MAP-2001 (TrEMBLrel 16, Last annotation update)
TYROSINE-PROTEIN FINASE 14K1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conway G., Marqoliath A., Wong-Madden S., Roberts R.J., Gilbert W.; "Jakl kinase is required for cell migrations and anterior specification in zebrafish embryos ";
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, MUTAGENESIS, AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachydanio rerio (Zcbrafish) (Zebra danio).
Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryjii; Neopteryjii; Tyleosfei; Euteleosfei; Osfariophysi;
Cypriniformes; Cyprinidae; Pasborinae; Danio.
                                                                                                                                                                                                                                                                                                                Eukarysta, Metassa, Chordata, Craniata, Vertebrata, Bureleostomi:
Mammalia, Estberia, Primates, Catarrbini, Hominidae, Homo
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C
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Best Local Similarity 30.6%, Pr.J No 1.36.62;
Matches 15; Conservative 16; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   916 WPMLLNMRDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSEAVPLLVKVIK 964
                                                                                          Score 67; DB 2; Length 644;
                                                                                                                 23: Indols
                                                                                                                                                                                                                                                                                                                                                                              Gorlich D., Prehn S., Hartmann E.,
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF039023; AAC14260.1: -
                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1105 | 1105
| 1105 | AA, | 124738 MW. | 206466000000000007 | 00064.
                                                                                                                                         16 FILLIVELSOVPLAKOTLITHOVKDIOFROPIOSLVTKSVKVPAPYPG 208
                                                                                                                                                        Płam, PPO2449, Glyoc bydro_42, 1
SCOURNCE - 668 AA, 76788 MW; GR256PR1CO6C4P17 CPC64;
                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Lust sequence update)
01-AUG-1999 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 94:3082-3087(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE, PS00038; BELIX_LOOP_HELIX; UNENDWN_1
     65:5443-5450(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1153 AA.
                                                                                                                                                                                                                              PPT; 1105 AA
                                                                                                                    io; Mismatchos
                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel, 13, Last am
RAN-GTF BINDING PROTEIN (FPAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97250493; PubMed:9096349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 443-1153 FROM N.A.
                                                                                            0.68;
      Appl. Environ. Microbiol. 65
EMHL: AF184246; AAF16519 1;
InterProj [PR003476; -.
                                                                                            Ouery Match
Best Local Similarity 28.3%;
Matches 13; Conserrative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                 PRELIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR003015;
                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                      668 AA,
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCB1_Tax10=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FISSUE-GASTRULA;
                                                                                                                                                                                                                                                                                                                                             NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              012990; 073880.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SECUENCE
                                                        SPQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012990
                                                                                                                                                                                                                                              060518;
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ASSOCIATED (BY SIMILARITY).

-!- DEVELOPMENTAL STAGE: PRESENT IN THE UNPERTILIZED EGG THROUGH TO THE BLASTULA STAGE WHERE IT 13 DISTRIBUTED UNIPORMENT. LEVELS PHOP THEN GRADUALLY INCREASE PROMITY. PEMAIN VEPY 1.7M HINTI: 10 HOURS. THEN GRADUALLY INCREASE FROM 12 HOURS WITH A RAPID INCREASE AT 48 HOURS. AT 48 HOURS IT IS CONCENTRATED IN THE REGION OF THE GILL ARCHES. ALSO PRESENT IN THE ADULT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY. PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- DOMAIN, FOSSESSES INC. PHOSTHOSFERASE DOMAINS. THE SECOND ONE PROBABLY CONTAINS THE CATALYTIC DOMAIN, WHILE THE PRESENCE OF SLIGHT DIFFERENCES SUGGESIA DIFFERENT ROLE FOR DOMAIN 1.
-1- SIMILARITY, WITH HONRECELTOR TY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00109; PROTEIN_ALMANGE.....
SMART: SM00219, TyrKC: 1
Transferace; 1yrosine protein kindsc, ATP-binding; Phosphorylation;
Transferace; 1yrosine protein.
SH2 domain; kepeat; Developmental protein.
DOMAIN 336 SH2 (ATYPICAL).
SH2 (ATYPICAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K--E- LOSS OF AUTOPHOSPHORYLATION AND
                oates A.C., Brownlie A., Fratt S.J., Irvinc D.V., Lian F.C., Paw B.F.
Dorian K.J., Johnson S.L., Postlethwait J.H., Zon L.I., Wilks A.F.;
"Gene duplication of schiafish JAKE Lamologs is peromposive by
                                                                                                                                                                                                                                                                                                    TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 67; DB 13; Length 1153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFECTS IN EARLY DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 649 T > I (IN REF. 2).
770 770 T -> S (IN REF. 2).
799 799 S -> T (IN REF. 2).
111 111 111 L -> I (IN REF. 2).
1133 AA; 132480 MW; 736D52e3D03E7450 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1207 VTLILELIQHKKKLRSPQILVPTLFNLLSRCLEPLPQEQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1098 VTRLVKVLEEGKRLPPPDDGSEQLYNLMRRCWEATPEKR 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY). ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                il; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1189 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00069; pkinase; 2.
PPRSTTE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PKUJEIN_KINASE_DOM, 2.
PROSITE; PS00109; PROTEIN_KINASE_IYR; 1.
MEDLINE=99445372; PubMed=10515866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZFIN; ZDB-GENE-980526-142; jakl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000719; -. InterPro; IPR001245; -.
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11150
886
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Best Local Similarity
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Wakasuqi T., Naqai T., Kapoor M., Suqita M., Hto M., Hto S., Tsudouki J., Nafashima K., Tsudouki T., Suzuki Y., Hamuda A., ohta I., Inamura A., Yoshinaqa K., Suqinra M., "Complete nucleotide sequence of the chloroplast genome from the queen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1453 BESVQHQ1QSLMNILQYLURI PBEYFFTIPFAVSENKSESQBFMLQVFNVFTHTSPQLRB 1512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Viridiplantae, Chlorophyta, Trebouxiophyceae, Chlorellales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           534 EESITINKLKKVIDIISSKSSNPTL/FATFPKFAFI NFØSYKMI LQTFSFKSFYQVVFKS 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
ePertEll Will Pressible Pole in THEOMysome EYMAMICS BY SIMILARITY TO
YEAST PDSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zimmermann W., Wambutt R., Wood V., Rajandream M.A., Barrell B.O., Subirted (SPE-2600) for the FARL, Orenther Fibble databases. EMBL: ALA41624; CACO85601; - SEQUENCE 1205 AA: 138874 MW: 935DABHDE0A5E30FF CRC64;
  'CIF150, a human cofactor for transcription factor III-dependent
                                                                                                                                                                                                                                                                               1492 SQEEMIQVENVETHTSKQLRHFKFLSVSFMSGLLSSNNFLKKVVESGOPET 1542
                                                                                                                                                                                                                                                                                                                            465 SMEEMLQVFNKLLSLASTASSQKF, SHMWSQMLVSLSGEFFSLSNVSGKDLSLS
                                                                                                                                                                            0.6%; Score 67; DB 4; Length 1199;
35.3%; Pred. No. 1.40+02;
ive 7; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0.6%; Score 67; DB 3; Length 1205; Best Local Similarity 23.4%; Pred. No. 1.46+02; Matches 15, Conservative 18 Nismatches 3, 154-18
                                               CELL. BIOL 18:248-239(1998).
AF026445; AAC02966.1; -:
JENCE 1199 AA; 136993 MW; 82DA6EAA189D3EF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi, Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomyceticese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01 JAN 1998 (TrEMBLrel. 05, Last Sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRI: 1205 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 AA.
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                                                                                                                                                                     Query Match
Best Local Similarity 35.3%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                             initiator function.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCB1_Tax1D=4896;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             594 IKYL 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPAC110.02
                                                                                                     SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9HFF5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSHFF5
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       SORET
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                                                                                                                                                  Eukaryoja, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi,
Mammalii, Eutheria, Primates, Catarrhini, Hominidae, Homo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enkaryola, Metazoa, Chorsata, Craniata, Vertebrata, Enteleostomi,
Mammalia, Entheria, Primetes, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              455 SMBPMLQVIRKOU, ASTALAQEE JAHAMAQAEVA KASTANASTRIQ 50,5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.5. SMEEMLQVENKLLSLASJASSQKFQSHMM×QMLV×1SGFLKSLSNVSGKDT 515
                                                                                                                                                                                                                                                                                                                                                                                                                               Match Longth 1189; Loral Statistics 11.46.02; Longth 1189; Loral Statistiffy 45,3%; Pred. No. 1.46.02; and etc. Posservative 7; Mismatches 26; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                covery Match 0.63; Score 67; DB 4; Longth 1199; Hes? Local Similarity -85.48; Fred. No. 1.4e+02; Matches -16: Conservative 7; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massmalia: Entheria: Primates: Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          Martines E., de H., Lao Y., Ynan C.-X., Roeder E.S.,
Schmilted (167) 1997; to the BMH, Abenkrek Appel databases.
DMM: APOLOZOL, AAY-MISSE, SEGEN AS USADANY CROSS.
SEGEN'E. IEM AA: 135434 MW. SEGALANY USADANY CROSS.
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EMBL: AF082894; AAC13540.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kautmann J., Abrens K., Koop R., Smale S.T., Muller R.,
of IMN For (TEMELTO), 65 (Totaled)
OF DATE TOWN (TEMELTO), 05 Last Sequence update)
OF ADD TOWN (TEMELTO), 07 Last amountation update)
TAIA BINDING PROJETN ASSECTATED FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of AGS 1998 (ITEMBLED, 07, Created)
of ADS-1998 (ITEMBLED, 07, Last sequence update)
of MAY-2000 (ITEMBLED, 13, Last annotation update)
THE-NSSOCIATED FACTOR INFILISO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of DN-1998 (itEMBLIDE), 06, (Touted)
of EBN-1996 (itEMBLIDE), 06, Last, sequence update)
of NN-1998 (itEMBLIDE), 08, Last annotation update)
%-FAN-198-0F INITIALSE FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRI; III'' AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRI; 1155 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDICINE VALUE (29) PURMOD 34 LBB 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEEL IMINARY;
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                                                                                                                             Monte Sapiens (Human).
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                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                    NCHI, LAXID BELLE,
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PRELIMINARY;
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InterPro: IPR002501;
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
alga Chlorella vulgaris: the existence of genes possibly involved in chloroplast division.", Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Transposon insertions in the Flavobacterium johnsonae fts% gene disrupt qliding motility and cell division."; Submitted (JUL-1999) to the EMBL/GenBank/EDBS databases. EMBL, AF169967; AAD50463.1; -
                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria, Proteobacteria, alpha subdivision, Sphingomes group,
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38,5%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches 19; Indels
                                                                                                                           0.6%; Score 66; DB 8; Length 68;
                                                                                                                                                        11; Indels
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InterPro: IPR063396; -...
Plam. PF02464; CinA. 1
Hypothetical protein.
SEGUENCE: 220 AA; 23680 MW; 09880764F7148568 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
                                                                              68 AA, 8230 MW; CR82F:E33A36EE71 CR064,
                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLiel, 13, Created)
01-MAY-2000 (TrEMBLiel, 13, Last sequence update)
01-MAK-2001 (TrEMBLiel, 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 AA.
                                                                                                                            Overy Match 0.6%; Score 66; DB 8 lest Local Similarity 44.8%; Pred. No. 7.4; Marches 13; Conservative 5; Mismatches
                                                                                                                                                                                       69 LPSOLARTLERSVQTKAVNKQLDENISLF 97
                                                                                                                                                                                                         FRT
                                                                                                                                                                                                                                                                                                PRT;
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MEDLINE=99350425; PubMed-10419959;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181:4598-4604(1999).
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                                               EMBL, AB001684; BAA57855.1;
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Kempf M.J., McBride M.J.;
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Hest Local Similarity 38.5%
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                            Zymomonas mobilis.
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                                                                 Chloroplast.
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                                                                                SEQUENCE
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong Y., Park S.W., Choi S.Y.; "Expression of the CIP1 yene induced under cadmium stress in Candida
                                                                                                                                                                                                                                                                                           16 KPLKWSSFQAVNKLKYLLINKVGLPKKFKIGHAGTLDPLATGLILLICTGKFTKKISFLQG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Candida sp.
Eukuryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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Eukaryota, Fungi, Ascomycota, Popiromyrotina, Sordariomyrotes;
Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Scote 66, DB 3, Length 296;
26.0%; Pred No. 39;
                                                                                                            Query Match
Best Local Similarity 25.3%; Pred. No. 29;
Matches 23; Conservative 16; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25; Indels
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NCBL_DaxID=39398;
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EMBL: Y13973; CAA74306.1; -.
SEQUENCE - 296 AA; 3.2338 MW; ВЕЧРОННОЙЦНЯЙТО ОРО64;
PÉGN; PEG1509; TruB_N; 1.
SEQUENCE 229 AA, 25872 MW; CFDAE756579RAC74 CPC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAF-2001 (TrEMBLrel 16, Last annotation update)
RELATED TO IMPORTIN BETA-2 SUBUNIT (TRANSPORTIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           76 QAKEYTGTFYIGATTPSYDLETEIDQTFPTE 106
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Matches 13; Conservative
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1156 10SppgFP 1163

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Phabditidaes Beloderimaes Saemorhabditis.
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                                                                                            Length 921.
                                                                                          7.18. September 104 3 Lough 921
47.18. Pred. N. 1.4e+02;
115e [5] Mismatches 13, helels
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Sammarted (1987) no entre EMBL/Shookaniy/Debat databasess EMBL: ALMSISTED (ASSISTATE CASSISTED)
                                     ALL AND I LAND MWD COMPETELD 965 B419 CROS4.
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21-JAN 1996 (Irimmirel, 15, Last Septence update)
51-MAR 2-01 (Tremedial, 16, Last annotation update)
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-1. SIMITARITY: 10 HELLTASE OFTERMINAL DOMAIN.
EMBL: DEAL23: CARGGOODER.
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                                                                                                                                                                                                                                                                                            PRT; 1241 AA.
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                                                                                                                                                                                                                                                                                        PRELIMINARY;
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InterProp IPROUITED
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Begit Lozal Similarity
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TOTALLS.
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Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Crystal structure of Thermus aquaticus core KNA polymerase at 3.4 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toyoda H., Kohara M., Kataoka Y., Suganuma T., (mata T., Imura N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequences of all three policying serotype appearance implication for genetic relationship, gene function and anniquency determinants."
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE:99428144; Pubmed-10499798;
Zhang G., Campbell E.A., Minachin L., Richter C., Severinov K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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                                                                                                                                                                                                                                                                                                                     Thermus/Deinococcus group; Thermus aroup; Thermus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 66; DB 2; Length 1524;
13.3%; Pred. No. 2.5e-02;
ive 9; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nomoto A.; Submitted (APR-1985) to the {\tt EMBL/GenBank/DDBJ} databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GGT 1999) to the EMBL, Generally, DEEC dutubuses.
                                                                                                                   01-001-2000 (TrEMBLrel. 15, Created)
U-MR-2001 (TrEMBLrel. 16, List sequence update)
01-MR-2001 (TrEMBLrel. 16, List annotation update)
RNA POLYMERASE, BETA-PRIME SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel, 01, Created)
01-NOV-1996 (TrEMBLrel, 01, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT: 2206 AA.
                                                                PRT: 1524 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1523 QLISSNNFLKKVVRSGGPRITKGLDEPLLE 1552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          546 PLINPNNPLKKLLAQCAPETLIPNEKPMLQ 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=84216300; PubMed-6202874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mol Biol 174.561-585(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Hest Local Similarity 43.3%;
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL: X00596; CAA25247.1; -.
HSSP; Q84790; 1PVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Y19223; CAB65466.3;
InterPro; IPR000722; -.
InterPro; IPR002879; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY:
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000081; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiqenic determinants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resolution.";
Cell 98.811-824(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human poliovirus 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          Thermus aquaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=12086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PV3 POLYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minakhin L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Darst S.A.;
                                                                                                                                                                                                                                                                                                                            Bacteria;
                                                                                           C9KWD6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             084792
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                                                         Q9KWU6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 60
RESULT 59
                                                                                                                                                                                                                                                        RPOG.
                           O9KWU6
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ANAIN-HARMELET SE HOUT R.A., Evans C.A., Genagne J.D., MEDLINE-20196005; Pubbed-1073132;
Adams M.D., Celniker S.E., Hout R.A., Evans C.A., Genagne J.D., KA. Adams H.D., Celniker S.E., Hichards S. Ashburner M., HenderSon S.N., Souteon C.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Ropers Y.-H.C., Hazel R.G., Champe M., Pfeiffer B.D., RA Brandon R.G., Ropers Y.-H.C., Hazel R.G., Nortman J.R., Anders S. Hell, G., Nolson C.R., Baldwin D., RA Abril J.E., Adbayani A., An B.-J., Andrews Plannkoch C., Baldwin D., RA Ballew R.W., Basan A., Baseldale J., Baykaring D., Baldwin D., Ballew R.W., Banos P.V., Berman B.P., Handdari D., Bolshakov S., RA Berson K.Y., Banos P.V., Berman B.P., Handdari D., Bolshakov S., RA Bertis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Rayles C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Cherry J.M., Cawley S., Dunkov B.C., Dunn P., Bartis K.J., Evangelista C.C., Ferraz C., Perriera S., Dunkov B.C., Dunn P., Bordson K.J., Evangelista C.C., Ferraz C., Perriera S., Fleischmann W., RA Posler C., Gabrielian A.E., Garte N.M., Glasser K., Anderson R., Goode A., Gong P., Gorreil J.H., Gu Z., Guan P., Hatris M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      493 PVRILLAMNHLKKIMETSKEGVLESFIKEAVLABLODDNIDVVLSAISAFEIFKEHFSSEV 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rteryjota, Rooptera, Endopteryjota, Diptera, Brachycora, Museumorpha.
Ephydroidea: Drosophilldee, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433 ESKYPRTLDVVLEEHLKETADLKKUELLHÜFVSLSTSGGKYGFLADSDTSTMLSLNHPLA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sideo
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                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 66; DB 14; Length 2206;
17.8%; Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78; Indels
                                                                                                                                                                                                                                                                                                                                                                     2200 AA, 116295 MW, 0004278973A88679 CECF4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 2470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Mismatches
                                                                                                                      Pram; PF00073; rhv; 3. Pram; PF000848; Cys-Protease-3C; 1. Pram; PF00686; RNA dep_RNA_rol; 1. Pram; PF00910; RNA_helicase; 1. Pram; PF0047; Prica_PZA; 1. Pram; PF0152; Prico_PZB; 1. Pram; PF0152; Prico_P1A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Onery Match 0.63
Best Local Similarity 17.83
Matches 23, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                  Probom; PD001125; -; 1.
Probom; PD001274; -; 1.
Probom; PD001306; -; 1.
InterPro; IPR000605; -.
                                                                                                       InterPro: IPR003593; -.
                                                                                                                                                                                                                                                                                                                                   SMART; SM00382; AAA; 1.
                                                            IPRU02527; -.
                                                                                 InterPro; 1PR003138;
                                           IPRODINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                553 TISNLLNLF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       693 QLRRMLEFF 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID 7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GG5092 PROFEIN.
                                                                                                                                                                                                                                                                                                                                               Polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
                                           InterPro;
                                                                  interPro;
                                                                                                                                                                                                                                                                                                                                                                           SECONDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VK45
Q9VK45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG2097
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Harris N.L., Harvey D., Heiman T.J., Hernandez J. R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alali M. Kaligh F. Parpen G.H., Kee J. Kenison J.A., Kelchum K.A.,
R.A. Kimmei B.E., Kedira C.H., Kraft C., Kravilz S., Fulp D. Lai Z.,
R.A. Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
R.A. Liu X., Mattei H., Merlin R., Merherson D.D.,
R.A. Meikliew C., Milahina T.C., Merhend M.P., Mepherson D.L.,
R.A. Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.L.,
R.A. Raisalon M., Pithman G.S., Pan S., Porlard J.M., Nelson D.L.,
R.A. Falizzole M., Pithman G.S., Pan S., Porlard J., More R., Shen H.,
R.A. Shue B.C., Sider Kiamos I., Simpson M., Skupski M.P., Smith T.,
R.A. Shue B.C., Sider Kiamos I., Simpson M., Strong R., Son E.,
R.A. Shue R.C., Stapleton M., Strong R., Son E.,
R.A. Syltskas M., Moodage T., Worley K.C., Wu D., Yang S.,
R.A. Wassarman D.A., Weinstock G.M., Weissenbach J.,
R.A. Yeh R. F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., A.,
R.A. Myors R.W., Rubin G.M., Venter J.C.,
R.R. Zihence Sequence Of Drosophila melanogaster.";
R. Schence L.J. Schaffer B., Venter J.C.,
R.S. Shience Saylence Of Drosophila melanogaster.";
R. Schence L.J. Stapleton M., Wenter J.C.,
R. Schence L.J. Stapleton M., Wenter J.C.,
R. Schence L.J. Stapleton M., Zhou X., Zhu X., Smith H.O.,
R. Schence Saylence Of Drosophila melanogaster.";
R. Schence L.J. Schaffer B., Shience L.J. Schaffer B., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kume S., Muto A., Aruga J., Nakagawa T., Michikawa T., Furuichi T.,
Nakade S., okano H., Mikoshiba K.;
"The Xenopus 1P3 receptor: structure, function, and localization in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus Jaevis (African clawed froq).
Ekarjota, McLazoz, Chordata, (rinninia, Vertebrata; Foreleastodi);
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 66; DB 5; Length 2470;
34.3%; Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                281031 MW; SP78D2ECC07C7FF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NDV-1996 (TrEMBLAG). 01, Last sequence update) 01-MAR-2001 (TrEMBLAG1. 16, Last annotation update) INOSITOL 1,4,5-TPIPHOSPHATE REFERTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2070 LEKTPRSSPYVPPAALITVLALAEKUKENYIVUUP 2104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1123 LVPVLDAFPFLPPQAMTTTPSTAKOLGKKYLVFVP 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 2693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00915; P13.4_KINASE_1; 1. PPOSITE; PS00916; P13.4_KINASE_2; 1. PROSITE; PS50290; P13.4_KINASE_3; 1. SMART; SM00146; P13KG; 1. SEQUENCE 2470 AA; 281031 MW; 5078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93258819; PubMed-8387895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00454; PI3_PI4_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE003638; AAF53237.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P42345; IFAP.
FlyBasc; FBgn0032466; @G5092.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D14400: BAA03304.1; -. InterPro: IPR000493; -. InterPro: IPR000699; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Conscrvative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003151; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    occytes and eqgs ";
Cell 73:555-570(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02259; FAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PP00515; TPR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1PP001440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1PR000403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPR003152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sest Local similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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Unro Ku. Lakufashi Mu. Sekhos Mu. Buba Sull. Ankai Au. Kosoni Hu.
Hoseyama Au. Pukor Su. Mani Yu. Nishijima Ku. Nakazawa Hu.
Cakuniyi Mu. Masuda Su. Punalishi In. Innaka Iu. Kusah Yu.
Tamazaki Kosoli Mu. Seriki Mu. Akibo hi Hu.
Mikiasara Iu. Kamata Ku. Sake Yu. Kibo hi Hu.
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24, 648; Prod. No. 185
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Bigothotical protein.
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(1-N.V.-1996. (FEBBGLOCE, CL. Last. sequence update).
M. N.V. 1994. (FEBBGLOCE, CO. Last. amoltation update).
M. AA. AND. M. BB. TENES.
M. MA.A. AND. M. BB. TENES.
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MEDLINE 98344137; PubMed 9679194;
MEDLINE 98344137; PubMed 9679194;
Mawaladayaa Y., Sawada M., Bolibawa H., Halbayaa Y., Hino Y.,
Tamadareto a., estime M., Edela a. I., bessel H., Hesoyama A., Medai Y.,
Sakai M., Gqura K., Otsuka P., Nabasawa H., Takamiya M., Ohfoku Y.,
Fundhabai I., Lanaka T., Kodon Y., Vanazaki J., Eushida N., Colonia A.,
Acki K.-I., Yoshizawa T., Nathura Y., Pokk F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.,
Tompitch sequence and dene organization of the genome of a hyper-
thermophilic archaebacteriam, Pytococcus hotikoshii of y.";
DNA Res., 5555-76(1998).
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                                                                                Trinh S., Haggood A., Royssot G., "Conjudal transfer of the 5-nitroimidazole resistance plasmid p1P417 from Bacteroides vulgatus BV-17: characterization and macleolide sequence analysis of the mobilization region.";

EMBL: X92849; CAA64434.1: -.
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Archaeoi: Euryarchaeola) Thermococeales; Thermococeaeoae; Pyrococeus,
NCRI_Tamib-53953.
                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 65; DR 2; Length 2011; 35,3%; Pred. No. 34;
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Fron-sultur: Hypothetical protein.
SEQUENCE 286 AA; 31564 MW; C991CC1680F75cCA CRC64;
                                                                                                                                                                                                                                                                                           201 AA; 22826 MW; 40F2DAF6628A0B41 CRC64;
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01-AUG-1998 (TIEMBLEEL, 07, Last sequence update)
01-667-2000 (TIEMBLEEL, 15, Last annotation update)
HYPOTHELICAL 31.6 KDA PROTEIN PHOSE2.
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                                                           MEDLINE 97113421; PubMed 8955281:
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Best Local Similarity 26.0%;
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Best Local Similarity 35.0%;
Matches 12, Conservative
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SECUENTE PROM N.A.
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RESULT
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                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metasoa, Arthropoda, Trachoata; Hovapoda, Inserta,
Puteryata, Mecoplera, Endopleryasta, Diptera, Brachysera; Museomorpha;
Ephydroidea, Drosophilidae, Drosophila.
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                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                   287 AA.
                                          PRT;
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PRINTS; PR00925; MILOCARRIER.
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                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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CG11196 PROTEIN.
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O: Gaps

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481 TSLALSLABPLAPVELLAMNBLEFTMFTSFFTVFFSFFFPAVLAPFGDPRIDVVLSATSA 540
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Enterovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114; AQTVSSVFKGISVNAEQVETELEPPPARPH CTVVQQERPQFRAGEKSON ESVQE 1198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 6%; Score 65; DB 14; Length 302; 21 0%; Prod No. 54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48; Indels
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Submitted (MAP-2000) to the EMBL/GenHauk/DDRT databases.
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E. 433 AA; 46877 MW; FOD18C4E56AHEBBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          302 AA; 33372 MW; AARPKO79RRCK6EIC CRC64;
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01-oct-2000 (TrEMBLrel 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
MFTHYL-ACCEPTING CHEMOTAXIS PROTEIN.
                               01-0CT-2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
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nos 15; Conservative 15; Mismatches
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 PRT;
                                                                                                                                                                                                                                        MEDLINE-20364294; PubMed-10906191;
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Interproj IPRO01676; -.
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 PRELIMINARY;
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Nishakara I., Namari K., Sarai, S., Lakohashi Polji A., Hara H.,
Nishakara I., Namari K., Sarai S., Lakohashi Polji A., Hara H.,
Arita M., Nihakara Y., Caniga S., Kama P., Hara H.,
Arita M., Nihakara I., India S., Kisa N., Sair K., Yamamari G.,
Nikaran Rasa A., Nikaran Y., Nishamari K., Masahara K., Masahara S.,
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Safaari G., Andrew S., Andrew M., Masahara A.,
Safaari G., Andrew S., Andrew M., Masahara M.,
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The AVERGE CONTROL OF THE TOTAL OF THE THE THE THE TOTAL OF THE TAXABLE OF TA
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"An interface in the structure and function of the scryl-FRNA
synthetase is not responsible to the evolution of CDG codon
reass among in the sponsible to the evolution of CDG codon
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EMBL. AND ALD ASSETT AND ASSETT ASSETT AND ASSETT ASSETT AND ASSETT ASSETT AND ASSETT AND ASSETT ASSETT
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NPG legific 5476;
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of MAR 2001 (TERMILOL, 16, Last sequence update)
el-MAP 2001 (TERMILOL, 16, Last annotation update)
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Nature 1., ishikasa E., Shimsa M., Fikuma K., Hirusawa M., Miyajima N., Tabaka A., Kotani H., Nomera N., Obata O.: "Prediction of the coding sequences of unidestified buren across XIII. in complete sequences of incluse this chairs from brain which code for large proteins in vitro."; page 10 and proteins in vitro.";
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Nature 407;508-513(2000).
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Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homes
                                                                                                                                                                                                                           Archaea: Euryarchaeota; Thermoplasmales; Thermoplasmaceae;
Thermoplasma.
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PROSITE; PS01405; MPAA_NIFB_FQ0E, UNKNEWN_1.
Bypothetical protein.
Bypothet 571 AA; 65511 MW; 7603590167E4485F CR0543
                                                     01-MAR-2001 (TrEMBLE), 16, Created)
01-MAR-2001 (TrEMBLE), 16, Last sequence apdate)
01-MAR-2001 (TrEMBLE), 16, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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PRI:
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MEDLINE:20479972; Pubmed=11029001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTAM, PEU0397; WW: 1.
PRINTS, PRO1217; PRICHEXTENSN.
FRINTS, TEOOBOG, VINCOLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL445065; CAC11808.1; -
                                                                                                                                                     HYPOTHETICAL PROTEIN TA0670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KIAA1014 FROIEIN (FRAGMENT).
                                                                                                                                                                                                                     Thermoplasma acidophilum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY
PRFLIMINARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR002965; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interFro: IPRO00385;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro: IPR000633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUCCESSOR FROM N.A.
LISSOR-BRAIN:
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  NCB1_Tax1D-2303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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O9VPR5
                                                                                                                                                                                                                                                                                                     CC2807
                                                                                                                                                                                            RESULT 75
                                                                                                                                                                                                            O9VPR5
                                                                                                                                                                                                                                     ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.15°
                                                                          Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse ear cress).
Enkayota, Viidipjantac, Enkaropsikut, Trachesphyta, Spersatrphyta,
Magnoliophyta, endicopyledoms, corc endicots, Rosidac, eurosids II;
Frassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                      Enkaryola, Metazoa, Chordata, Craniata; Vertebrata; Enteleostomi;
Mammalia; Entheria; Primates, Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. COLUMBIA;
Edunsley S.D., Lin X., Ketchom K.A., Crosby M.E., Branden R.C.,
Sykos S.M., Kaul S., Mason T.M., Korlayoge A.P., Adams M.D.,
                                                                                                                                                                                                                                                                                                                                                                                 Blum H., Bauersachs S., Mowes H.W., Gassenhuber J., Wiemann S.;
Submitted (JAN 2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL137480; CAB70761 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 SKEGVDESFIKEAVLARIGIDNIDVVESATSAFELFKEHFSSEVTISNDLML 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.4 AQEMPORTIARYTHYDRIOTISNSTESSETSTASLOFFESFSCOVSSSSIMPL 685
                                                                                                    509 SKEGVBESFIKEAVLARLGDDNIDVVLSATSAFETFKEHFSSEVTISNLLNL 560
                                                                                                                  358 AOENRUETLARQTI.KERTGTÜSNSTESSETSTGSI.CKESFSGQVSSSSLIMPI. 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%, Score 65, DR 4, Torighh 1013;
30.8%, Fred. No. 2.16+02,
tive 12, Mismatches 24, Indels
                                              0.6%; Score 65; DB 4; Length 737; 30.8%; Pred. No. 1.5e+02; time 12; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1013 AA; 109874 MW, 36F15450746830FF CR364,
        SEQUENCE 737 AA; 80758 MW; 75458EnbzAbCA55z CKC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61-AUG-1996 (TrEMBLEEL, 07, Created)
01-AUG-1998 (TrEMBLEEL, 07, Last Sequence update)
01-MAY 2000 (TrEMBLEEL, 13, Last annotation update)
                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1217 AM.
                                                                                                                                                                                              PRT, 1013 AA.
                                                                                                                                                                                                                                                                 HYPOTHETICAL 109.9 KDA PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00866, VINCOLIN.
PROSITE; PS01159; WW_DOMAIN.1; UNKNOWN_1.
PROSITE; PS00303; WW_DOMAIN.2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUTATIVE IBP-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 36.8% Matches 16, Conservative
                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY,
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          Interpro; JPR000633; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001202; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00397; WW; 2.
                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR002965;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID: 9606;
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                                                                                                                                                                                                                                                                                                                                                                        TISSUE-TESTIS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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NON_TER
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                                                                             Matches
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RX Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Lip.M., Hoskins R.A., Galle R.F.,
RA Ananatides P.C., Schorer S.E., Lip.M., Hoskins R.A., Galle R.F.,
RA Ananatides P.C., Schorer S.E., Lip.M., Hoskins R.A., Galle R.F.,
RA Ananatides P.C., Schorer S.E., Lip.M., Hoskins R.A., Henderson S.N.,
RA Sutron G.G., Worthman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Abrill T.F., Adhayani A.A., Holsell R.G., Champe M., Preiffer B.D.,
RA Abrill T.F., Adhayani A.A., Baxendall F.C., RayerAtharoglu L. Rayer R. G.L.G.,
RA Beesson K.Y., Benos P.V., Berman B.P., Handari D., Bolshakov S.,
RA Berkery B., Basu A. Rayendall F., Cadlenker P. Rondra T.,
RA Burtis K.C., Husam D.A., Burthan M.P., Protter P., Cadler R.A., Chandra I.D.,
RA Burtis K.C., Prophy S., Dahke C., Davenport L.B., Davies P.,
RA Detkier R.D., Fricher A. Freng E., Mays A.D., Dex I. Dict. S.M.,
PA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
PA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
PA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
PA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
PA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
PA Cherry J.M., Cawley S., Belman T.J., Herrarda C., Ferrierra S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Herrarda C.J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Herrarda C.J.R., Koulp D., Lai Z.,
Lasko P. Lei Y., Levitsky A.A., Howland T.J., Well M.-H., Degwam C.,
RA Mishina N.V., Mayan R. N., Mayan M. N., Melssen D.B.,
RA Mishina N.V., Mayan R. N., Mayan R., Shen H.,
Shie B.C., Spradling A.C., Squeletier E., Shen H.,
Shie B.C., Spradling A.C., Stapleton M., Strong R., Shen B.,
Shier B., Spradling A.C., Stapleton M., Strong R., Shie B.,
Shier B., Spradling A.C., Stapleton M., Strong R., Wan O., Sheng H.,
When P. P., Though W., Chou W., Chou S., Chon S., 
                                                                                                                                                                                                                                                                                                                                                                                                                          1688 PFVLVLXTAVKLIAPEPKEEKNVIGSALLOTAEVTSTLEALAIPOLPSLAPELLTIMKN 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaijota, Metagoá, Arthropoda: Tracheata: Graapoda: Insecta;
Pterygota, Neoptera, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Prosophilidae; Prosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                554 PEVHPTYNALMSRLTHQDQDQRVKECATTCMGLVISTFGDQLRAELPSCLPVLVDRMGN 612
                                                                                                                                                                                                                                                          Length 1217;
                                                                                                                                                                                                                                                                                                   Best Local Similarity 28.8%; Fred. No. 2.5e+02;
Matches 17; Conservative 11; Mismatches 31; Indels
                                                                                  EMBL; ACCOA136; AAC18930.1; -. SEQUENCE 1217 AA; 134620 MW; AA23DAE4A94EELEA CRC64;
Somerville C.R., Venter J.C.;
Schmitted (TTM-1999) to the EMPI/GenRank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-HNN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The genome sequence of Drosophila melanoquaster."; science 287:2185 2195(2000).
                                                                                                                                                                                                                                                          0.6%: Scare 65: DB 10;
28.8%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1349 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                        Çuery Mateb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9VPR5;
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Amanatibes B.C., Scherer's F. Li D.W. Highlins B.A., Galle B.F.,
S. George B.A., Lowis S.E., Richards S., Ashburner M., Henderson S.N.,
S. Strin G.J., Worlman G.R., Yandeli M.D., Zhana O., Chen L.X.,
A. Brandon R.C., Borger Y. J. C., Blarel B.C., Clampe M., Preiller B.D.,
A. Mill J.F., Aphayani A., An H.-J., Andrews Prannkoch C., Baldwin D.,
A. Antil J.F., August R.A., Berrediler, B.B., Andrews Prannkoch C., Baldwin D.,
A. Barllew R.M., Besu A., Berrediler, B., Shanarin D., Folshakov S.,
A. Berrediler, B. Berrediler, B., Braker D., Bersley R.M.,
A. Berson K.Y., Bernos R.V., Bernan B.P., Broktier A., Chandra I.,
A. Herris K.C., Bussam D.A., Burler H., Cadier R., Canter A., Chandra I.,
A. Cherry J.M., Cawley S., Lahkbe C., Pargenpar L.R., Brette P.,
A. de Pablos B., Delchert A., Berna Z., Mays A.D., Dew I., Dietz S.M.,
A. Adadson K., Lewin E.E., Dewnes M., Ondern Royle S., Dunkov B.C., Dunn P.,
A. Goder C., Gard R.S., Garg N.S., Gelbart W.M., Glasser K.,
A. Hurris N.J., Revener J. R., Gerrell J.R., S. C., Char, F., Barris M.,
A. Hurris N.J., Bernard J.M., Canger N., Bernard W.M., Glasser K.,
A. Hurris N.J., Bernard J.M., Canger N., Bernard M.,
A. Hurris N.J., Bernard J.M., Canger N., Bernard N.,
A. Hurris N.J., Bernard J.M., Canger N., Bernard N.,
A. Hurris N.J., Bernard J.M., Canger R.,
A. Hurris N.J., Harrow D., Bernard J.M., Canger R.,
A. Hurris N.J., Harrow D.,
Bernard J.M., Canger J.,
Bernard J., Bernard J.,
Bernard J., Bernard J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stitskas R. Lortor I. Inter B. Venter E. Wang A.H. Wang X., Wang C. Y. Wassarman D.A. Weinstock G.M., Weissrabach J., Wallams S.M., Weedery K., Williams S.M., Weedery E., Walle, Williams S.M., Weedery K., Williams S.M., Weedery E., Walle, Williams S., Yao Q.A., Zhong X.H., Zhong E.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.C., Cibas K.A., Myans E.W., Ruhin G.M., Wanter G.S., Zhu X., Smith H.C., Schiere Sequence of Ensembling metanomessater. The genome sequence of Ensembling metanomessater. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proryous as Neoptoras Endoptorydotas Diptoras Brachycetas Muscomorphas
Ephydroideas Drosophilidaes brosophila.
N'ML_taxID-7227;
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A., Gallo P.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           orosopbila melamoastor (Fruit 113).
Būkaryota, Metazoa, Arthropoda: Tracheata; Hexapoda; Insecta;
                                                                                                                   0.6%; Score 65; 18-5; Length 1349;
4.8%; Pred. No. 6002;
                                                                                                                                                                                                    20; Indels
                                                                                                                                                                                                                                                                                1813 LATTLAPHVLLPATERITEQIEKNWENHMSPEMSILGEHLGXMERE 1858
                                                                                                                                                                                                                                                                                                                                                         1164 VAESCRPFIVLPALMNEYRVPELNVQNGVLKSLSFLFEYIGEMGK: 1209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HELLIX, 1930 PELLIX: CHKIN-WH. 1.
A) 2430-40 MW; E3FBH4FEC7A25636 CRC544.
    Thought MW: APRING CINE 263 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O. MAYZEGE (TERMILLE), 3. Treated)
of MAY zees (TERMILLE), 3. Last sequence update)
of JSN-zees (TERMILLE), 3. Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fr. 1236 17 A
                                                                                                                                                         local Similarity (4.8%) Pred. No. (600), os 160 Conservative to Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRE: 2114 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITAR ZOLOGOGO, POIMON 107 (132)
Adams M.D., Colnifor S.F. Holt P.A., P.
Amanatibles P.C., Schorer S.F. Li P.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBLE AEOUSTON, AAPTRÓGLIÉ
Flybaser Francostoff, (112042)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY:
S. SEQUENCE LOTA AND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2114 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECTRINGS PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PP SIPE PSOUGHS.
SEQUENCE - ZIPE AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331Z047 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN HERKELEY;
                                                                                                                       Ouery Match
Best Lessie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QMAY445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23VY44
                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - 1VY4 -
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MEDLINE 98978014; FabMed 9714232;
Tokita P., okamato H., Liraka H., Kishimaro I., Tenda F., Miyakawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila metanegaster (Fruit 119).
Enkaryota Metazea Arthropedia Trachesta: Hexapeda: Insecta:
Petryodia: Neoptera: Endopterygota: Diptera: prachycera: Muscemerpla:
Ephydroidea: Drosophilidae; Drosophila.
                                                5.41.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0: Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The entire nucleotide sequences of three hepatitis o' zirus isolates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (ITEMBLIEL. 08. Last sequence apdate)
51 MAE 2001 (TIEMBLIEL. 16. Last annotation apdate)
GENEME FOLYPROTEIN (CONTAINS: ENVELOPE GLYCOPFORTIN EL/NSI (GP68)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECHENCE From N.A.
MEDIALE-2024512: FubMed-10881435;
MEDIALE-2024512: FubMed-10881435;
Median 2., Frado A., McLaia J., Nash H.A., Kaabe T.;
"Mishroom body detect, a gene involved in the control of neurobiast
"Mishroom body detect, a gene involved in the control of neurobiast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses, ssenta positive strand viruses, no PNA etage; Flaciniiidae;
Hepacivirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 65; DB 5; Length 2501;
41.7%; Pred. No. 60.02;
Score 65; DB 5; Laugth 2116;
Pred. No. 5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16: Indels
                                           ie; ladels
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2501 AA: 286525 MW: F3E087071R771EC2 CRC64:
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                                                                                                                                                                                                                                                                                                 01-0CT-2000 (TrEMBLE), 15, Created)
01-0CT-2000 (TrEMBLE), 15, Last sequence apdate)
01-MAR-2001 (TrEMBLE), 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proliferation in Prosophila, oncodes a colled-col
Proc. Matl. Acad. Sci. 5.8.A. 97:8122-8127(2000).
EMBL: AF174134; AAF88146.1; -.
Flybase: Fhqu0002873; mud.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1485 USFNKSFSQEEMLQVFNVFTHTSKQLRHFKFLSVSF 1520
                                                                                            1485 VSENKSESOERMIQVENVETHISKOLRHERFISVSF 1520
                                                                                                                    :11 || |:|: | :111 || 1111: | 1111 || 1111: | 1657 || LSFGSSEPPRETILIERGENINT SKIPARFKFIJORF 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2042 ISFGSSEPPREILRPPGEHNNISKTPAKFKFITGAF 2077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTITE: PSOCORS: HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PR1; 3019 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 Mismatches
                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLIFel: 08, Created)
                                      ur.
  0.6%;
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Matches 15, Conservative
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003015;
Onery Match
Hest Local Similarity
Matches 15, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hepatitis C virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN THEROR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGB1_Tax1D=7227;
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                                                                                                                                                                                                                                                                                                                                                                          MUD PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                             CONCM7;
                                                                                                                                                                                                                                                        CWCM20
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                                                                                                                      ENVELOPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Envelope protein; Glycoprotein; Nonstructural protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euglenodoa; Kinetoplastida; Trypanosomatidae: Leishmania.
                   durentic groups."

J. Gen. VICOL. 79:1847-1847(1998)

J. Gen. VICOL. 79:1847-1847(1998)

J. Gen. VICOL. 79:1847-1847(1998)

J. Gen. VICOL. 79:1847-1847(1998)

CONTAINED WITHIN THE GENOME POLYPROTEIN THAT CONTAINS: CAPSID CONTAINED WITHIN THE GENOME POLYPROTEIN TE. BUNELOPE CHYCOPROTEIN PROTEIN: UNIVERSITY OF THE VIEWS FROM ST. NGAA, NGAB, NGSA AND NGSB. THE VIEW OF THE VIEWS IS COVERED BY A LIPOPROTEIN ENVELOR THAT CONSISTS OF TWO PROTEINS: PROTEIN M AND GLYCOPROTEIN E (BY
in genetic groups 7-9 and comparison with those in the other eight
                                                                                                                                                             SIMILARITY).
SIMILARITY: TO HEPATITIS C VIRUS NON-STRUCTURAL PROTEIN E2/NSI
                                                                                                                                                                                                 -i. SIMITÄRITY. TO HEPATITIS C VIRUS ENVELOPE GLYCOPROTEIN El.
-i. SIMILARITY: TO HEPATITIS C VIRUS RNA DEPENDENT RNA POLYMERASE.
EMBL; D84262; BAA32664.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 65; DB 14; Length 3019;
42.9%; Pred. No. 7.4e+02;
ive 7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (FFEMBLrel. 15, Last sequence update)
01-OCT-2000 (TFEMBLrel. 15, Last annotation update)
PROBABLE CODED FOR BY C ELEGANS CDNA YK38H3.5 (FRASWENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Coat protein, Envelope protein: Objects: Transmembrane. Polyprotein; EnA-directed ENA polymerase; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 AA, 6315 MW, EE34B6A2678549D2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00290; IG_MHC. UNKNOWN 1.
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PF01542; HCV_core; 1.
PF01543; HCV_capsid: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 0.6%;
Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FMBL; AL160493; CAB97624.1;
NON_TER 53 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00998; HCV_RGRP; 1.
Pfam; PF01001; HCV_NS4b; 1.
Pfam; PF01506; HCV_NS4a; 1
Pfam; PF01506; HCV_NS5a; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01560; HCV_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCV_NS2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00487; DEXDC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                   IPR002522; -.
                                                                                                                                                                                                                                                                                                                                                                               IPR002521: -.
                                                                                                                                                                                                                                                                                                                                                                                                                 IPR002531; -.
                                                                                                                                                                                                                                                                           InterPro; IPR000745; -
                                                                                                                                                                                                                                                                                            IPR001410; -
                                                                                                                                                                                                                                                                                                                                             1PP002518; -
                                                                                                                                                                                                                                                                                                                                                               [PRO02519; -
                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002868;
                                                                                                                                                                                                                                                                                                              IPR001490;
                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; 1PRO03006;
                                                                                                                                                                                                                                                                                                                               1ppnn2166.
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                                                                                                                                                                                                                                                              1A1V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD186062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN = FRIEDLIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01538;
                                                                                                                                                                                                                                                            HSSP; P27958;
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                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                InterPro;
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Pfam;
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                                   Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "structural analysis of Arabidopsis Challana chromosome ^{6} X. Sequer features of the regions of 3,076,755 by covered by sixty PI and TAC
                                                                                                                                                                                                                                                                                                                  buxaryota, Viridiplantae, Embrycph,tu, Trachesphytu, Spormafophyta;
Magnollophyta, eudicosyledons; eutc endicuts, Fosidae; eurosids II;
Brassicaies; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ye M., Zhang Q.H., Zhou J., Shen Y., Wu X.Y., Guan Z.Q., Wang L., Fan H.Y., Mao Y.F., Dai M., Huang Q.H., Chen S.J., Chen Z., "Human tull length club chara cloned liow cd34 stom cells."; submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases. EMBL: AF161525; AAP29440.1; - SEQUENCE 219 AA, 24571 MW, C9969FPKAFPF126 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa, Chordata; Craniata; Verrebrata; Euteleostomi.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 64; DH 10; Length 109; 37.5%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
0.6%, Score 64; DB 4, Length 219;
Best Local Similarity 31.1%; Pred. No. 51;
Matches 14; Conservative 11; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15, indels
0.6%; Score 64; DB 5; Length 53; 36.6%; Fred. No. 10; tive 7; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AB019236; BAA97301.1; . SEQUENCE 109 AA; 12343 MW; 63C5E26DBC71B32E CRC64; SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                   Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1456 VQNQIQSLMNILQXLLKLFEEKEETIFFAVSFUKSESQEE 1495
                                                                     78 ERSVQTKAVNKQLDENISLFLIHLSPYFLLKPAQKCLEWLI 118
                                                                                                                                                                                                                          01-0CF-2000 (TrEMBLrel. 15, Created)
01-0CF-2000 (TrEMBLrel. 15, Last sequence update)
01-0CF-2000 (TREMBLrel. 15, Last annotation update
GENOMIC DNA, CHEOMOSOME 5, PI CLOME.WKR3.
Arabidopsis Lhaliana (Mouse-ear cress).
                                                                                                        13 ERSMLTTTEDSTLRVRLEQFLTF1.SPH1.FI.TAAQQVFEFLV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VOFLDOALIAVLKCIGLLCOPAKKTAPSPVTFNOPEEGEE 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 219 AA
                                                                                                                                                                                                  109 AA.
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                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PET;
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20181125, PubMed-10718197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY,
                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7:31-63(2000).
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ses 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                          Rest Local Similatity
                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Res.
         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSPC177.
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                                                                                                                                                                                                                    091, V88;
                                                                                                                                                                                                      09LV88
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                                                                                                                                                                  RESULT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4atches
                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STEWN KAN STEWN ST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITNE FAZISTIJ, Pripad 2323579;
Sapta A.K., Aukin J.E., Wayo M.M.;
"Isolation of a baman vinentin chwa with a long stroncoding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ГИІ за слосян.
Sampylobarter рејилі.
Karteria: Proteobarteria: epsilon sabdirision: Campylobarter group:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domo sapiros (Himan).
Enkaryota Metazoa: Chordata: Craniatas Vertebrata: Euteleostomi;
Mammalia: Estinosia: Pilmates: Catarrana; Hominidaes Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDITURE 2015:0012: Fuldwed 10688204;
Parklill 1. Wick Riw., Mideall R., Ferley J.M., Pluncker J.,
Busklam D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jarels K., Karlyshev A.V., Modle S., Pallen M.J., Penn C.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    guail M.A., Rajandream M.A., Rutherford K.M., Van Vliet A.H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2090 ALAEKLKENYTULPESTPETAFLMEDPPEFVERGOOKTIGGI PTVLOOP 2139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Shore 64; DB 4; Length 400; 42.0%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PP SITE: PS90426; TF: 1.
Colled coil: Beptad repeat pattern; Intermediate filament.
                               1790 EKILSEMGSASQANIRITSEKFITATUTAPPVLIPAIKELYEGIE 1834
                                                                               RO DNIALESENMEDANTILESEMENTE CONTRACTOR TO THE CONTRACTOR OF THE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300 AA; 3555 MW; D40F65BB70CA43.7 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                           od N.V. 2006 (HEMMALTOIL OL. Last sequence applate)
of MAR-2001 (HEMMALTOIL 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO THE INTERMEDIATE FILAMENT FAMILY.
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of off-confidence. 5, created)
of MAK 2004 (IEEMBLIC). 6, last sequence update)
of MAK 2004 (IEEMBLIC). 6, last amoutation update)
METHIONYL INNA FORMYLIRANSFERASE (EC. 21.2.9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from a bunar esteosarcoma cell line (MG-53). To dene 85:30\pm604\,(1999) .
                                                                                                                                                                                                                                                                                                   PRI: 400 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               PANA SOFT (TREMBEROLL SIL Prouted)
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Piam, PP-M551; formyl_framst; l.
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EMBL: ALI39074; CAB72582.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIMENIIN (HUVIMA) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Obery Match
Bost Local Similarity (2.08
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                       FREELIMINARY;
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09PJJR;
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015868
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MEDILINE=20406833 PubMed=10952301;
MEDILINE=20406833 PubMed=10952301;
MEDILINE=20406833 PubMed=10952301;
MEDILINE=20406833 PubMed=10952301;
MEDILINE=20406833 PubMed=105.0 Verteron J.D. Ghayum L.A.,
Gill S.R., Nelson K.E., Read I.D., Tettelin H., Kichardson D.,
Ermolacva M.D., Vummathevan J., Fest S., gin H., Branderon D.,
McDonald L., Utterback T. Floishmann R.D., Nierman W.C., White D.,
Salzberg S.L., Smith B.D., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                         448. EPETAGEPPOETERGEVSTSTSCOPPOETADEGENAMMETARVETAMMEGEN 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 54; DB 2; Length 363;
34.1%; Pred. No. 90;
                                                                           Query Match 0.6%; Scare 64; DR 2; identify 66;
Best Local Similarity 28.1%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fend S., Chen G., Barthold S.;
"GdB clone from Borrelia burgdofferi.";
Submitted (MAY-1997) to the FMBL/Geneenk/DDBJ databases.
EMBL AF005055, AAD01225.1;
305 AA; 34069 MW 770DE65961EE5009 CF:64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 463 AA; 41909 MW; D8330154940932CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTBETICAL 41.9 KDA PROTEIN (FRAGMENI).
Borrelia burgdotteri (Lyme disease spirochete).
Bacteria: Spirochaetales: Spirochaetuceae: Borrelia.
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01 MAY 2000 (TrEMBLIE), 13, Last sequence update)
01-MAY-2000 (TrEMBLIE), 13, Last annotation apdate)
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01-MAR-2001 (Tremmirel, 16, Last annotation update)
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                                                                                                                                  12; Mismatches
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                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Constant vation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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NON_TER 1
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                                                                                                                                                                                                                                                                                                    508 ISKE 511
                                                                                                                                                                                                                                                                                                                                                           77 EIKD 80
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SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9R7H6;
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                                                                                                                               Matches
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EMBL; AE004198; AAF94343.1; -.

InterPro; IPR000192; -.

TIGR; VC1184;

Nature 406:477 483(2000)

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Isogai i., ola I., Hayashi K., Suşiyana I., Ols A. T., Suruki Y., Nishikawa I., Nayai K., Sugano S., Aotsaka S., Yoshikawa Y., Matsunawa H., Ishii S., Kawai Y., Sailo K., Yamanoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuko Y., Sasaki N.; Nahamoro D., Makamatsu A., Nabo human cDNA sequencing project."; Submitted (FER-zuu) To The EMMI/Gaubank/DRU databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 SGPEKLIALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPRELALVVLSFIPPRD41QA 150
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01-0CT-2000 (ILEMBLel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 16, Last annotation update)
CDNA PLJ11071 FIS, CLONE PLACETON 4937, MODERATELY SIMILAR TO SEL.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryotu; Metazea, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2090 ALAEKLKENYIVLLPESIPFLAELMEDECFEVEHQCQKTIQQLETVIGEP 2139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.6%; Score 64; DB 4; Length 553; 27.5%; Pred. No. 1.5c+02;
                                                                                                                                                                            promit PF00038; filament; 1.
PRINTS; PR01248; TYPEIKERATIN.
PROSTTE; PS00226; IF; 1.
Coiled coil; Heptat pattern; Intermediate filament.
SEOURNCE 466 AA; 53651 MW; BAB540200556015A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
0.6%; Score 64; DB 4; Length 466;
Best Local Similarity 32.0%; Pred. No. 1.2e+02;
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Bird C.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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                                             -i- SIMILARITY: TO THE INTERMEDIATE FILAMENT FAMILY. EMBL, AL133415; CAB87963.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          12, Mismatches
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PROSITE: PS00078; WL_KEPEAIS, UNKNOWN_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2000) to The EML: BMBL; AK001933; BAA91986.1; -. InterPro; IPR001680; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00320; GPROTEINBRPT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lb; conservative
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Repeat; WD repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00400; WD40; 7.
Pfam; PF00646; F-box; 1.
                                                                                                              InterPro; IPR001664; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001810;
                                                                                                                                                     1PR002957; -
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MEDLINE-9844137; PutbWad-9679194;
Kawarabayasi Y. Sawida M. HeriPiwi H. Halbawa Y. Hibo Y. Kawarabayasi Y. Sakine M. Baba S.-T., Kosuqi H., Hosoyama A., Naqai Y., Sakini M., Ogura K., Nakasawa H., Takamiya M., Ohfiku Y., Punahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki W. H., Shidayi H., Hounis W., Pebb F T., Horikoshi K., Masuchi Y., Shidayi H., Piwohi H., Piwohi H., Piwohi H., Piwohi H., Shidayi H., Piwohi 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                        o; Caps
                                                                                                                                                                                                                                                                                                                                                                                1337 EDDITSEÇVENKTVKMVITALIQEDSCUSLEVSRNVEHIVVKLISVEVDALPHVPRH 1393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Archaea; Euryarchaecta; Thermococca; Thermococcaceae; Pyrococcus
NCBI_Tax10-53953;
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ċ,
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20.0%; Prod No 1 Lo-02;
ative 14; Mismarches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 24.6%; Pred Ho 1 le-02;
Matches 14; Conservative 13; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01189; Noll_Nop2_Sun; 1.
NCE 456 AA: 51637 MW; 0295234B1EF4AF3C CRC64;
                                                                                                                               Pfam; PF00256; aminotran_5; 1.
SEQUENCE 416 AA; 45878 MW; 7511A8A160C3208B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16, Last annotation update)
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
450AA LONG HYPOTHETICAL EMI PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
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EMBL: AP000003; BAA29945.1; -.

1PR001678;

InterPro; SEQUENCE

InterPro; IPR00005

5:55-76(1998).

SEQUENCE FROM N.A.

PH0851.

Conserrative

Best Local Similarity

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Matches

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(Treated) D.D.T.

01-60T-2000 (TrEMRLFP) 15. 01-60T-2000 (TrEMBLFEL: 15, 01-MAR-2001 (TrEMBLFEL: 16,

BA124N14.1 (VIMENTIN).

Homo sapiens (Human).

SEQUENCE FROM N.A.

NCBI\_Tax1D=9606;

PRETURNARY

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очитиз

RESULT 87

PRI; 450 AA.

PRELIMINARY;

RESULT 86 058581

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"Fix+ and Prox Lexpression during lens regeneration from Cynops iris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Kenegers eveners evidence for a genetic program common to embryonic force development. Partie (1997).

EMEG. Ako editor HARD All 19 (1997).
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Eukriye'is Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
Marnollophyta: endicotyledoms: eore endicots: Rosidae: eurosids II;
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of JAN | SAN (TEMMILLE) | C. Last September update)
of MAR JOO (TEMMILLE) | C. Last amount on opdate)
PEPLICATION CONTROL PROTEIN HOMOLOG (REFLICATION CONTROL PROTEIN )
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Enkarget is Met Leas chostatas chanistas Verterratas Exteleostomis
Amphibias Battrichias Anusas Mesobattischias Pipoideas Expidaes
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25.28; Fred. No. 2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EV Arabi kopsis sequencina project;
Scandico (2001) o (1001) e (2001) sedapkyddat da abaecs
EMBL: 297 (46) (ARG-2401) (-)
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                           of MAR 2001 (ITEMBLE). 16, Progred)
of MAR 2001 (ITEMBLE). 16, bast sequence update)
of MAR 2001 (ITEMBLE). 10, bast annotation update)
plox 1 FROIEIN.
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N'ET LIVIE CO.:
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Host Local Similarity 26.0%.
Materies 180 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                Xemopodinae: Xemopus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria, Thermus/Deinococcus group; Deinococcaies; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome sequence of the radioresistant bacterium Deinococcus
6.6%, Score 64; DB 10; Length 771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.6%; score 64; DF 2; Longth 789; Best Local Similarity 33.3%; pred; No. 2.2e+0.2; Matches 13; Conservative 8; Mismatches 18; Indels
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Nakaroons K., Takuki Y.,
WABTIONIY TO The EMEDINARIY DUBU databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              789 AA; 87421 MW; 3CA32BCZF43EEBD1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Cleated)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                         01-07F-2000 (FEMBLEEL, 15, Created)
01 OCT-2000 (FEMBLEEL, 15, Last sequence update)
01-MAR-2001 (FEMBLEEL, 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium Group;
Bacillus/Staphylococcus Group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1479 LIKLPEEKKELLIPKAVSENKSESQUEMILOVENVELHISK 1508
                                  10; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.16-02;
                                                                   CPP CWOODALDINVINCED REPORT FOVANGEMENT LIABBIENT 674
                                                                                                  487 GWKKALOSLNERFAEGKKIGKENEKPCILLIDELDV 522
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                                                                                                                                                                                          78'3 AA
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                                                                                                                                                                                            PR1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plam; PF01580; FtsK_SpoiliE; 1. SMARE; SM00382; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submiliter (MARK-Jons) on the EME
EMBL: APOULSIS: BABO6114.1) on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-DI-GMP PHOSPHODIESTERASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .571 1577(1999).
                36.18;
                                  13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=C 125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Deinococcus radiodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; 1PR002543; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003593;
                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                     NCB1_[ax10~86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_Tax [D-1299;
                                                                                                                                                                                                                                                                                  SPOILIE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 286
                                                                                                                                                                                                                                                                                                                                                                                                                                          Takami H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN R1;
 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                    SPOILIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9RTX3;
                                                                                                                                                                                                           09KA95;
                                                                                                                                                                                          Q9KA95
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                                  Matches
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EMBL: AE002006: AAF11189.1:

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                                                                                                                                                                                                                                                                                                                                                                            CONA ENGIGORO FIS, CLONE NTORPROCIOS, WEAKLY SIMILAR IN DEGI PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses: ssRNA positive-strand viruses, no DNA stage, Picornaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Caps
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1018 LMKVLQGVNGEMVLSOLI PMAPQTLPFTQFFFTAVLFFFAMVLHLTLGKYNFFSVSL 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Buovilainen A., Kinnunen L., Poyry T., Laaksenen L., Roivainen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                ..
                                                                                                                                                                                                        0.6%; Score 64; DB 4; Length 852;
22.8%; Pred. Ho. 2.4e<sup>+</sup>02.
Live 19; Mismatches 25; Indels
                                                                                                                                                   0.6%; Score 64; DB 2; Length 790;
34.0%; Pred. No. 2.2e+02;
ive 9; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AK028151; BAB14432.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102A3C36218F812B CRC64;
                                                                                                                790 AA; 86721 MW; P4953E2567442F89 CRO54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NVV-1996 (TrEMBLEEL. 01, Created)
01-NVV-1996 (TrEMBLEEL. 01, Last Sequence update)
01-0CT-2000 (TrEMBLEEL. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrei, 16, Last sequence update)
01-MAR-2001 (TrEMBLrel, 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 878 AA.
                                                                                                                                                                                                                                                                                                         PRT; 852 AA
                                                                                                                                                                                                                                                                                                                                     01-MAR-2001 (TrEMBLrel, 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDI.INE-94160574; PubMed-8116248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98441 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPSID PROTEINS (FRAGMENTS).
                                                                                                                                                                   34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Gimilarity 22.8%
Matches 13, Conservative
                                                                                                                                                                     Local Similarity 34.0 ses 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                            PPFLIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-ocT-2000 (TrEMBLrel.
                                                                     Ptam; PF00563; DUF2; 1.
Ptam; PF00990; DUF9; 1.
SMART; SM00267; DUF1; 1
                InterPro; IPROU0160; -.
InterPro; IPRO01440; -.
                                            IPR001633; -.
                                            InterPro; IPR001633; -
Pfam; PF00515; TPR; 2.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     852 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TavID-12086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human poliovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                     NCB1_Tax1D=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN SAURETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterovirus.
    TIGK; DR1629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                       Query Match
                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  084893;
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                                                                                                                                                                                                                                                                                                                        09н911;
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                                                                                                                                                                                                                                                                                RESULT 93
                                                                                                                                                                                   Matches
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"A set of ordered cosmids and a detailed qenetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
EMBL; AL160431; CAB77429.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 PVPILAMNHLKKIMKTSKEGVDESFIKEAVLARLGDDNIDVVLSAISAFEIFKEHFSSEV 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 PSDTVQTRHVIQPRSESESTIESFFAPGACVATIGVDNBQPTTRAQKLFAIWKLIYKDIV 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     433 ESKYPRILDVVLEEHIKEIADLKKQELFHQFVSLSTSGGKYQFLADSDTSLMLSLNHPLA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       573 QSALPQGIKELISEVAQGALTLSLFKQQDSLPDTKASGPAHSKEVPALTAVETGATNPLV 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria: Firmicutes; Actinobacteria: Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycelaccae, Streptomyces.
NCBI_TaxID=1902;
"Poliovirus type 3/Saukett: antigenic and structural correlates of sequence variation in the capsid proteins."; Virology 199:228-232(1994) EBMB: L28985, AAA19633.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                            o 0.6%; Score 64; DB 14; Length 878; Similarity 17.8%; Fred No 2.50002; Conservative 26; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-A3(2);
Cerdeno A.M., Parkhill J., Barroll B.G., Bajandream M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1059 AA; 118514 MW; E62438A859106E3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2);
Seeger K.I., Harris D.;
Submitted (MAP-2000) to the EMBLASABAUK/DABI databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                        97210 MW; 03E3BC722A181A27 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel 15, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) DNA-DIRECTED RNA POLYMERASE BEIA' CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1059 AA.
                                                                                                                                                                                                                                                       CAPSID PROTEIN.
                                                                                                                                                                                                                                                                                                         CAPSID PROTEIN.
                                                                                                                                                    CAPSID PROTEIN.
                                                                                                                                                                                                      CAPSID PROTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01 oct-2000 (TremHirel, 15, Created)
01-oct-2000 (TremHirel 15, Last sequ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDI.INE=97000351; PubMed=8843436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed RNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces coelicolor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPET [MINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1059
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341
>578
579
>878
                                                                                                                         HSSP; Q84790, 1FVC.
                                                                                                                                                                                                                                                                                                                                                          878 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      553 TISNLLNIF 561
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578
579
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Adams M.D., Collinger S.E., Holf R.A., Evans C.A., Gorayne J.D.,

RA Adams M.D., Collinger S.E., Holf R.A., Evans C.A., Gorayne J.D.,

RA Adams M.D., Collinger S.E., Eithel R.D., Hans W., Herderson S.N.,

RA Server C. R.A., Martin S.E., Fither B. S., Ashburnor M., Herderson S.N.,

RA Mindel, E.C., Martin S.E., Fither B. S., Ashburnor M., Herderson S.N.,

RA Mindel, E.C., Martin S.E., Martin E.G., H. Lan R., Herderson S.N.,

RA Abril J.P., Addayani A., An H.-J., An Hews-Plannkorth C., Raidwin D.,

RA Abril J.P., Addayani A., Bax-ndale B., G., H. Lan R., Boasiny E.M.,

RA Hersen R.M., Bass A., Bax-ndale B., Raidwar D., Holshaker S.,

RA Mortis R.M., Bass A., Bax-ndale B., Raidwar B., Boasiny E.M.,

RA Hersen R.M., Bass A., Bax-ndale B., Raidwar B., Boater R., Chindra B.,

RA Hersen R.M., Bass A., Bax-ndale B., Raidwar B., Boater R., Boater B.,

RA Hersen R.M., Sarley S., Lahlbor B., Canton R., Boater R., Dietz R.,

RA Hersen R.M., Sarley S., Lahlbor B., Berran B., Berran B., Berranan R.,

RA Gorard C., Botter B.E., Boater R.M., Boater R.M., Berran B., Berranan R.,

RA Hirtis R.J., Beard R., Sorrell J.H., Son Z., Shan P., Harris M.,

Adday R.M., Bass R., Borrell J.H., Son Z., Shan P., Harris M.,

Adday R.M., Bass R., Borrell J.H., Son Z., Shan P., Harris M.,

Adday R.M., Bass R., Borrell J.H., Son Z., Shan R., Barran C.,

RA Lin X., Matrix B., Welland R.A., Berran C., Reinnisco J.A., Perchym. P.,

RA Lin X., Matrix B., Welland R.A., Harris S., Borrell R., Shen R.,

RA Lin X., Matrix B., Welland R.A., Harris R., Marker R., Shen R.,

RA Rimsel B., Welland R.A., Harris R., Marker R., Shen R.,

RA Rimsel B., Welland R.A., Harris R., Wensen M.G.,

RA Rimsel B., Welland R.A., Harris R., Wensen M.G.,

RA Rimsel B., Welland R.A., Harris R., Wensen M.G.,

RA Rimsel B., Welland R.A., Harris R., Wensen M.,

RA Shirkana R.A., Welland R.A., Britan R.A., Harris R.,

RA Shirkana B., Welland R., Shen R., Shen R., Shen R.,

RA Shirkana R.A., Bernell R.A., Shen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theret X.E., Zhond F.N., Zhond W., Zhand G., Zhao Q., Zhond L., Tidos R.A., Myers E.M., Zhond W., Zhou X., Zhu S., Zhu X., Smith H.M., Tidos R.A., Myers E.W., Bubin G.M., Venter J.C., Shou X., Smith H.M., "The een and sexponence of Densophila melanomatter."; Section 2.2 "Life Late Late Computer (1) Phys. 2. "Left Late Late Computer (1) Phys. 2. "Left Late Late Computer (1) Phys. 3 Phys. Left Late Computer (1) Phys. 3 Phys. 2 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bakaryotas Metazoas Arthropodas Fracheatas Hexapodas Insectas;
Prergaco s. Neopreras Endeprergastas Dipleras Brashyceras Muscomorphas
Episydos bens Drosephilidaes Prosophila.
N'EL EAXID 7227;
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ., Wang A.H., Wang X.,
Weissenbach J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is F. Dertor C., Dirner R., Venter E., Ward A.H., Wang X., Y., Wassammi, D.A., Weinstock G.M., Weissenberh J., Ses M., Weisser C., Weinstow G.M., Weinser C., Weinston C., Weinston C., Stand C., Zhang C., Zheng V.A., Yell E. F., Gazert C.S., Chats M., Zhang G., Zhao Q., Zheng
                                                                                =
6.074; Smith 64; 186.2; Length 1559; 6.074; Pred, N., 889.02;
                                                                        7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of MAY_2000 (FrEMBLEEL, 14, Freated)
of MAY_2000 (FrEMBLEEL, 14, Last sequence update)
of BUN_2000 (FrEMBLEEL, 14, Last amoutation update)
                                                                                                                                                                                                                                                                                                                                                                                                                       PPI: 1154 AA.
                                                                    12: Mismatches
                                                                                                                                                     1524 JESSUNPLEKEVESSBPETCKSUEDRILLE 1552
                                                                                                                                                                                                                             445 BVINPNNBIRFILLILIAPELIVNNEKRMIG 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inforbro, PPRODOTA:
PP-SITE: PS-0077: JAFGE, UNKN-WN 1.
SE, SENPE - 1154 AA; 1702: 1 MW: 98
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                            oni Sir Anrice (6.79)
Olio Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       PRETLIMINARY;
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RKA MADRINE-BENGLINE;
RKA Adams M.D. Celniker S.E. Hout R.A., Evans C.A., Gocaphe J.D.,
RA Adams M.D. Celniker S.E. Hout R.A., Evans C.A., Gocaphe J.D.,
RA Adams M.D., Celniker S.E. Hout R.A., Evans C.A., Gocaphe J.D.,
RA CAMBRIAGES D.G., Scherer S.E. Li P.W., Hoskins R.A., Gallerson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Hondon R.C., Royer E.G., Bayer E.G., Nelson M., Piciter R.D.,
RA ADELL J.F., Again A., Bazendale J., Bayer R. Houthon R.C.,
RATELL J.F., Again A., Bazendale J., Bayer R. Holsen M., Politer P.,
RA Hollis R.C., Honson D.A., Hutler B., Cadiou E., Gonter A., Gandard E.,
RA Hondra R., Basendal R.P., Berman R.P., Browstein P., Brottier P.,
RA Hortis R.C., Honson D.A., Hutler B., Cadiou E., Conter A., Chandra I.,
RA Gerry J.M., Cawley S., Dalike G., Davier T.L., Ber S.M.,
Cherry J.M., Cawley S., Dalike J., Dawier R.L., Daw I., Bietz S.M.,
Cherry J.M., Cawley S., Dalike J., Davier R.L., Davie S.,
RA Gerry J.M., Cawley S., Dalike J., Berras R.L., Davie C., Barris R.J.,
Poston R., Doup L.E., Downes N., Damar Rochen S., Pleischmann W.,
RA Glock A., Sobri P., Gerraz C.C., Perriac S., Perriac S.M.,
BARTIS R.L., Harrey D., Heimar J.J., Hernanded J.R., Harres M.,
RA Jalal M., Rahish F., Karpen G.H., R. Z., Liang Y., Lin X.,
RA Jalal M., Rahish F., Karpen G.H., R. Z., Liang Y., Lin X.,
RA Mount S.M., Mishiaa N.V., Moharry C., Morthey D.M., Nelson D.L.,
RA Mount S.M., Mishiaa N.V., Moharry C., Morthey D.M., Nelson D.L.,
RA Halance B.R., Releas R.A., Harry C., Morthey D.M.,
Ratars R.A., Mitman G.S., Pan S., Pollard J., Puril V., Rosse M.G.,
RA Halance B.R., Reland R.A., Philance B.R., Marken B.R., Reland R.A.,
Ratars R.A., Markhy B., Murphy L., Muzhy D.M., Nelson D.L.,
Ratarskolo M., Mitman G.S., Pan S., Pollard J., Burley D.M.,
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                                                                                                                                                                                                                                 1091 NNAVHYMORTTEYKTTETSOTMON SENVI PEMEDETESVELODI POOKREDYLLKITYE 1340
                                                                                                                                                          390 NNLOHLLASIJ FERYTSYSSQEEM (SNKVSLIJNFQPLDI IPLI FSKYPRTIDVVI FPHLK 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Arthropeoda, Tracheata, Hexapoda, Insecta, Pleryaota, Neoptora, Endopteryota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reinert K., Remindton K., Saunders R.D.C., Scheeler F., Shon H., Shue B.C., Siden-Klamos L., Simpson M., Skupski M.P., Smith I.,
0.68; Score 64; DB 5; Length 1154;
                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strong R., San E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, C.eated)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The genome sequence of Drosophila melanogaster.";
                                     29.4%; Fred. No. 3.4e+02;
Live 10; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spier E., spradiing A.C., stapleton M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanoqaster (Fruit tly).
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-!- SIMILARITY: TO EF-HAND FAMILY.
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                                                                                   20; Conservative
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                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P02588; llnx.
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    Owery Match
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199
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                                                                                                                                                                                                                                  NCBI_TaxID=11246;
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                                                                                                                                                                                                                                                                                                                                             STRAIN-9314893;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     387 SLKNMLDHILLASILFEBYISYSSQEEMDSNKVSLINMQFLPLIRLLESKYPRTLDVVLER 446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alveolata, Apicomplexa, Haemosporida, Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; tudels
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SEQUENCE 1979 AA; 237745 MW; 5C6CD6307AFF7D37 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1779 AA: 199146 MW: 8062479CA02PA652 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1230 CONTLORESTED PROGRAMMY PROGRAMMY TANDER STEELS TO LISTON 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBL: 10, Created)
01-MAY-1999 (TrEMBL: 0, 0, Last sequence update)
01-MAY-1999 (TrEMBL: 10, Last annotation update)
01-MAY-1999 (TrEMBL: 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268 MINULILVAKENQESÇQYKDLIKQLVISDLIEPGQERSPDG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 64; DB 5; 1
36.6%; Pred. No. 5.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Mismatches
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                                                                                                                                                                                                                               PRIME 1900450; RECOVERIN.
PROSITE: PS00018; EV_HAND: UNKNOWL_1.
PROSITE: PS00294; PRENYLATION, UNKNOWL_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel, 10, Created)
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EMBL; AE001375; AAC71819.1; -.
                                                                                                                                                                                                                                                                                                            PROSITE; PS00294; PRENYIATION, PROSITE; PS00972; GCH_2_1 1. PROSITE; PS00973; GCH_2_2: 1. PROSITE; PS50235; GCH_2_3: 1. Calcium-binding.
                                                                                                                                   PFam; PF00036; efhand; 2. PFam; PF00442; UCH-1; 1. PFam; PF00443; UCH-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Onery Match
Best Local Similarity 36.6°
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY,
                                                                 IPR001394; -.
                                    IPR001230; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum.
Eukaryota: Alveolata:
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   InterPro; IPR001125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                        InterPro;
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 63; DB 14; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Obery Match
Best Local Similarity 40.9%; Pred. No. 61;
Matches 18; Conservative 2; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. GATION T. MURILLO D.A., Patarroyo M.E., GATIORROYO M.A., Patarroyo M.A.; Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                               Bovine respiratory syncytial virus.
Viruses; ssRNA negalive strand viruses; Monenegamirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                        Larsen L.E., Gottshalch E., Blixenkrone-Moller M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF054668; AAC36678.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1152 KGISVNAEQVRIELEPPDKAKPLGTVQQKRPQKMQQKKSQDLES 1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 AA; 22428 MW; 6CD5A57112F5C748 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        Nonstructural protein.
SEQUENCE 136 AA; 15244 MW; AEB6A89D7FADDD24 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 KGIKALLEQVEAEKKKLPKUNTTNTPLTDEQQKAAQKKIADLES 71
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PV200 WIGH-BINDING REGION ( (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PV200 HTGH-BINDING PEGION ! (FPAGMENT).
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
NONSTRUCTURAL PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.55% cov.c. ... 40;
Rest Lonal Similarity 28.18; Pred. No. 40;
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Eukatyota, Metazoa, Phordata, Praniata, Vertebrata, Euteleostomi,
Mammasia: Euteria, Primates, Catarrhini, Hominidae, Homo.
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Mimmalis: Estaria; Primatos; Catarrhini; Hominidae; Homo.
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Substituted (CMS for C) in the CMBC/CS density durind density BMBC (1995-20) Annual Composition (CMS for C) in the New TERM (C) in the Composition (C) in the C)
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MERLIANS 9829989; pubMed-9644230; carnier T., Churcher C., Harris D., Corlo S T., Prower P., Parkhill J., Carnier T., Churcher C., Harris D., Corlo S.V., Barlis E., Gas S., Barry C.E. III. Tekaid F., Badcock K., Basham D., Brown E., Chillingworth T., Comior R., Caries E., Ewills K., Feitweil T., Certies S., Hamlis N., Holroyd S., Hornsby T., Jagels K., Krodh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Kajandaram M.A., Kogers J., Taylor K., Whitehead S., Barrell B.G., Squres S., Sqares K., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Museomorpha;
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Actinomycetaies, Corynebacterineae, Mycobacteriaceae, Mycobacterium.
NCRI_TaxID+1773;
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Nature 49:157-544 (1998).
RMHL: 295446: CAROBRA6.1; ...
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                                                                                                                                                                                                                                                                                                                0.6%; Score 64; DB 4; Lynath 209;
41.9%; Pred. No. 65;
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Submitted (NoV-1999) to the EBBL/GenBank/Tobbs databases.
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SEGUERCE 211 AA; 23989 MW: D58979862788689F SEC64;
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W) = 060B1*2470F2BA169=**RC64;
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01-JUL-1997 (TFEMBLEEL, 04, Lest sequence update)
01-JUN-2000 (TFEMBLEEL, 14, Lest annotation update)
HYPOTHETCAL, 23, 9 KDA PROTEIN.
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01-MAY-2000 (TrEMBLrel. 14, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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                                                                                                                                                                       PROSITE: F390092: NG_MTASE: DRI
SEQUENCE 209 AA: 24719 MW;
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                                                                  EMBL; AF201938; AAF86874.1;
InterPro; IPR000051; -.
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A WING_LANGED BOOSEPHILIDARY DESCRIPTION.

WAS ADARD MENN, CACHERES S.E. 1911 F.M., HORSENS R.A., GOLDE R.F.,

WAS ADARD MENN, CACHERES S.E., 1911 F.M., HORSENS R.A., GOLDE R.F.,

WAS ADARD MENN, CACHERES S.E., 1911 F.M., HORSENS R.A., GOLDE R.F.,

WAS ADARD MENN, CACHERES S.E., 1911 F.M., HORSENS R.A., GOLDE R.F.,

WAS ADARD MENN, CACHERES S.E., 1911 F.M., HORSENS R.A., GOLDE R.F.,

WAS ADARD MENN, CACHERES S.E., HOLL G., WOLSENS C.E., MIKIOS G.L.G.,

WAS REALL J.E., MONTEN J.M., HORSENS D.E., MIKIOS G.L.G.,

WAS REALL J.E., HORSENS P.M., HORSENS D.E., MIKIOS G.L.G.,

WAS REALL J.E., HORSENS D.M., HORSENS D.E., MIKIOS G.L.G.,

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WAS REALL J.E., HORSENS D.M., HORSENS D.E., MIKIOS G.L.G.,

WAS REALL J.E., HORSENS D.M., HORSENS D.E., CONTROL D.E., CONTROL D.E.,

WAS REALLY D.M., LONGES G.M., HORSENS D.M., MONTEN R.M., GLABARICH A.M., CONTROL D.E.,

WAS REALLY D.M., HORSENS D.M., MONTEN R.M., GOLDSON D.E.,

WAS REALLY D.M., HORSENS D.M., MONTEN R.M., MONTEN R.M., GOLDSON D.E.,

WAS REALLY D.M., HORSENS D.M., MONTEN R.M., MONTEN R.M., MONTEN R.M.,

WAS REALLY D.M., HORSENS D.M., MONTEN R.M., M
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Obsery Match

0.6%, Score 63; DB 5; Longth 231;

Bush Local Similarity 25.4%; Pred. No. 73;

Matches 15; Conservative 10; Missatches 34; Indels 0; Caps 0;

03 738 KRIESVITAVEIPSEMHEIMPROTIVEDTHYPHYNSTRYAVENSVETUTSIEKE 796

Db 67 KREESINGAYELESTINGSTRUKGSVETAGGVHINAERVVEDAGTKETYKSEF 125
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RESULT 106
054493
AC 054493 PRELIMIDARY, FRT, 232 AA.
AC 054493.
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAY 2000 (TIEMBLREL. 13, Last annotation update)
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MEDIINE-20196006, PubMed-1073132;

AGENTRE-20196006, PubMed-1073132;

AGENTRE-20196006, PubMed-1073132;

AGENTRE-20196006, PubMed-1073132;

AGENTRE-20196006, PubMed-1073132;

RA Amendides P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.E.,

RA GCOTGE R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA SULTON G.G., Worthman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Abril J.F., Agbayani A., Rayarell M.D., Zhang Q., Champe M., Pfeilfor B.D.,

RA Abril J.F., Agbayani A., Rayarell M.D., Zhang C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., Rayarell M.D., Rolson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., Rayarell M.D., Rolshakov S.,

RA Abril J.F., Agbayani A., Rayarell M. P., Payravi Parcell I., Rosalevy M. P.

RA Burlis K.C., Busam M.P., Horder H., Cadiou E., Center A., Chandra I.,

RA Burlis K.C., Busam D.A., Muller H., Cadiou E., Center A., Chandra I.,

RA GLERY J.M., Cawley S., Pahller H., Cadiou E., Center A., Chandra I.,

RA GLERY J.M., Cawley S., Pahller T., Parantrarel I. R. Barrich P.,

RA GLERY J.M., Cawley S., Pahller T., Parantrarel I. R. Parioc P.,

RA Fogler C., Gabrielian A.E., Downess M., Dugan-Rochas S., Dunkov B.C., Petrazor C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryela, Melazea, Arthrepeda Trachesta, Bexapoda, Insecta;
Freiyyola, Nooleesa, Endopleryyota, Diptera; Brachyeesa; Museumerpha;
Epiyabidiolot; Frosephilidae, Drosophila.
Newi Taxib-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 63; DB 2; Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16; Indels
                                                                                                                                                                                                                                  Krismer B., Mentenbruck L., Goetz P.;
Submitted (APF 1907) to the UMER (GenRack Typk: databases.
                                                                                                                                                                                                                                                                                                                                                                    SCED PROTEIN.
P441E32P48PP1225 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OI MAY 2000 (TrEMBLrel. 13, Created)
OI-MAY-2000 (TrEMBLrel. 13, Last sequence update)
OI-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG7582 PROTEIN.
                                                                      Rarieria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylosocous group; Staphylorocous.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 441 DVVI EFHLIRETADLIKROFI FHOFVSLSTSGGKYQFL 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No.
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232 AA, 24319 XW
                                                                                                                                                                                                                                                                                          EMEL; AP109218; AAB94657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Bost Local Similarity 41.7%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                  Staphylococcus carnosus
SCHU PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                     SECUENCE FROM N.A.
                                                                                                                                  NCRI_TaxID=1281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=RERKELEY;
                                                                                                                                                                                                                 STRAIN=TM 300;
                                                                                                                                                                                                                                                                                                                                                                                                SEGMENTE
                                                                                                                                                                                                                                                                                                                         Signal.
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31.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 242:331-336(2000).
                                                                                  PULATIVE HYDROLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHOUTENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             NCB1_fax[D= 4702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PICKE87 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBL_TaxID= 458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIORF87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O9R6H2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (772 PHF)SPTESTINS_VIHINE ISEMEAN_ANDRICHENTIAL APPENDENTIAL 1831
State B. L. Siben Kiamos in Simpson M., Skapski M.F., Smith T., Spiret B. Spradfind A. L. Stajbeton M., Strone P., Sun E., Spradfind A. L. Burner E., Wond A.H., Wang X., Stirksas R., Torton C., Burner E., Wonder E., Wond A.H., Wang X., Wild Laws S.M., Woodner D., Weilstock G.M., Weissenbach J., Wild Laws S.M., Woodner D., Weilstock G.M., Weils D., Yang S., Yao Q.A., Feldinaws S.M., Woodner D., Weilstock G.M., Weilstock G.M., Shore W., Zhou G., Zheo Q., Zheng L., Zhen X., Zhen H., Shore W., Zhen K., Zhen B., Zheng L., Zheng L., Zheng R.A., Zheng R.M., Shore M., Zheng C., Zhe X., Zheng L., Sheng R.M., Shore M., Zheng C., Zhe X., Zheng L., Sheng R.M., Shore M., Zheng C., Zhe X., Zheng L., Sheng R.M., Sheng R.M., Wonder J.D., J., The strong September G.M., Worter J.D., J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [Shizaki K., okuyama H., woita N.; [Shizaki K., okuyaki K., okuyaki K., okuyaki K., okuyaki K., okuyaki K., okuyaki Mariana Shizaki MF 1.", Horosahexterici arida pa darina barteriam Vibrio mariana shizaki MF 1.", EMBL: About G. G.; Paako (G.); [Shizaki K., okuyaki K., okuy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SdP() ()
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sdp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Professarteria; gamma subdivision; Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            orn (1974) Shorre 6.0 DB 5; Laurdh 254; Estalluring a cask from the No. 81; [14] [14] Subservative tree [18] Minner share of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score var TeP 2) Length 287;
Fred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13: Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     136 TOTEMPET OSLVTESVEVEAFYPISSALE PVOLANIAS UVSALVAAED 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.04 | CACLEVISUALIAVIMEVSVPLPCARLOIMITYYAAJFALSTADD 24.1
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PPISIES PSOCITY BRIALLANDAMASELAS 1.
SECTEMPE 202 AAS CHILLIAMS ABERANDELASEBS CROSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA: 28582 MW: 2F861FEF561AC484 CROS4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of MAY 2000 (TrEMBLED), 16, Greated) of MAY 2000 (TrEMBLED), 16, List sospence update) deory-2000 (TrEMBLED), 5, List annotation update)
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                                                                                                                                                                                                                                                                                                                           Settemor 287;2145 2145(2003),
EMRG ABOCK770; AAF56916;1;
F1pkisor FBGoote9681; 537582.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Through Mittach
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Mathematical
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Suzuki K., Ohta N., Hattori Y., Traji M., Katob A., Yoshida K.; "Nevel structural difference between nopaline and ortopine type till genericand separation at genetic and physical map and Separation of the tructural and top gree clanders of a low i placed pit in AACHAA."; Hiochim. Hiophys. Acta 1396:1-7(1998).
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Battori Y., Syzuki K., Obra N., Hraji M., Katob A., Yoshida K.;
"Genome structure of pli-SAURA(1): Stratedy for DNA sequencing of a Japanese cherry-li plasmid.";
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                                                                                                                                                                                               Eukaryota, Viridiplantae, Emb yophyta, Tracheophyta, Spermatophyta;
Magneliophyta, eadicotyledons: core endicats; Residae; eurosids it:
Brassicales; Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Murphy G., Ridley P., Hudson S., Bancroff L., Mowes H.W.,
Rudd S., Lemcke K., Mayer K.F.X.;
K.A.C.C.-I (ACL.2002) And P. PHRISCHER P. T.F. F. P. P. Ses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pTi-SAKURA.
Bacteria, Proteobacteria, alpta sabdilision: Rhizokjarear group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suruki K., Hattori Y., Oraji M., Ohta N., iwata K., Morata K.,
Katoh A., Yoshida K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 63; DR 10; Length 404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EU Arabidopsis sequencing project; Steeling (ADC) Sees; to the FMR4 (Seese, 2004) databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sopre Flord (APC) 2000 1990 FMP (Sobrigher) (1995) databases
EMBL ALS91712; CAC05469.1) 1
Hydrolase (APC) AA) 34559 MW: 1348BSZAZ66534PP PRO54;
SEQUENCE 304 AA) 34559 MW: 1348BSZAZ66534PP PRO54;
01-MAR 2001 (TrEMBLrel. 16, Last sequence apdate)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1276 DILDEEKFNVELIVQCIRLSEMPQTHHHALLLGIVAGIFP 1416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09R6H2;
01-MAY-2000 (TFEMBLICEL 13, Created)
01-MAY-2000 (TFEMBLICEL 13, Last sequence update)
01-MAR-2001 (FFEMBLICEL 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 DEIDEKRELIKSILKERRISELPRIKEKSLITWGREDQIFP 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Symp, Ser. 37:159-160(1998)
                                                                                                                       TSR8_230.
Arabidopsis thaliana (Mouse-ear eress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98193120; PubMed 9524202;
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SHOUENCE FROM N.A. STRAIN-MAFF301001; SECUENCE FROM N.A. STRAIN MAFF301001;

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170 CVPLARGELII HCYKGGGEMIGELGSGVTKSVKVFAEGFGGSSAQLKVLLAFYAGT1VSALV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 GLQNMKPTAYSQVIPQVVPTTFVALLTSAFLPIGVEYAAAGAMISVVLGELASLLYMIVM 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pajunen M.I., Kiljunen S.J., Skurnik M.; "Complete genomic sequence of the lytic bacteriophage phi-Yeo3-12 of Yersinia enterocolitica serotype 0:3.": Superijated (PPE 1997) to the FMEL/ConRank/DDBJ databases. EMBL, A155,805; CAR67627.1; - SEQUENCE 535 AA, 58649 MW; 03FMABBBDBBDBDCCC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1551 LETVLGY1SAVAQSMERNAPKLTVKFWEALL SKAYDULHKVNALLETETFT PVIRGLY 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     319 (LAAF) SYAPM MSAVQPPFEPPVTAFF1PVASPLEDTLGGVYSTI SQFTQ1 PLWRUL 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 535;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 63; DB 2; Length 522;
22.9%; Pred. No. 1.8e+02;
Ee 19; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obery Match 0.6%; Score 63; DB 9; Length 535; Rest formal Similarity 25.9%; Pred. No. 1.9e+02; Matches 15; Conservative 17; Mismatches 26; Indels
                                                                                                                                                                                                                                                               STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAP-2000) to the EMPL/Gentuck/EDPRI databases.
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01943; Polysacc_synt; 1.
SEQUENCE 522 AA; 56157 MW; 29756518FF145ABF CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMRLrel 16, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-000-2000 (TrPMRLrol 15, Croated)
01-00T-2000 (TrEMRLrol 15, Last Sequence update)
01-MAR-2001 (TrEMRLrol, 16, Last annotation update)
                                                                                                                                           Racieria, Firmicutes, Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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                                             01-MAR-2001 (TrEMBLACT, 16, Last an INVOLVED IN SPORE CORTEX SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 AAEDVSDRIIAKLPPYTQFGFR9 252
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                                                                                                                                                                                                                                                                                                                                      EMBL; AP001511; BAB04952.1; -.
InterPro; IPR002797; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.9%;
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Matches 19, Conservative
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                                                                                                                         Bacillus halodurans.
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                                                                                                                                                                                             NCBI_TaxID-86665;
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                  SPOVB.
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       Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
"Genome structure of pTi-SAKUKA (IV): Characteristics of tra region.";
Nucleic Acids Symp. Ser. 39:187-188(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Hetagoa; Arthropoda; Tracheata; Hevapoda; Insecta;
Prerygota, Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                      Hattori V., Suruki K., Ohta N., Braji M., Kafoh A., Yoshida K., "Genome structure of pTi-SAKUKA (V): Complete macheolide sequence of plasmid pil-SAKURA's vir region in Agrobattelium Lumefacieus.", Nucleic Acids Symp. Scr. 39:265-266 [1998].
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Begun D.J., Whilley P.;

"Reduced X Inhed muchedide polymorphism in Drosophila simulans.";

"Reduced X Inhed muchedide polymorphism in Drosophila simulans.";

Proc. Natl Acad. Sci. 0.S.A. 97.5960.5965(2006).

EMBL: AF255319; AAF68615.1; -.

Flybase: Fkgn0041641; pyakkmiranda.
  Obta N., Suzuki K., Hatteri Y., Braji M., Katoh A., Yoshida K., "Genome structure of pTi SAKUKA (111). Characteristics of T-DNA.", Nucleic Acids Symp. Ser. 39:185-186(1998).
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46.7%; Fred. No. 1.20:62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bength 358,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%, Fred. No. ..eeroz,
tive 4; Mismatches 12, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches 13, Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 AA; 38508 MW; DF1B307751CF087B CR364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (FFEMBLEEL 15, Created)
01-0CT-2000 (TFEMBLEEL 15, Last sequence update)
01-MAR-2001 (TFEMBLEEL 16, Last annotation update)
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PKT, 366 AA.

PRELIMINARY,

09NGB0; OWNCHO

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RESULT 111

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OSCHOOLS O

Drosophila yakuba (Fruit fly).

SECUENCE FROM N.A.

NCBI\_TaxID-7245;

MIRANDA (FRAGMENT).

1176 TVQQKPPQKMQQKKSQDF#SVQEVGSYWQ 1205

14; Conservative

Matches

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Onery Match Best Local Similarity

366

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PRELIMINARY;

Q9KD10; Q9KD10;

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RESULT 112

OBKDIO

0.68; score 63; ws 2; 1 40.08; Pred. No. 1.2e+02;

PROSTIE; PSU0120; LIPASE\_SER; UNKNOWN\_1.

SEQUENCE

Plasmid.

Z Z

InterPro; IPR000379; Interpro: IPR000734;

Local Similarity 40.0% ses 14; Conservative

Query Match Best Local S

Matches

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(rosephila virillis (Fruit 113).
Bukaryeta, Meraraa, Arthospoda, Trachesta: Hexapada, Tugeeta,
Pletyjeta, Neopera: Endopteryota, Diptera: Brachycera, Muscomorpha;
Ephyaroidea: Arosephilidae: Drosophila.
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                                                                                                                                                                                                                          FINE PELIGIAN FONTON INTERFALL MINE FROIDIN (BY SIMILARITY).

P. SIMILARITY: FOURTH FRANSMEMBRANE CHANNEL MIP FAMILY.

EMBL: AFOLG (A) ANY MEMS.]:

EMBL: AFOLG (A) ANY MEMS.]:

EMBL: AFOLG (S) ANY MEMS.]:

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Bukaryota: Viridipiandae: Phulyophyta: Tracheophyta: Spermatophyta:
Mannollophyta: englestyledans: eore endreots; kosidae; eurosids III:
Riassivales: Brissivacae; Arabidopsis.
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FMBL ACCASA, AARLEGA, AARLEGA, C.D., FREINGARK/IOBA databases.
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                                                                                                                                                                           product, PPS BRAIN, are conserved between prosophila vivilis and trosophila methoruster.";
bene zo nee ?(( eq),
                                                                                                                            MEDGINE OGGIOGS FORMER OFFILE).
BOILTS F.A., Zhatof Y., Reseant J.A., Cabin V.;
"The peer Coffettor and eytoplusmic domains of the neurogenic gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 o. (*) Secret 64: 58 5; Lemith 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Fred. No. 2.5e+02;
14: Mismarches 27; Endeds
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RICHMOLD IIA., BIOCCKOF A.B.:
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Artester) FPR (CPS)
Asteren (FPR) (2007)
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Infortency TPP codes
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SIPAIN OV, POLUMBIA:
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                                                                                                             SECUENCE FROM N.A.
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N'81_faxto 7244:
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1506 TOPET BHEFFE SVETIMEST FFRHHEFPRVDS THE LLESTEDGLETTVETS AVAGAM 1900
                                                                                                                                                                                Drosophila melanogaster (Frui: 11y).
Bukaryota: Metazoa: Arthropoda: Trachoata: Hexapoda: Insecta:
Pteryoda: Neopleta: Endopteryota: Especia: Heachycera: Muscumesplas:
Ephydroidea: Drosophilidae: Ecosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HESCHREGOSOTIST, FOLHER 979°205;
Ohno K., Hirose E., Inoue Y.H., Takisawa H., Mimerra S., Hoshimoto Y.,
Kiyono T., Nishida Y., Matsukaare A.;
"CDNA closhing and expression during development of brosophila
melanousster MCM3, MCM6 and MCM7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Su T.F., Yakubevich N., o'Farrell P.B.; "Cloning of brosophila MCM honologs and analysis of their requirement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5. IT IS
                                                                                   Guery Match 0.6\% Score 63: DB lo; Length 725; Rest Local Similarity 26.7%; Pred. No. 2.7c+02; Matches 20; Conservative 12; Mismatches 43; Indels
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21,7%; i.e.d. Bo. 4.1e-02;
affye 1e; Mismatches 18; indels
Pfam; PF00378; BCH; 1.
Pfam; PF00725; 8ECH; 1.
SEQUENCE 725 AA; 78839 MW; AB079FB354CB394C CRC64;
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01-MAR-2001 (TrEMBLiel, 16, Last sequence update)
01-MAR-2001 (TrEMBLiel, 16, Last unnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                           01 AUG 1999 (Trimmirel, 11, Last sequence update)
01-MAR-2001 (Trimmirel, 16, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1997 (TrEMBLIel, 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PKI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97368134; PubMed-9224961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    during embryogenesis.";
Gene 192:283-289(1997).
EMBL: AB010107; BAA34731.;; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 410-444 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTIE: PS00847; MCM_1; 1.
PROSTIE: PS50051; MCM_2; 2.
SEQUENCE 819 AA: 90895 MV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FlyBase; FBqn0024332; Mcm3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 13, Conservative
                                                                                                                                                                                                                                  1566 ERNADKLIVKFWRAL 1580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U83492; AAC47651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCM3 OR DMMCM3 OR 004206.
                                                                                                                                                                                                                                                                    363 VRKGSMSOEKFEKTM 377
                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene 217:177-185(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plam; PF00493; MCM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; 1PR001208;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MCM3 (MCM HOMOLOG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECURINGE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                          P91675;
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SEQUENCE FROM N.A.
                                                                      SEQUENCE FROM N.A.
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"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty it and 7AC clones.";
                                                                                                                                                                                                                                                                                                                                                                        1145 UTVSSVFKGISVNARQVRIELEPPDBKAKPLGTVQQKRRQKMQQKKSQDLLESVQRVCCSYW 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chao D., Brook, S., Reckler F., Chin C., Chiou J., Choi E., Conn L., Shinn P., Altati H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Coepaler A., Hanser N., Hewing R., Koe T., Tam R., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shinn P., Brooks S., Buellier E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonerales A., Hansen N., Hawing B., Koo T., Laur H., Lee J., Lorz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Ngyyen M., Palin C., Elann P., Sakaro H., Schwartz J., Southwick A., Thorvai A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genomic sequence for Arabidopsis thaliana BAC F15H18 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                         300 ETHEKQELELKINAQEAKVELLEQVKNSFLPVVFAKFLEKI ©FTKTKPWFKRQTYKRFL 359
                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota, Viridiplantae, Elbryophyta, Tracheophyta, Spermitephyta;
Magnellophyta; eudleotyledons; cere eudleots; Rosidae; eurosids II;
               Arabidopsis thallana (Mouse-ear cress).
Enkaryota: Viridiplantae: Embryochijia, Trishesphyta: Spermatophyta:
Magnollophyta: cudicotyledoms; cere endicots; Mosidae; enrosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                 Sato S., Nakamura Y., Kaneko I., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                            0.6%; score 63; DB 16; Length 967,
23.9%; Pred. No. 3.76.02;
                                                                                                                                                                                                                                                                                                                                          18; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boker J.R.)
Supmitted (NOV-1999) to the EMBLZGenBank/DUBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1999) to the EMBLAR-mbank/DübJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JAM 2000) to the EMBI/GenRapk/PNPI databases
                                                                                                                                                                                                                           DNA Res. 7:31-63(2000).
EMBL; A8019225; BABILIO7.1; -.
EMBL; A8005707; BABILIO7.1; JOINED.
SEQUENCE 967 AA; 108786 MW; 2E03D8016D5A0D15 CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1003 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thallana (Monse-ear cress).
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01-0CT-2000 (TrEMBLEEL 15, Created)
01-0CT-2000 (TrEMBLEEL 15, Last sequ
                                                                                                                                     MEDLINE-20181125; PubMed 10718197;
                                                                                                                                                                                                                                                                                                              0.05
Best Local Similarity 23.9%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360 NHÖTEALQELK 370
    KINESIN-TIKE PROTEIN
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                                                                                                            SECUENCE PROM N.A.
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                                                                                                                          STRAIN-COLUMBIA;
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MEDITNE-20196006, PubMed-10731132;

K MEDITNE-20196006, PubMed-10731132;

K Admars M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,

K Admars M.D., Celniker S.E., Li P.W., Hoskius R.A., Galle R.F.,

K Grorde R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

K Grorder R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pieffer B.D.,

K Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pieffer B.D.,

K Brill J.E., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

K Abrill J.E., Agbayani A., Raxendale J., Bayraktaroglu L., Reasley E.M.,

RA Rallow R.M., Basu A., Butman B.F., Blandari C., Belstabery S.,

K Borkeva D., Botchan M.R., Rourk J., Brokstein P., Brottier P.,

Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

K Borkeva D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

K Gherry M., Cawley S., Delly S., Mays A.D., Dew I., Delly S.,

K Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

K Godzieliend A.E., Gally M.S., Gelbart W.M., Glaser K.,

R Hostin D., Houston R.A., Howland T.J., Wein, W.M., Glaser K.,

K Hostin D., Houston R.A., Howland T.J., Weil M.-H., Ibeqwam C.,

K Harris N.L., Kalbett G.D., Kraft C., Kravitz S., Kulp D., Lin X.,

K Laske F., Lei Y., Levilsky A.A., Li i., Li E., Liand A., Lin X.,

K Laske F., Lei Y., Levilsky A.A., Li i., Li E., Liand A., Lin X.,
                                                                                                                                                                                                                                                               Cheuk R. Shinn D., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheu S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing H., Koo T., Lam B., Idea J., Lora C., Li J., Liu J., Liu J., Howing H., Koo T., Lam B., Hoyen M., Palm C., Fham P., Sakano H., Schwartz J., Southwick A., Threologis A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J., Sakano H., Kou G., Davis R., Federspiel N., Theologis A., Beker J., Sakano H., Ku G., Davis R., Federspiel N., Theologis A., Reker J., Sakano H., Federspiel N., Theologis A., Reker J., Sakano H., Ku G., Davis R., Federspiel N., Theologis A., Reker J., Sakano H., Federspiel N., Theologis A., Reker J., Sakano H., Federspiel N., Phenitted (Tun-Zunu) in the FMHL/Genfauk/DDBJ databases.
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Pucrygotu, Negicia, Endigierygota; Dipfera: Brachycera; Museomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Palm C., Pham F., Sakano H., Schwartz J., Scuthwick A., Thewerl A., Toriumi M., Vaysberg M., Yu G., Davis R., Ederspiel R., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 63; DB 10; Length 1003;
48.1%; Pred. No. 3.9e*02;
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ATP-Dinding; Coiled cuil, Microtubules; Motor protein.
SEQUENCE: 1013 AA, 114706 MW: 3CPEP2596F323B17 CPC64;
                                                                                                                                         Submitted (JAN-2000) to the EMBL/SchBauk/FOR: databases.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRODISO; KINESINHEAVY.
PHOSITE: PS50067; KINESIN-MOTOR_DOMAIN2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 PSSMLKMVEDLISVGEEESFNLKQKVT 703
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Matches 13; Conservative
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NCB1_Tax1D=9606;
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09H588;
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                             RESULT 121
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A Milkelor B., Milkelor B., Worder M.P., More's M.P., More's D.,
A Mount S.M. Milkelor N.V., Moderry C., Morris G., Moshreti A.,
A Mount S.M., May M. Murpey B., Murpey B., Morris G., Moshreti A.,
A Mount S.M., Moy M., Murpey B., Murskern D.R., Parleb J.M.,
A Palazzolo M., Pittman G.S., Fan S., Pollard J., Puri V., Reese M.G.,
A Rethert R., Remindron A., Sauders R.D.C., Scherer P., Smith T.,
Spite P., Standing A.C., Stapleton M., Strong B., Smith T.,
A Spite P., Spradling A.C., Stapleton M., Strong R., Smith T.,
A Strissas K., Terror J., Furner R., Venter E., Wand A.H., Wand X.,
A Williams S.M., Woodader L., Worley F., With P., Yens E.,
Yel J., Yek R. F., Zarrel J., Worley F., Williams S.M., Woodader L., Worley F., Williams S.M., Woodader F., Wolley F., Shou N., Smith H.D.,
A better X.H., Abong F.N., Shou W., Zhou S., Zhu X., Smith H.D.,
A bittes R.A., Myers E.W., Fould M., Zhou S., Zhu X., Smith H.D.,
C., Chilles Godge September of Intosophila melanogaster.";
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Mannellophytus endleafylodouse eere endleets: Residoe; engelek II)
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Lubata S., Mowes H.W., Rudd S., Lemeke K., Mayer K.E.X.;
Submitted (AMS 2009) to the EMBG, "Year E, TSBG databases."
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(4.8) Pred. No. 4,70992;
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45,5%; Pred, No. 4.46+02;
From 9; Mismartches II; Redels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTYBOSC: FRONTO-30249; CM.1203.
SECHENTE : 1134 AA: 120731 MW: A0872E0389550738 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypotherical protects.
SEQUENTE: The AA: 19142 MW: 07 0P041994200E580 08054;

    to the BRBL/Shitkink/Clark for Black

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NCB: LaxID 4702:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ET Arabidopsis sequencina project:
Sataritical (Ann. 2000) to the BHELOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 247:2185 2195(2000).
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Matches 17: Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL: AEDO1484; AAE47376 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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Hest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpres IPROCESS
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PEGUL 
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STRAIN-BERKELEY,

A MAILE E. G. Scherer S.E., Ho I E.A., Evans C.A., Goragne J.L.,

RA Adams M.D., Celunker S.E., Ho I E.A., Evans C.A., Goragne J.L.,

RA Adams M.D., Celunker S.E., Ho I E.A., Hoskins E.A., Galle K.E.,

RA Adams M.D., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,

RA Brandon R.C., Rouers V.-H.C., Hazel M.D., Champe M., Heilter B.D.,

RA MAD K.H., Doyle C., Paxter E.G., Hell G., Champe M., Heilter B.D.,

RA Abril J.E., Adbayani A., An H.J., Adriews Thankoop, C., Baldwin D.,

RA Abril J.E., Adbayani A., An H.J., Adriews Thankoop, G., Baldwin D.,

RA Berson K.Y., Bornes P.V., Berman B.F., Handrif L., Boisbakev S.,

RA Buttis K.C., Husam D.A., Butler H., Caldien E., Conter A., Chandra L.,

RA Cherry J.M., Cawley S., Dahike C., Davenpent L.R., Davics P., Ontor A., Chandra L.,

RA Gebrus J.M., Cawley S., Dahike C., Davenpent L.R., Davics P., Ontor A., Chandra L.,

RA Deblos R., Food L.E., Powers M., Borna Reha S., Fleischmann W.,

RA Dorbin K.J., Evanbaelista C.C., Perraz C., Perriera S., Fleischmann M.,

RA Dorbin K.J., Evanbaelista C.C., Perraz C., Perriera S., Fleischmann M.,

RA Dorbin R.J., Bornelman A.E., Gerban R.E., Gerbatti W.M.,

RA Dorbin R.J., Bornelman A.E., Gerban R.E., Gerbatti W.M.,

RA Dorbin R.J., Bornelman A.E., Gerban R.E., Gerbatti W.M.,

RA Dorbin R.J., Bornelman A.E., Gerbatti W.M.,

RA Dorbin R.J., Bornelman A.E.,

RA Dorbin R.J., Bornelman A.E.,

RA Dorbin R.J.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enkaryota, Metagea, Althrepset, 127,
Prerygota, Neopiera, Endopterygota, Hiptera, Brachycera, Muscomorpha:
Ephydroidea, Drosophilidae, Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sdeg
                                                                                                                                                                                                                                                                                                Bukuryola, Mefazoa, Cherdata, Chamiata, Vertebratu, Eureleostomi;
Masmalia, Dutheria, Primatus, Catarrhici, Rominidae, Bamo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 PLFSQLAKTLERSVQTKAVNKQLDENTSLFLJHLSPYFLJJKPADKGLEWLIHR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         295 PLEDYFERCKENGAFIVLVDNYVKEEEGIGVVHQAPYFGAEDYRVCMDFNIIR 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 63; D8 4; Length 1272;
28.3%; Pred; No. 5e-02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        145599 MW; 743886370496DA21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2008) to the EMBL/PerBack/Table databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLEE), 13, Created)
01-MAY-2000 (TrEMBLEE), 13, Last sequence update)
01-MAK-2001 (TrEMBLEE), 16, Last annotation update)
                                                                                                                01-MAR-2001 (TrimMirel, 16, Tast sequence update)
01 MAR 2001 (TrimMirel, 16, Tast annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Obery Match
Best Local Similarity 28.3%; Pred. No. 34 34
Openavalive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1426 AA
                                                                                                                                                                                    BA6203.2 (ISOLEUCINE-TRNA SYNTHETASE).
                                                                        01-MAR-2001 (TrEMBLrel, 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Frui 11y).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMHI, AL136097; CAC12710.1; -.
Aminoacyl tRNA synthetaso.
SRQUENCE 1272 AA; 145599 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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.. Moshreti A.

West 11

.. Milshina N.V., Mcharry C.

Merkulov G

3.75 MIVDELL 1812

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1080 TYAVCTSTSTTTFORSHEAVEASLFAITRTKSNLGKNIRE 1119

RESULT 124

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Mount 3.B., May M., Murth, B., Murth; I., Murny D.M., Nelson D.I., Nelson D.E., Nelson E.A., Nixon K., Nusskern D.P., Pacleb J.M., Palazzolo M., Pithman G.S., Pan S., Poollard J., Puri V., Reese M.G., Perington K., Saunders K.D.C., Scheeler F., Shen H., Shie B.C., Siden-Kramos L., Singson M., Skupski M.F., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.F., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.F., Smith T., Spier E., Spradling A.C., Stapleton M., Stupski M.F., Smith T., Spier E., Wang Z., Wang X., Wang 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 LEBLICTOPSFEQFEAPLIFSQLAFTLFBSVQTFAVNKQLDENISLFLIHLSPYFLLKPAQ 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            858 VERLIALDRITOHCOPSQVKHMMKVIEFQFORDFISLLPRELALFVLSYLEFKDILRAAQ 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones.",
INNA Res. 5:297-308(1998).
EMBL: AB015479; BAB085561; -.
SEQUENCE 1332 AA, 150795 MW; 75476C170CE81704 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enkaryola, Viridiplantae, Embryophytu; Tracheophyta: Spermatophyta,
Magnoliophyta; endicotyledons, core endicots; Rosidae, carosids II;
Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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30.0%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 6%; D6 5% Length 1326% Best Loral Gimilarity 26.2%, Prod 26.5% of 20.02% Marches 17% Conservative 10% Mismatches 38%, Indels Matches 17% Conservative 10% Mismatches 38%.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; WD repeat.
SEQUENCE 1326 AA; 141360 MW, 3F420873CFA3027F CRC64,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TTEMBLEEL 16, Last annotation
GENOMIC DNA, CHROMOSOME 5, PL CLONE:MTEL7.
Arabidopsis thallana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrHMBLrel, 16, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDILINE-99087489; PubMed-9872454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50181, FBOX; 1.
PROSITE; PS00678; WD_REPEATS; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; 1PR001810; -. Pram; PF00400; PF00400; PF00400; PF0040; F Pox. I. PRINTS; PR00120; GPROTEINBRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; Fkgn0035516; cc15010.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Science 287:2185-2195(2000).
EMBL, AE003480; AAG22246.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Trembirel, 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Hest Local Similarity 30.08
Matches 12, Conscrative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_Tax1D=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 KCLEW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           918 TCRSW 922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09FJ71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :-
O
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Marie F. Ainschaff R. Anderson K. Haymes C., Perks M., Bullen F., Ainschaff R., Anderson K., Baymes C., Perks M., Coper J., Coulson A., Craxton M., Dear S., Durbin R., Favello A., Fulton L., Carden P., Hawkins T., Hillier L., Jier M., Johnston L., Lancs M., Kershaw J., Kirsten J., Laister N., Latreille P., Lidytrina J., Lloyd C., Memurray A., Mortimore B., O'Callaghan M., Latreille P., Farey C., Pithen L., Porpra A., Sannders D., Shownkeen R., Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J., Thomas K., Vaudin M., Vaudhan K., Waterston R., Weinstock L., Wilkinson-Sproat J., Wohldman P.; In of C. elegans M., Weinstow B., Certiguous nucleatide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukarjota, Metapei, Hematoda, Chromodoroa, Phabditida, Rhabditoidea;
Rhabditidae, Pelodenimae, Caenorhabditis.
                                                                                                                                                                                                                                                                       Enkaryota, Metacca; Nemateda; Chromadoroa; Phabdilida: Phabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 0.6%; Score 63; DB 5; Length 1398; Local Similarity 29.3%; Prod No. 5.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1398 AA; 156597 MW; 31C7EDE541A8EDBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ephmitted (NOV-1995) to the EMRE Membaph MODRI databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               428 LSAWETAMEETIEPVPPRELKMIKOSALLKTFADOLNVGAP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               637 LRGWEEALENVIKSTKPGKLIGVANQKMIELLADNINLGDP 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE, PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1461 AA.
                     PRT; 1398 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLIFE) 05, Created)
01-MAY-1999 (TrEMBLIFEL, 10, Last Sequ
01-OCT-2000 (TrEMBLIFEL, 15, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00664; ABC_membrane; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 368:32-38(1994).
EMBL, 268113; CAA92148.1; -.
HSSP; P13569; 1NBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC_tran; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001140; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR003593; -.
                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00382; AAA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPR003439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WICC6.1 PROTEIN.
                                                                                                                                                                                                Enado 2 PPOTRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ainscough R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                         019048:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              018191
                                                                                                                                                                                                                                    E03G2.2
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                     019048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
019048
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Drossphila mei meeaster (Fruit II).
Enkuryova: Met need Alfhropoda: Tracheata: Hexapoda: Insectar
Pretpyova: Megrer r: Endopferyova: Dipperar Brachycera: Mascemerpha: Epryproiden: Ersepartidoc; Drossphila.
N'BC, Laxto (2.27).
                                                           Setro
                                   David Similarity (9.4%) Ered. No. 5.00+62; Longth 1461; ovs. 13; Ausselfallye. 7; Milmerth
Schmitter (2011-1992) to the EMPLANDER FARGE Batabases. Employees of TABLA47.11.

Interpretation (Decoded State of March 1994 FCZ BARDE CAFE CRESA)

SECRENCE 1461 AA: 164 64 MW. 1994 FCZ BARDE CAFE CRESA.
                                                                                                                                       6. Created)
[3. Last sequence update)
[4. Last annotation update)
                                                                                                                         PPI; 2445 AA.
                                                                       47 THE ACREDITIONED EVOK TENNET (STUZAMVVKILITEVT 1911)
                                                                                136 ABITPENILERSKHEPSVV3-VDAAFVMESGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AEU 44 GE AAF46127.13
                                                                                                                                      01 MAY 2000 ([FEMBLED])
01 MAY 2000 ([FEMBLED])
84 JUN 2 000 ([FEMBLED])
                                                                                                                          PPELLIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Physical and Physics of 1945.
                                                                                                                                                                                                                     SECUENCE IF M N.A.
                                                                                                                                                                                                                            STRAIN REPRETERS
                                                                                                                                                            MALLE PROTEIN.
                                                          Mat the S 1 %
                                             CHARLY MARKET
                                                                                                                                23 × 19M/ 5
                                                                                                                       1.48.4
                                                                                                                                                                   77771
                                                                                                          RESULT 126
                                                   Heist
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-i - CATALYTIC ACTIVITY: PROTEIN TYRUSINE PHOSPHATE · H(2)0 = PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eskaryota, Metarca: Chordata, Craniata: Vertebrata: Buteleostomi;
Mammalia; Eutheria; Cetartioductyla; Ruminantia; Pecora; Bozoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RADIXIN, AND TALIN.
-!- SIMILAKITY: BELONGS TO TH; NON-KECEPTOR CLASS OF THE PROTEIN-
TYROSINE PHOSPHATASE FAMI X.
                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 63; DR 5; Length 2435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-IYROSINE PHOSPHATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SMO0194; PTPC; l.
Structural protein; Cytoskeleton; Bydrolase; Colled coll.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 504 (201ED COLL (POLENTIAL).
1761 1793 (201ED COLL (POLENTIAL).
2484 AA; 276382 MM; 45A92F0D4F1ED13G (RC44;
                                                                                                                                                                                                                                                                                      272993 MW; A76617A66265617BB 17R164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vega Q.C., Waiton K.M., Dixon J.E.,
Submitted (FEE 1995) to the EMMI/General-Lids databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (TrEMBLEE), 01, Proated)
01-NOV-1995 (TrEMBLEE), 01, List sequence update)
01-MAR-2001 (TrEMBLEE), 16, List annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-TIKE LOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                            1.10.03;
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PROSITE: PS00661; BAND_41_2: FALSE_NED.
TRACTIE; PS00661; BAND_41_3:
TRACTIE; PS00683; TYE_PHUSPHA'ASE_1; FALSE_NED.
PROSITE; PS50056; TYE_PHUSPHA'ASE_2; 1.
PROSITE: PS50056; TYE_PHOSPHA'ASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 2484 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 OLLEKIQKEPTAVLKPEAMVLHLTLGKYNEFS 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 ULWEGILKURGSLMRTEGMVYPLTLSUYYEFS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BA14 TYROSINE PHOSPHATASE (EC 3.1.3.48).
                                                                                                                                                       PLUMIT PEROSON FOR LEADS: 3.
PRINTS: PROOLZO: NACHANNEL.
PROSITE: PSCOOLS: CASHELE: UNKNOWN.:
PROSITE: PSCOOLS: GARDH: UNKNOWN.:
RECORDER: 2435 AA: 272993 MW: A746FA
                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HANI. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00102; Y_phosphatase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS: PR00945; BAND41.
PRINTS: PR00700; PRTYPHPHTASE
                                                                                                                                                                                                                                                                                                                                                                                Overy Match
Bost Local Similarity 43.88;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U20807; AAA73516.1; -...
HSSP; Q06124; 2SHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PP00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE + PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro: IPRU01478; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinde; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000242;
IPPOA0294;
LaterPro: IPROco173;
                           IPR000636;
                                                          IPR000901;
                                                                                                                                                 1PR002111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Priam; Price5y5; PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCRI_TaxID=9914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1341
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                                  InterPro:
                                                             InterPro;
                                                                                         InterProp
                                                                                                                        InterPro:
                                                                                                                                                 InterPro;
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Pfam; PFC0385; chromo; 1.

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RX MEDLIANS_20196005; PROMERO_1073132;
RA Adams M.P. Celnikers S.F. Holt R.A. Fevans C.A. Gocayne J.D.,
RA Adams M.D. Celnikers S.F. Holt R.A. Fevans C.A. Gocayne J.D.,
RA Anamaldes D.G. Scherer S.E., Li P.M., Hoskins R.A., Calle R.F.,
RA Anamaldes D.G. Scherer S.E., Richards S., Ashburner M., Headerson S.N.,
RA Anamaldes D.G. Scherer S.E., Kichards S., Ashburner M., Headerson S.N.,
Barandon R.G., Worthan J.R., Yandell M.D., Champe M., Pfeilter B.D.,
RA Harley B.M., Rasu A. An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bleeson K.Y., Berus F.V., Berman B.P., Bhandarl D., Bolshakoy S.,
RA Berson K.Y., Berus P.V., Berman B.P., Bhandarl D., Bolshakoy S.,
RA Berson K.Y., Doup L.B., Downes M., Dugdar-Rocha S., Durkov R. Chandle I.C.,
RA Burtis K.C., Busam D.A., Butter H., Cadiou E., Celtter A., Clandia I.C.,
RA Burtis K.C., Busam D.A., Butter H., Cadiou E., Celtter A., Chandle I.C.,
RA Burtis K.C., Busam D.A., Butter H., Cadiou E., Celtter A., Chandle I.C.,
RA Glodek A., Gorn F., Locked M. P., Bornes R., Pleistulman M.,
RA Glodek A., Gorn F., Correll J.H., Gu Z., Chan P., Harris M.,
RA Glodek A., Gorn F., Correll J.H., Gu Z., Chan P., Harris M.,
RA Glodek A., Gorn F., Karpen G.H., Browne C.J., Roberton D.L.,
RA Mustin D., Houston K.A., Howland T.J., Will M., Glasser K.,
A. Lau X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.
RA Las X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.L.
RA Kimmel B.E., Scharling A.C., Stapleton M., Strong R., Shin B.,
Sylier B., Spradling A.C., Stapleton M., Strong R., Shin B.,
Sylier B.C., Spradling A.C., Stapleton M., Strong R., Shin B.,
Raten X.H., Zhoria F.N., Robing W., Weissenber J., Wang X., Yuk, R., Wang X., Yuk, R., Shine B., Strikh H.O.,
Ra Suleskas P.C., Shaden Klaman D.A., McHarley G., Rub S., Zhu X., Shin B.,
Rathen R., Shine B.C., Shaden Klaman D.A., Weinsenber P., Shine B.,
Rathen R., Shine B.C., Shaden Klaman D.A., Weinsenber B., Wang S., Zhu X., Shill H.,
Rathen S.M., Wong W., Weinschild M., Weinsenber P., Shill H., Shine B., Shill M., Shill M., Shill M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  septera, Endopteryjora, Diptera, Brachycera, Muscomorpha,
Drosophilidae, Drosophila,
                                                     Gaps
                                                     С,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bukaryota: Metazoa: Arthropoda: Trácheata: Hexapoda: Insecta:
Pterygota: Neoftera, Endoptrrygda: Diptora: Brachycera: Musov
0,6%; Score 53; DB 6; Length 2484;
                                                     17 indeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of Drosophila melanogaster."; science 287:2185 2195(2000).
                                                                                                                                                                                                                                                                                                                                                                            0.MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                       1926 LLEVIHYVNGVSTQGMTLEBAKRTLEMSLPSVVLKATRD 1964
                                                                                                              355 VVSTITHHVTGEETEGMDGQIYKRHLEAILTKISLKNNLD 393
                             Pred. No. 1.1e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                   PPT: 2703 AA
                                                           8. Mismatohos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
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                             35.98;
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                         PPELIMINAPY
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        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUTION FERM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID-7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG3660 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea;
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                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Morinaga T., Yasuda H., Higashio K., Tamacki T.;
"A human alpha-fetoprotein enhancer-binding protein, ATBF1, contains
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMAPT: SM00389; HOX; 1.
DNA-binding; Homeobox; Metal-binding; Nucleur protein; Ziuc-finger.
VARIANT 2460 2460 A -> V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria, Primates, Catarrhini; Hominidae; Homo.
W.M.L.yaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
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                                                                                                                                                                           0.6%; Score 63; DB 5, Length 2703; 39.5%; Pred. No. 1.2e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 \qquad \qquad A \implies V. Fig. (47 MW) - K23.46903F0065BAB CRC64)
                                                                                                                                                                                                                                                 7; Mismatches 19; Indels
                                                                            2703 AA; 295070 MW, 3A5D59DF278E7224 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  2185 LUSGIPAQNNISELFSLANFLEFSQFSSQFEFMSEFGSTRTER 2227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0cr-2000 (TrEMBLiel. 15, Created)
01-0cr-2000 (TrEMBLiel. 15, Last sequence updatc)
01-MAR-2001 (TrEMBLiel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                   382 ILLINISLANNELDHILLASTAFETTISYOSQEEMOSHKVSLLNTQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OL-MAR-ZUUI (TERMILEEL, 16, LASE ANNOTATION UPGALE)
ALPHA-FETOPROTEIN ENHANCER BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOL. CELL. BIOL. 11:6041-6049(1991).
-!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-!- SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
EMBL; DIU250; BARNINGS 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     four homeodomains and seventeen zinc fingers.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 3201 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 2783 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE, PSUGUZE; MINC_FINGER_C2H2; 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel, 01, Created)
01-NOV-1996 (TrEMBLrel, 01, Last Sequ
01-MAR-2001 (TrEMBLrel, 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92049333; PubMed-1719379;
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                    PROSITE; PS50013; CHROMO_2; 1. ATP-binding; Helicase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00046; homeobox; 4. ptam; PF00096; zf-C2H2; 16.
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                                                                                                                                                                                                                        Best Local Similarity 39.5%
Matches 17; Conservative
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SEQUENCE 2/83 AA;
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1174 FOLVOGERPERM JERSZERIKYLINOMENT (L. 1200-material) (A. 120-12) (A. 120-12
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Lamacki I.;
"Ponitation and characterista for of an ATMPL isotome that expresses in a
feet and differential son-dependent annines.";
I. Bret. Them. 270:228405-28448(1995).
                                                  Drosophila mejanoaaster (Froit 193)
Eskargeta: Metacoar Althropoda: Iracheata: Hexapoda: Insecta:
Ptergeda: Meopleri: Endeptergesla: Hiptoria: Brachgeera: Museomeorpha:
Ephylioteka: Prosophilldae: Drosophila.
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"A bound adopted to operate a condition protein, AFBFL, contains
bent behavedomeins and seventeen zinc tingers.";
Med. edit. Wiol. High History (1991).
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EMBGL ARCHES JORGES AARELISE, D.
ETJESARE EKIROLZON OF dominio.
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Mimmailas Eusasias Primatess Catarrhinis Hominidae, Homos
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01-NA 1999 (Tremmirel, OL, Last sequence update)
01-NA 2001 (Tremmirel, D. Last amicralion update)
2INC FINJER HOMEGRANIN ERGIEIN (WISSO-HIGDIOSGIEZO I PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 64; DB 5; Longth $201;
23,6%; Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatehes 36; Indels
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Francist Prio271; helicolese_Cril.

Prio1112; Prio272; barilloaning and an analysis of the prio1112; Prio272; barilloaning and an analysis of the prio1112; Prio272; barilloaning and an analysis of the prio1112; prio112; prio272; barilloaning and an analysis of the prio112; prio11
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MEDGINE (AGG-0778) PARMAD 3532926;
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Best Local Similarity 25,640
Autones 17, domentalize
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                                                                                                                                                                                                                                                                                                                                                                                SEJUEN'E FEMNAA.
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주문문항 항공주도도도당한다고요를 보고도로 보고도를 받는다.
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"An abnormal ketamine response in metanis detective in the ryanodine
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Rhabditidae; Peloderinae; Caecorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00389; HOX; 1.
FRA biddin, Bohes-kox, Mctai binding, Nocledar protein, Einerlinger.,
VARIANT 3528 4529
SEQUENCE 3763 AA; 404468 MV; OP6ZAP4704D5P856 cRe64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oucry Match 0.6%; Score 64; DB 4; Longth 3703; Best Local Similarity 27.9%; Pred. No. 1.70.03; Matches 19; Conservative 13; Mismatches 6; Endeis
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J. Mol. Biol. 0:0 0(1997).
-i- SIMILARITY: TO EF-HAND FAMILY.
"The sequence of Homo Sapiers FAC close L'Esplace.";
Symmitted (UNN-1998) to the PMSD/Abendark/Adds databases.
                                                                               Saturitied (CCN 1998) to the PMRC/Sections/1966 databases.
[5]
                                                                                                                                                    Waterston R.)
Schmiffed (MOV-1998) to the EMBL/Chemannk/Gempf dividence.
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01-MAY-1997 (TrEMBLIE). 03, Last sequence update)
101-MAY-2001 (TIEMBLIE). 16, Last annotation update)
PYAN-OHDE PEGEPPOR.
                                                                                                                                                                                       PRT; 5071 AA.
                                                                                                                                                                                     Plan: PF00046: homeobox; 4.
Plan: PF00096: 7-72H2: 20.
PROSTE: PS00027: HOMEOBOX_1: 2.
PROSTIE: PS50071: HOMEOBOX_2: 4.
PROSITE: PS00028; ZINC_FIN3ER_C2H2: 14.
                                                          SECUENCE OF 1151-4703 FROM N.A.
                                                                                                                                SECUENCE OF 1151 - 4704 FROM N.A.
                                                                                                                                                                                                                      EMBL: 1.328.52; AAC14462.1; -.
EMBL: AC004943; AAC79153.1;
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InterPro; IPRO00107; -.
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                                                                                                                                                                                                                                                           HSSP; P06601; 1FJL.
InterPro; 1PR000822; -.
InterPro; 1PR001356; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR000699; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1784 TETLLQUQ 1791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                             Waterston R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sakabe Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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InterPro, IPP003608; -.
Pfam; PF00036; ofhand; 2.
Pfam; PF00622; SPRY; 3.
Pfam, PF01365; RVDR_ITPR; 2.
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           1518 KALIGLAMKILGGMISMERTIVTSPIPLVENGLAIVLEKKETGGEAGAGAGAGAGALATIKIL 1627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bakaryota, Mitubod, Nematoda, Chromadoren, Bbakditida, Flib4litbidea,
Khabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                  Guery Match 0.6%; Score 63; DB 5; Length 5071; Best Local Similarity 26.5%; Fred. No. 2.4er03; Matches 18; Conservative 13; Mismatches 37; Indeis
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Submitted (MOV-1996) to the EMBLyGermank/DUBJ databases.
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                                                                                                                                                                                                                                             5071 AA; 576357 MW; 145EF32288613324 GRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997 (TrEMBLrel. 02, last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                PRINTS, PRO0795; KYANODINEK.
PROSTTE, ESGOALW. LE HAND, SAKNOWE.2.
PROSTTE: POOJ186; ECE.2; UNKNOWE.1.
PROSTTE: POOJ066, HMC_COA_REDICTASE_1; UNKNOWE.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 5107 AA.
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EMBL: 064854; AAB18.1; -.
InterPro; 1PK000107; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL N2;
MEDLINE-94150718, PubMcd 7906338,
           Pfam, PF00622; SPRY; 3,
Pfam, PF01365; RYDR_ITPR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                            SMART; SM00472; MIR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans.
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                                                               PF02026; RyR; 4.
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InterPro: IPR001682;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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25.0%; Pred. No. 2.5e<sup>1</sup>03;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.6%; Score 63; DB 5; Length 5107; Bost Local Similarity 26.5%; Pred. No. 2.5e+03; Matches 18; Conservative 13; Mismatches 37; Indels
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Pfam; PF92026; Myr; 4.
PROSITE: PSOG018; EF_HAND; UNKNOWN_1.
PROSITE: PSOG66, HMG_CGA_FEDUCTASE_1; UNKNOWN_1.
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MEDITUR-94150718; PubMed=7906398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.
17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 64; DN 5; Length 0994;
25.0%; Pred. No. 4.5e-04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 62; DB 10; Tength 75; charity 38.2%; Pred. No. 27; charity 6; Mismarshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14, Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6994 AA; 775364 RW; 90036449255599240 TR054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nebentuchr A., Lommax T.L.,
Submitted (SEP-1997) to the EMBL/Combank/DABH dutabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1157 MARQVPIELEPPPRAKPY CTVQOKPPQKMQQKRSQCLESVQEVC 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQÜENCE 75 AA; 8724 MW; 9742A03141141173 CRO540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01 AUG 1992 (TERMELTEL, 07, Created)
01-AUG-1998 (TERMELTEL, 07, Last sequence update)
01-MAR-2001 (TERMELTEL, 16, Last amnotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001 (TrEMBLEEL, 16, Cecated)
01-MAR-2501 (TrEMBLEEL, 16, Last sequence update)
01-MAR-2001 (TrEMBLEEL, 16, Last annotation update)
PNAS-114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS50088; ANK_REPEAT; 22.
PROSITE: PS50297; ANK_REPEADION: 1.
PROSITE: PS50017; DEATH FAMAIN: 1.
PROSITE: PS00572; GLYCASYL, BYDRACH I CONKARALZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               992 PHEADALLIANDSSYNDTENTACTARRYDGW TOZST 1914 HT 111 HT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PKI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL: AP022019; AAC13259.11; -...
Mendel: 2877; !...
InterPro: IPR003411; -...
Pram: PP02309; AUX_IAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LISSUE-ELIOLATED HYPOCOTYLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Most Local Similarity 25.0%)
Matches II; Cosservative I
EMBL, 021733, AAB38384.1,
HSSP, P42773, 11HB.
InterPro: IPR000488; -.
InterPro: JPR000956; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00531; death; 1.
Pfam; PF00791; 205; 1.
PRINIS; PR00001; GLABLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00005; DEATH; 1.
SEQUENCE: 6994 AA; 775:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       Ptam; PF00023; ank; 24.
                                                                                                                                                                                                           1PR001460; -.
                                                                                                                                                                                                                                                                 InterPro; IPR002110; -.
InterPro; IPR002383; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 14: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAAH (FRAGMENT).
                                                                                                                                                                                                                           InterPres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Onery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
NON_TER
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 141
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"PRIAS 2, human acute promyelocytic leukemia cell line NR4's apoptosis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Cherdata, Craniata, Vertebrata, Eureleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                 Yn W. Q., Chai Y. B., Sun B.-Z., Zhu F., Liu X.-S., Li Z., Lu F., Yan W., Yang H., Zhao Z.-L.:
Yan W., Yang H., Zhao Z.-L.:
Expansion of the EMELYCLERIC databases.
EMBL, AP275810. ACC BC 11.
EEGGERIC 131 AA, 14441 MW, 8238A68FE8C19045 CPC64;
                Eukaryota; Metazoa; Chordata; Craniata; Verlebrafa; Euteleostomi;
                                                                                                                                                                                                                 e,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 62; DB 4; Length 139; 41.2%; Pred. No. 55;
                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                      0.6%; Score 62; DB 4; Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Mismatches 13; Indels
                                                                                                                                                                                                                 13: [mde] s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2000) to the EMBL/Genbank/5DEJ databases.
EMBL: AF229832; AAF42917.1; -.
NOW TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15344 MW; FUBAE51E1A0FE11C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1958 (TrEMBLrel. 05, Last sequence update)
01-NoV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLEEL 15, Last sequence update)
01-0CT-2000 (TrEMBLEEL 15, Last annotation update)
APOPTOSIS-RELATED PROTEIN PNAS 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria: Pirmicutes; Bacillus/Clostridium group,
Bacillus/Ctaphylococcus group; Bacillus
NCBI_FaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1801 OANTRETSLKKTLATTLAPRVLLPATKKTYKOTE 1834
                                                                                                                                                                                                                                               1801 ÇANTRITSEMETEAPTEAPPVLIPATERYEGIE 1834
                                                                                                                                                                                                                                                                                                                                                 139 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 QARYTIQSLEPTETTVPAMFIGVEMFKAYFOVF 44
                                                                                                                                                                                                     Pred, No. 51;
7; Mismatches
                                                                                                                                                                                                                                                               3 QANYTIQSERDIETIVDAMEESVERMERAVEVK 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel, 05, Created)
                                                                                                                                                                                                                                                                                                                                                                            01-0CT-2000 (TrEMBLrel: 15, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRI
                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                       Query Match
Best Local Similarity 41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%
Best Local Similarity 41.2%
Matches 14; Conservative
                                                                                                                                                                                                                    14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID: 9606;
                                          NCB1_TaxID=9606:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 related gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YERD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN 168;
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RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azcredo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Bourist K., Bernstein C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S. Bruschi G.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S.D., Bringhol J., CounterLon I.F., Counmings N.J., Daniel R.A.,
RA Brilan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Brilan K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Ghim S.V., Glaser P., Golfcau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Mchas R., Lapidus A., Lardinols S., Rumano M.,
RA Mchas M., Lewine A. Liu H., Masuda S., Mauel C., Medique C.,
RA Mcdias N., Mellado A., Lardinols S., Mauel C., Medique C.,
RA Mcdias N., Mellado A., Lardinols S., Manel C., Medique C.,
RA Mcdias N., Mellado A., Lardinols S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R. Liu H., Masuda S., Manel C., Medique C.,
RA Mcdias N., Mellado R., Pornelle D., Porwollik S., Prescott A.M.,
RA Mccecan E., rujic P., Pounelle D., Porwollik S., Prescott A.M.,
RA Schorin A., Tanconi E., Tanahashi H., Takemaru K.,
RA Sato T., Scanlan E., Schronter R., Scotto P., Sadaie Y.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Tarahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanahacka T., Tarahashi H., Pasumoto K., Yata K.,
Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
Pannel E., Wollikawa H.F., Sumstein E., Yoshikawa H., Danchin R.,
Pannel E., Wollikawa H.F., Sumstein E., Yoshikawa H., Danchin R.,
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Pteryqota: Neopteia, Endoptorypota: Diptora, Brachycera: Muscomorpha:
Ephydroidea: Drosophilidae: Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Z99117; CAB14688.1; -.
EMBL; Z99118; CAB14705.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 AA; 19729 MW; 02F3FC9457D5BC55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLEEL, 13, Created) 01-MAY-2000 (TrEMBLEEL, 13, Last sequence update) 01-MAY-2000 (TrEMBLEEL, 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1301 HHHALLLCTVAGIFPDKVLHNIMS 1325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE 20196006; PubMcd-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 HHHALLRACDISSTEDDRILASVSS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CG9782 PROTEIN (FRACMENT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPOTENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STPAIN=REPKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_Tax1D-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168;
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MARTHELL FORGER N. MARTHELLEN, MICHAEL M. Melsen C.E., Mikhos G.L.G., MARTHELLE, Autogenia A., An H. J., Andrews-Plannkoch C., Baldwin D., PA Mallew M.M., Massach, Barshadari J., Baylandari C., Baldwin D., Barshada M.M., Barshada B., Brendin L., Bershey E.M., Barshada M.V., Bernanda A., Barshada B., Brendin L., Bershey E.M., Barshada J., Barshada M., Bernanda B., Brendin D., Brendin J., Bernanda J., Barshada M., Barshada M., Barshada M., Barshada J., Barshada M., Marshada M., Marsh
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MEDINE Occursory publicd 97 841 85;
Stephania R.S., Kalmin S., Lummel C.J., Fun J., Marathe R., Aravind C.,
Mitheil W.R., wild per L., Intessor R.L., Zhao g., Koodin E.V.,
Divis R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  daps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (4) Smale 62; DH 5; Londth 23D; 146; Ered, No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14: Mismatches 25: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231
231 AA) - 24564 MW) - 928A265E904184F0 (3RC64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z6025 MW: A44936B44EP0P6B0 CR051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oB, Last Sequence appare)
14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Racteria: 7D mydiales: Chlamydiaceae; Chramydia.
NYGE (axii. 8) &
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New Tek 24
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Science 242:74-75 (1799).
EMBC: AE of Ges. AAC #[28.];
LaterEnco. Press [4.9]
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s 145 conservative i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMHL: AE004502: AAF48640, L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINAFY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Al Nov 1934 (ITEMBLIEL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Trembile)
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17.
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Eukaryota: Viridiplantae; Embryophyta: Tracheophyta; Spermutophyta:
Magnoliophyta; Liliopsida; Posles; Poaceae; Ehrhartoideae; Orygeae;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Embryophyta: Trachesphyta: Spermatophyta:
Magneliophyta, eudiostyledons sore eudirots; Residae; eurosids 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yao J., Dong Y., Kvarnheden A., Morris B.;
"Socia apple MADS box genes are expressed in different parts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 23.5%; Score 62; DB 16; Length 242;
Matches 16; Conservative 16; Mismer 1
                                    7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (SFF-1997) to the PMRE/Caster-Lynger databases.
EMBL: AJ001682: CAA04520.1: -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01 JAN-1998 (TrEMBLEC), 05, Created)
01-JAN-1998 (TrEMBLEC), 05, Lest sequence update)
01 MAR-2001 (TrEMBLEC), 16, Lest annotation update)
                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Last annotation update) MDMADS9 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                     01-N-V-1998 (TrEMBLrel, 08, created)
01-N-V-1998 (TrEMBLrel, 08, List sequence update)
Score 62: 148-2:
                                                                                                                                                                                                                                                                                                                                    Malus domestica (Apple) (Malus sylvestris).
                                    9: Mismatches
                                                                       1918 LMKVLQGVNGEMVLSQLLPMAEQLLEKT 1045
                   Pred No.
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                                                                                             54 TMDIIQCI SNOTTI QQILGESDVI.EEI | 81
                                                                                                                                                                                                      P.K.I
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PROSITE; PS50065; MADS_BOX_Z; 1.
SMART; SMO044Z; MADS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33266; Maldo:MADS;33266.
 0.68
                   42.98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam; PF00319; SRF-TF; 1.
                                    Carretive
                                                                                                                                                                                                                                                                                                                                                                                           Rosales; Rosaceae; Malus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SPONFNCE FROM N.A. STRAIN CV. CRANNY SMITH;
                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01486; K-box; 1
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Ouery Match
Rest Local Similarity
Matches 12: Courery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P11746; 1MNM.
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                                                                                                                                                                                                                                                                                                                                                                                                          NCBL_TaxID=3750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MADS OR M79.
                                                                                                                                                                                                                                                                                                                   MUMADS9.
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024234;
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                                                                                                                                                                 RESULT 143
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1823 LEATEKTYKYTEPENMENHMOPPMSTLOPHICKMMMPERLTSHOSOLTAMPELEALDPPAGHS 1882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINI 20026330, rubM.d 10552041,
Suqa H., Hoshiyama D., Karaku S., Katoh M., Mubokawa M., Miyata T.;
"Protein tyrosine kinase cbNAs from amphioxus, hagfish, and lamprey:
                                                                                                                   1. SIMITAETTY, 10 THE MAIS DOMAIN PAMILY OF TEANSCRIPTION PACTORS.
EMBL, Y15008; CAA75241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eptatretus burgeri (İnshore haqfish).
Esku: Jolu, Motusou, Chorduta, Gramiata. Hyperetreti, Myxiniformos;
Myxinidae: Eptatretinae; Eptatretus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  isoform duplications around the divergence of cyclostomes and quathostomes.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 62; DB 10; Longli 249;
21.8%; Pred. Rc. 1.1e<sup>+</sup>02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Pred. Mo. 1.16*02;
tive 20; Mismatches 48; indels
                                                                                                                                                                                                                                                                                                                                                 SMART; SM00432; MADS; 1.
DNA-binding; Nuclear protein; Transcription regulation.
SECCEMPT: 249 AA, 28762 MW, 76961830ADA3338 CR664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TIEMBLiel. 13, Last sequence update) 01-MAR-2001 (TIEMBLiel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00219; TyrKc; 1.
ATP-binding; Transferase; Tyrosine-protein kinase.
                                                                                                 -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 AA.
                                                       Zhāng Y., Liu M., Gu H., Chen Z.;
i. Bull. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE, PSS0011, PROTEIN_KIHASE_DOM; 1. PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
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                                     STRAIN CV. ZHONGHUA 8, TISSUE-FLOWER,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKT;
                                                                                                                                                           HSSP: P11746, 1MNN.
Mendel: 24350, Grysa,MADE;24350.
Interpro: 1PR002100; -
Interpro: 1PR002487,
                                                                                                                                                                                                                                                                                     PRINTS, PKGG404, MADSGOMAIN.
PROSITE, PSG0350, MADS_BOX_1; 1.
PROSITE, PS50066; MADS_BOX_2; 1.
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PKINIS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                Pfam; PF00319, SKF-TF, 1.
Pfam; PF01486, K-box; 1.
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Best Local Similarity
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               SEQUENCE FROM N.A.
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                                                                           Sci. Bull.
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MEDLINE-9929935; PubMed-10369927;
McOneen.K.L., Lohwasser S., Takei F., Mager D.L.;
"Eapty-saion analysis of now Ly49 genes: most transcripts of Ly49; lack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      665 IELLADNINLGDPSSMLKMVEDLISVGEEESFNLKQKVTFHVILSVLVSCCSSLKETHFP 724
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                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukuryolu, Metaroa, Chordata, Craniata: Vertebrata, Euteleostomi;
Mammalia: Eutheria, Rodenlia, Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kanckon 1 Muramoto K. Kamio V.; "Gene of Luke-like component of Panton-Valentine leukocidin in Staphylococcus aureus P83 is linked with lukm.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zon D , Kaneko J , Narita S , Kamio Y.; "Complete nucleotide sequence and molecular characterization of prophage PW83paro carrying lukm-lukF-PV(p83) gene cluster in Staphylococcus aureus strain P88."; Supmitted (JHN-2000) to the EMML/GenEank/DDRJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 62; DB 11; Length 266;
25.0%; Pred. No. 1.1e+02;
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1210 ILELLOHKKKI.PSPOTLVPTI.FNIJ.SPCI.RPI.POROGNMEYTK 1252
                  183 VLERVQEEYEMFEFFEFFFFTINIAMQ~WEQEPFFFFFFF 230
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01-04T-2000 (TrEMRLrel. 15, Last annotation update)
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01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-007-2000 (TrEMBLrel, 15, Last sequ
                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                           the transmembrane domain ";
immugogemetics 40,685-691(1999).
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                                                                                                                                                                                                       LY49J PROTEIN.
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Lyer M., Word L.H., Jackson M., Hojek L., Mikkedson F.;
"Isolation and Sequence analysis of a chark encoding an adentic
notelestide transforcator from Flagmodium falciparum.";
                                                                                                                                                                                                                                        2086 TIVLALAEKLÄENY IVELPESTPELAELMEPPEEVERGEGGKITGGELIV 21 🐴
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                                                                                                                                Length 267;
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29.7%; Pred. No. 1.4e+32;
ive 11: Mismarches 15; Indeis
                                                                                                                                John Share 62 1B 9: length 267;
Jisher Pred, Ma. 1.20002;
1190 - 14: Mismatches - 23: Indels
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PRINTS: PROBOGO, MILOGRARHER,
PROSTIE: PSOCIES, MILOGRAFIER, UNENGREE.
SECHENCE OF AA, 43756, MW: 1873687AZ782E9985 280564;
                                                     Theo A MW = 8782 or oct 1010 059 (38264)
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N.V. 1996 (TEMBLES), (1, Last seperate update)
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APP/ATP FEANSPERER ON AGENTIALF FRANSPORASE
Brosei, Bierechnel, Brachem, 61:1960 1962(1997).
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Eur. J. Hiochem. 228:46-91(1995).
EMBL: X8355;; CAA58541.1; ...
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EMBD: 1043€5: AAA52221.12 ·.
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InterPro: IPRe02867;
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"Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,881,565 bp covered by twenty one physically assigned P1 and 1AC clones."; DNA Res. 5.131-145(1998).

EMHI, AB010700; BAB08629.1: -.

SEQUEN'E 313 AA: 34523 MW; EBER436AB6A94A97 CKC64;
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Enterovirus,
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OT-MAR-2001 (TERMILLE). 16, Last sequence update)
OT-MAR-2001 (TERMILLE). 16, Last annotation update)
GENOMIC ENA, CHECOLOS ME 5, Pl CitoREMUDZI.
Arabidopsis thallama (Mouse-ear cress).
Eukaryota: Viridiplantae: Ranspophyta; Tracheophyta: Spermatophyta;
Mannollophyta, endicinyledons: core endicots, Rosidae; entosids II:
Brassjeales; Mrassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko I., Kotani H., Nakamura Y., Sato S., Asamizu E., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kew 0.M., Crainic R., Mendelson E.;
"A highly evolved derivative of the type 2 oral poliovaccine strain
isolated from sewage in Israel: molecular and antiquenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN PV/A745 3/ISR98;
Staiman L.M., Manor Y., Handshor R., Telpoyroux F., Medonoudh M.J.
Halmut T., Silberstein L., Allandari J., Fisher I., Robinov J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1801 QANIRLTSLKKTLATTLAPRVLLPATKKTYKQIEKNWKNHMGPFMSILQEH 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 0.6%; Score 62; DR 10; Length 313; Best Local Similarity 27.5%; Pred. No. 1.4e^{+0.2}; Matches 14; Conservative 11 Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                          Length 401;
                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 6.2; DB 5; Legath 401
Best Loral Similarity 29.7%; Pred. No. 1.60462;
Matches 11; Conservative 11; Mismatches 15; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-200m, to the whelphose makables databases
                                                          PROSTIL, PSO0215; MITGCH_CARRIER, URKHAWH_1.
SEQUENCE 301 AA; 43712 MW; 1CAELAB47074A940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (TrEMBLECL. 16, Cheated)
01-MAR-2001 (TrEMBLECL. 16, Last sequence update)
01-MAR-2001 (TrEMBLECL. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1601 IPVIRGLVONPLPSVRRKALDLUNNKLQQNISWKKTI 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEST THE TOTAL STATE TO THE STATE OF THE STA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MELILINE-98 444 | 45; PubMed-9479 202;
PRINTS; PRO0926; MITOCARRIER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAPSID PROTEIN (FRAGMENT).
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                                                                                                              SEQUENCE
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1305 LILLGTVAGTFPDKVLHNIMSIFTFMGANVMRLDDTYSFQVINKTVKMVIPALIQSDSGD 1364
                                                                                                                                                        Enkaryoja, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi:
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12 LAVAGTRADVSPRQVATVIMPYETELGSSAFETVRQLQRAELTKQLARTLQGRUGSAARY 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neonotonia wightii.
Eukarysta: Viridiplantae: Embrycphyta; Tracheophyta: Spermatophyta;
Magnoliophyta: eddicotyledons; oche endicots: Rosidae; eurosids 1;
Pabales; Fabaceae; Papilionoideae; Neonotonia.
                                                                                                                                                                                                                                                                                                                                             "Expression and conservation of apolipoprotein AIV in an avian
                                                                                                                                                                                                                                                                         MEDLINE-98221191; PubMcd-9553114;
Steinmetz A., Rezmann M., Nimpf J., Aebersold R., Ducret A.,
Weinberg P.R., Schneider W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMRLrel. 16, Last annotation update)
01-MAR-2001 (TrEMRLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 62; DB l3; Longth 366; 25.0%; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 AA; 40852 MW; 847DB49F3E8D91CE CRC64;
                                                                             01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                        01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 AA.
                                                                                                                                                                                                                                                                                                                                                                                      Chem. 273:10543-10549(1998).
                                    01-NOV-1998 (TrEMBLrel. 08, Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINNE-20040642; Pubmed-10570164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam, PF01442; Apolipoprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Y16534; CAA76273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 25.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
PRELIMINARY;
                                                                                                                                            Gallus qallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                               TPROUDINA;
                                                                                                   APOLIPOPROTEIN AIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1365 SIEVSRNV 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 AEELQRRI, 79
                                                                                                                                                                                                                         NCB1_Tax[D-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein.
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                                                                                                                                                                                                                                                                                                                                                                       species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                         Biol.
                                                                                                                      APOAIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09SE57
093601
                                                                                                                                                                                                          Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Ainscouth K., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Cotlson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister M., Latreille P.,
Lightning J., Lloyd C., Memurray A., Mortimore R., of Callagian M.,
Landon N., Smith A., Sonnhammer B., Staden R., Sulston J.,
Thierry-Mics J., Thomas K., Vaudin M., Vauqhan K., Waltston J.,
Thierry-Mics J., Thomas K., Vaudin M., Vauqhan K., Waltston F.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
eleqans.";
                                                                                                                                                                                                                                                                                                                                 70 PSDTVGTEHVVGRESPSESTIESFFARTATVALIEVDARGETTFAQKLFAMMFITYRFFV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                        433 ESKYPRTLDVVLEEHIKETADLKKQELFHQFVSLSTSGGKYQFLADSDTSLMISLNHPLA 492
                                                                                                                                                                                                                                                                                          493 PVRILAMNELKKIMKTSKEGVPFSFIKFAVLARIGDBNIDVVLSAISAFELFKEHFSSBV 552
                                                                                                                                                                                                                                                 10 OSALPQCIEDLISEVAQGALTLSLPKQQDSLPDTKASGPAHSKEVPALTAVETGATNPLA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryeta: Metazoa, Memateda: Chreshabrea, Phabditida, Phabdifeidea,
                                                                                                                      // Match 0.6%; Score 62; DB 14; Length 348; Local Similarity 17.8%; Pred. No. 1.6e.02; etc. 23; Conservative 27; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 62; DB 5; Length 364;
35.1%; Pred. No. 1.6e+02;
Live 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT 1996) to the EMRL/ConRank/TUR! databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTam; PF00646; F-box, 1.
SEQUENCE 364 AA; 42740 MW; 861H009GCBC3D3F0 CRC64;
                                                              348 AA; 38758 MW; 0362DB14F4AK10EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE 94150718; Pubmed-7906398;
  EMBL: AJ288081; CAB77542.1; -. NON_TER 1 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%
Best Local Similarity 35.1%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 358:32:38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
                                             348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001810;
                                                                                                                                                                                                                                                                                                                                                                            553 TISNLLNLF 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  130 QURKKLEFF 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCB1_Tax1D-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T22G5.3 PROTEIN.
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RESULT 152

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EUNCTION: CYTOCHROBE C GXIDAGE IS THE COMPENSIVE OF THE RESPIPATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-3 FORM THE FUNCTIONAL CORE OF THE BUXYME COMPLEX. SUBUNIT 2 TRANSFIRE THE FLETTRING PFOM CYTOCHROMP C VIA ITS BINGLEAR COPPER A CENTER TO THE BIMETALLIC CENTER OF THE CATALYTIC SUBUNIT I (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FERRICYTOCHROME C (BY SIMILARITY).
--- COFACTOR: COPPER A AND HEME GROUP (BY SIMILARITY).
--- SUBCELLULAR LOCATION INTEGRAL MFMRPANE PROTEIN. MITOCHONDRIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY, 4 FERROCYTCCHROME C + O(2) - 2 H(2)O + 4
                                                                           Doyle 1.1, Painwr (p.)
"Intracellular gene transfer in action: Dual transcription and
                                                                                                                                            multiple silencings of nuclear and mitochondrial cox2 qenes in
Adams K.L., Song K., Foessler P G., Nugent J.M., Doyle J.L., \mathsf{Deyle} J.I., Palmer T D.,
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InterPro;

RESULT 153

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Prorphoris Newprora Endonterynotas Diptoras Brachyceras Muscomorphas Ephystosidos Diosophisidas Losophisidas Losophisidas Losophisidas Prosophisidas Prosoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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D
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Embrigatis Matazoa; Arthrapoda; Fracheatis Hexipada; Inserta;
INNER MEMBRANE (NY S-MILARITY).
1 SIMILARITY: DO THE CYTOCHRONE C OXIDASE SHRONT 2 FAMILY.
EMBLS AFFRZOS: AAPL4574 1; ...
INTOLEM. 1969 (1969).
                                                                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Shore 62; DR 10; Loneth 881;
7.1%; Prod. No. 1.70(02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       % Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shariffy, Lin S.I.;
Sabmitted (JUN-1995) to the EMBL/Oscaladayard databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07240024565BD85 CRC64.
                                                                                                                                                                                                                                                                                                                                                             *OBF4DEF96F4925C CRC64;
                                                                                                                                                                                                                                  Prostic records NATE 1.
788 to the tambhate. Micchaelfour, wideredectuse NATE to type claim the member inc.
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often-V 1996 (IrEMBLIEL 5), East sequence update)
often-MAY proced (IrEMBLIEL) 13, Last accordation update)
IRANSA YEARE.
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of PATEZ DO (TERMINAC), PS, Last Sequence update)
of MAEZ-PS (TERMINAC), PS, Last annotation update)
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Macilius/Staphylocorems group: Macillus.
McMt_TaxID-1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CV 1242 POROSMARY RELIGENTAL METAPLEM 1209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.KT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE MACH SEANGTERNAS DESCRIPTION
                                                                                                                                                                                                                                                                                                                                                       141 AA; 4284r MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           обоя; Acyl_franst: 1.
455 AA, 45026 MW,
                                                                                                                                                      Princ PEGGILS, COXZ; 1,
PRINTS; PROTISS; CYCOXDASETT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 MSRILLYANNETERELISSORE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                Courty March
Rest Local Similarity 57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: 142526; AAABISBB:1;
HSSP: P25715; IMLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 12: Caservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                             InterPres (PRe02429)
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Matches 14, Conserv
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                                                                                                                                                                                                                Prefermy Plancoul 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Martillus subtillis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-F23 4;
                                                                                                                                                                                                                                                                                                                                                          SECUENCE
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Best Londins
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045544;
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RX MDDLINE-20196606, PuthMed-1073-182,

RA Admis M.D. Celniker S.E., Ho r R.A., Evans C.A., Gocayne J.D.,

RA Admishaides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gatterson S.N.,

RA Admishaides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gatterson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RA Brithon R.G., Rogers Y.-H.C., Mazel R.G., Change W., Pitclifer R.D.,

RA Abril J.F., Adbayani A., An H.-M., Andrews-Phannkach C., Raiddwin L.,

RA Abril J.F., Adbayani A., Rawenda.e. J., Bayraktaroth L., Headdwin L.,

RA Brill J.R., Rose P.V., Herman H.P., Hohndari D., Bolshakov S.,

RA Bullow R.W., Benos P.V., Herman H.P., Hohndari D., Bolshakov S.,

RA Bulls K.C., Eusan D.A., Bull let H., Cadieu E., Center A., Chandra I.,

ROGESON K., Doup L.E., Downes M., Dusan-Bortha S., Power C., Gabriellian D.A., Bull let M., Galeu E., Center A., Doun P.,

RA Doubson R., Doup L.E., Downes M., Dusan-Bortha S., Power S.,

RA Harris N.L., Byangelista C.C., Perray C., Perricus S., Pleischmann W.,

RA Harris N.L., Harvey D., Heimar T.J., Hernander J.R., Horrism C.,

RA Jaaris N.L., Harvey D., Heimar T.J., Hernander J.R., Morkey D.,

RA Jaako P., Lei Y., Tevitsky A.A., Li J., Hernander J.R., Northwes M.S.,

RA Jaako P., Lei Y., Tevitsky A.M., Li Z., Liang Y., Jan X.,

RA Jaako P., Lei Y., Tevitsky A.M., Li J., Hernander J.A., Morshing D.L.,

RA Mernilov G., Milshina N.V., Moharis J., Morshol D.L.,

RA Mernilov G., Milshina N.V., Moharis R.D., Serledor F., Nebell H.,

Reinert K., Ferningston R., Sameders R.D., Durit V., Reese M.S.,

Reinert K., Ferningston R., Sameders R.D., Shulp D., Parl R.,

Reinert K., Ferningston R., Sameders R., Shulp D., Parl R.,

Reinert K., Ferningston R., Sameders R., Northwest R., Shulp D., Roller R.,

Reinert R., Ferningston R., Sameders R., Shulp D., Roller R.,

Reinert R., Shule B.C., Siden-Kiames L., Simpson M., Skupski M.P., Shull T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanoaster (Frui: 119).
Eukaryota, Metazoa, Arthropoda, Trachoata, Hexapoda; Inserta;
Pteryqota: Neoptera: Endoptervqota: Diptera; Brachycera: Muscomorpha;
Ephydroidea: Drosophilidae: Drosophila.
                       STRAIN-SIMB, SIM3, SIM4, SIM6, AND SIM7;
MEDITHE 20218743: PubMcd-10823947;
Medun D.J., Whitley P.:
"Reduced X-linked nucleotide tolymorphism in Drosophila simalans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.68; Score 62; DB 5; Donath 400; Best Local Similarity 46.78; Prod. No. 1.86-02; Matches 14; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                            400 AA; 45958 MW; BE367472D5255FPC (1964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY 2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2000 (TrEMBLrel, 14, Last annotation update)
CG6475 PROTEIN.
                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 97:5960-5965(2000).
EMBL; AP252721; AAF68504.1; -.
EMBL; AF252717; AAF68500.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRI: 441 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 TEQQQAVAKVQQQVESDI ESAVER (KSYWR 64
                                                                                                                                                                                                                                                                                         Elybase: FEGO0041661; DSim\miranda.
NoN_TER 1 1 1 1 NoN_TER 460 460 SECUENCE 400 AA; 45958 MW: RE367
                                                                                                                                                                                                                    EMBL, AF252718; AAF68501.1;
EMBL, AF252719; AAF68502.1;
EMBL; AP252720; AAF68503.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY:
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 157
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Mang A.H., Wang X., Wang A.H., Wassaniman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., Yeli K.F., Zaveti J.S., Zhan M., Zhang C., Zhang L., Zhang X.H., Zhang F.M., Zhang K., Zha X., Zha X., Zha X., Zha X., Zha X., Smith H.A., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1392 EHRREPTEVQUVDTIGAEKFIWILLITI.FEQYVTKTVLAAAYGEKDAILEADTEFWFSVC 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iseqawa Y., Makai T., Nakano E., Kaqawa M., Chen J., Moli Y.,
Sunaqawa T., Sashihara J., Edu T., Koseqe H., Yazanishi E.,
"A comparison of the complete DNA sequences between human herpesvitus
6 variant A and B.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Bukuryota; Metazoa; Arthropoda; Wracheata; Hoxapoda; Insecta;
Pteryqota; Neoptera; Endopteryqota; Diptera; Brachycera; Museomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caps
                                                                                                                                                                                                                                                                                                                                                                                                    Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                         374 TYKRELEATLIKISEKNUGELLASELITEN ISTSSOFOMIGUKVELLARQFIR 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 62; DB 14; Length 443; 30.0%; Pred. No. 2.1e<sup>2</sup>
                                                                                                                                                                                                                                                                                                                                                         0.6%, Score 62, DB 5; Longth 441;
20.4%, Prod. No. 20:02;
tive 15; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30.0%; Pred. No. 2.10.00.
Live 9; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Virol. 0:0-0(1999).
EMBL: AR021506; BAA76225.1; -.
SEUDENCE 443 AA. 51515 MW; 0DIP168070355191 CRC64;
                                                                                                                                                                                                                                                                                                50073 MW; AB74BA044714C0B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses, dstwa viruses, on RWA stage; Herpesviridae;
Retaherpesvirinae; Roseolovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel, 13, Greated)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-JUN-2000 (TrEMBLrel, 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-RGV 1999 (TERMELTEL 12, Last Bequence apdate)
01-RGV-1999 (TERMELTEL 12, Last annotation update)
44-6% inswrich, To US GRNE OF STRAIN ULIO2 OF HHV-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 491 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT, 443 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV 1999 (TrEMBLrel, 12, Created)
                                                                                                                                                                                          EMBL; AE003734; AAF55892.1; -
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                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 20.49
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                         Ptam; PF00201; UDPGT; 1.
PROSITE; PS00375; UDPGT,
                                                                                                                                                                                                                                        InterPro; IPR002213; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Onery Match
Rest Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human herpesvirus 6.
                                                                                                                                                                                                                                                                                                441 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                  SECUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Sirkhilms-Birkhelbri;

PA. Adams M. D. Colniber S. E. Holf P. A. Evans C.A., Gocayne J.D.,

Adams M. D. Colniber S. E. Holf P. A. Hoskins R. A. Galle R.E.,

Amadaidas P. G., Scherer S.E., Li P. W., Hoskins R. A. Galle R.E.,

Ban G. G., Wortman J.P., Yandell M. D., Zhang O., Chen L.X.,

R. Sutton G.G., Wortman J.P., Yandell M. D., Zhang O., Chen L.X.,

R. Brandon R. C., Evarta Y. H.C., Blazelj B.G., Champe M., Heiffor B.D.,

R. Adril J.F., Agbayani A., An H. J., Andrews Pfannkoch C., Baldwin D.,

R. Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

R. Ballew R. W., Baxendale J., Brokstein P., Brothier P.,

R. Barlis K.C., Busam D.A., Butler H., Cadicu E., Corter A., Chandra L.,

R. Butlis K.C., Busam D.A., Dutler H., Cadicu E., Corter A., Chandra L.,

R. Butlis K.C., Busam D.A., Dutler H., Cadicu E., Corter A., Chandra L.,

R. Adrews R., Doup L.E., Downes M., Daya R.D., Dw. I., Dictz S.M.,

R. Adrews R., Doup L.E., Downes M., Dayan Roche S., Dunkov B.C.,

R. Garriellan A. E., Garra N.S., Gelbart W.M., Glasser K.,

R. Garriellan A. E., Garra N.S., Glan P., Harris M.,

R. Garriellan M., Harroy D., Howland T.J., Wei M.-H., Ibeayam C.,

R. Jalail M., Kalush F., Karpen G.H., Ke Z., Kennson J.A., Ketchum A.A.,

R. Hunkel R. E. Kodira C. D., Kraft C., Kennson J.A., Ketchum A.A.,

R. Harris N.L., Harroy D., Holmand T.J., Wei M.-H., Ibeayam C.,

R. Harris N.L., Markel H., McIntosh T.C., McLeod M.P., McPherson D.,

R. Mount S.M., Moy M., Murphy B., Murphy L., Murny D.M., Nelberson D.,

R. Mount S.M., Markel M., Sannders R.D.C., Scheeltor F., Shen H.,

R. Keinert K., Remington K., Saunders R.D.C., Scheeltor F., Shen H.,

R. Keinert K., Sannders R.D.C., Scheeltor F., Shen H.,

R. Keinert K., Sannders R.D.C., Scheeltor F., Shen H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong K., Sun E., Farier C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Wacadage T., Werley K.C., Wu D., Yang S.-Yao O.A., Weils, K., Zhu, M., Zhang G., Zhac C., Zheng L., Zhong X.H., Zhong Y.H., Zhong K.M., Zhang G., Zhac C., Zheng L., Zhong X.H., Myers E.W., Rubin G.M., Venter J.C., Thu X., Smith H.O., Cibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pterygota, Neoptera, Endopterygota, Colcoptera, Polyphaga,
Elateriformia, Cantharoidea, Phengodidae, Phrixothrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             491 AA; 57573 MW; 8CB320ADBE95A0F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 62; DB 5; I
Local Similarity 28.6%; Pred. No. 2.30+02;
les 16; Conservative 9; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99315203; PubMed=10387072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase, FBqn0034023; C212960.
SPQUBNCR 491 AA: 57573 MW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Salpade 287-2185-2195(2000).
EMPL: ABOUSAID: AAFSRI32 1:
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                                               SECUENCE FROM N.A.
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NCBI_TaxID-7227;
                                                                            STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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RESULT 162
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                Action Microsoft and the Microsoft and Micro
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Bakaryota Merik si Arth.opoda Tidebata: Hexapoda: Insecta:
Preryota: Negreta: Endyteryota: Dipleta: Brachycera: Miscomorpha;
Epigdreider: Drosophillday: Dassophila.
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Viriant V.E., Rechard E.J., Charja Y., "Clouder, See price analysis, and expression of active thripotheta. Indicating the form of active thribotherases relationship between bioluminescence special and primary structures."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   c. 40 Share 62; like 5; Length 546;
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15: Mismatories ax ax Todals
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16. Last annotation update)
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                                                                                                                                                                    Візстичнізтту зм. 8271—8279 (1999)
ЕМИС, АБТ 39645, ААБЗ454111 г.
HSSP; РОВБ59; ПДТ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rest Local Similarity (2000) 489
Matches (150) Assertation
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NACHALPHA 96AA PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of MAY Zoro (TERMSTEE)
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Adams M.D., Celniker S.E., Hell F.A., Frans C.A., Gordyne J.E.,
Adams M.D., Celniker S.E., Hell F.A., Frans C.A., Gordyne J.E.,
Adamstides P.G., Schero S.E., Hell F.A., Frans C.A., Gordyne J.E.,
Adamstides P.G., Schero S.E., Hell F.A., Frans C.A., Gordyne J.E.,
Andardides R.A., Forthern S.E., Hell F.W., Heaster B., Henderse S.M.,
Sutton G.C., Wortman J.R., Yandell M.D., Zhana C., Chen L.X.,
A Hendon K.C., Rouser Y., Harzel F.E., Hell C., Nelson E., Hell C., Held M., Deither B.D.,
Anil J.F., Adbayani A., An H.-J., Andrews-Prannkorh C., Haldwin D.,
Bellew R.W., Hash A., Bernen B.P., Henders P., Miller F.M.,
A Heris K.C., Busan D.A., Bernen B.P., Henders P., Henders P.,
Burtis K.C., Busan D.A., Bull Y. H., Cadler, E., Centert A., Chandra J.M.,
Cherty J.M., Casley S., Bull Y. H., Cadler, E., Centert A., Chandra J.M.,
Ac Pablos B., Delcher A., Dent Z., Mays A.D., Dew L., Dietz S.M.,
Ac Cherty J.M., Casley S., Ballik C., Dayenpert L.B., Lebrors P.C., Dunn P.,
Ackelon B., Hong R.D., Bohlik C., Dayenpert L.B., Lebrors B.,
Ackelon B., Hong R.D., Christon K.J., Hennan R.M., Glasser K.,
Anderson R.J., Pennagelista C., Gabriellan A.E., Girq N.S., Gelbart R.M., Glasser K.,
All Cone R. Gorrell J.H., Gu Z., Guan P., Hartis M.,
Hostin D., Houston K.A., Howland T.J., Hennam C., Hermide J.F.,
Andellali M., Kalush F., Matper S.H., Merchise G.J.P., Hennam C., Henrick M.,
Andellali M., Kalush F., Matper S.H.,
Andellali M., Kalush F., Matper S.H., Merchise G.J.P.,
Andellali M., Kalush F., Matper S.H., Merchise G.J.P.,
Anderson R., Henrick C., Garrell J.H., Gu Z., Gun P., Henrick G., Merchise G., Mer
Ye J., Yel R. F., Easeri J.S., Zhan M., Zhang G., Zhao Ç., Zheng L., Zheng X., Zheng F.N., Zheng W., Zhao S., Zha X., Zhu K., Smith H.D., Glubs R.A., Myers E.W., Rubr G.M., Venter J.C.;

"The genome sequence of Dros phila melanomaster.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkarjota, Metazoa, Arthropoda, Trachcara, Bezapoda; Insecta;
Pterygota; Neoptera; Endopteryanta; Diptera; Brachycera; Muscomorpha;
Ephydroideu; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mainel M., Kalush E., Karpen (16.) Ke Z., Kennisen J.A., Ketehom K.A., Kimmel M.E., Edita (16.) East (17.) Lask (17.) Listed S., Ealp D., Eal Z., Lister V., Els Z., Lister V., Els Z., Ealp D., East (17.) Lister V., Els Z., Mattel B., Methosh T.C., Meleod M.P., Metherson D., Merkilov G., Milshina N.V., Mobarry C., Morris J., Mesherson D., Mennt S.M., Mey M., Merphy L., Mishy L., Mishy L., Mishon D.L., Palazzole M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sdps
                                                                                                                                                                                                           SCIENTE 287.2185-2195 (2000).
-!- SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE LIGAND-GATED JONIC CHANNELS FAMILY.
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D4BAlc:1654DF646 CRC64;
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01-MAY-2000 (TrEMBLEEL 13, Last sequence update)
01-MAY-2000 (TrEMBLEEL 13, Last annotation update)
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PRINTS, PK00252, NKICNCHANNEL.
PRODOM; PD002183; -; 1.
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SEQUENCE 552 AA; 62218 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000361; -
InterPro; IPR001175; -
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1566 ERNADKLIVKEWRALLSKAYDLLDKVNALLPTFTFIPVIRGLVGNPLPSVRRKALDLLNN 1625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Since
bitables mention, involved in cyclic beta justa binsynthesis.", J. Bacteriol.
 0:0-0(1999) .
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Mammalias Eutherias Primatess Catarrhinis Hominidaes Homos
                                                                                                                                                                                         Bartoria: Protespacieria; aipha subdivision; Rhizobiaosae group;
Phizobiaosae; Stnorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 27.7%; Pred No. 3 2e+uz;
Best Local Similarity 27.7%; Pred No. 3 2e+uz;
Matches 13; Conservative 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSTITE: PARTE, SMOO326, SH3; 1.
SMART; SMOO326, SH3; 1.
ALP-Dinding, Kinase, Receptor, Transferase; Tyrosine-Prince for AA, 71926 HW, 6AD0PB28221777DB CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 AA; 71500 MW; ChancerderaranaRA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-FFH-1997 (TrEMBLrel. 02, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 0.04; Score 62; DB 2; Local Similarity 27.4%; Fred. No. 3.2c+02;
                                                                                                                                                                    Rhizobium meliloti (Sinorhizobium meliloti).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 MALOCHREKEEGVLHEVRLADDFL 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON-RECEPTOR TYOSINE KINASE.
                                                                                                    PHOSPHOGLYCEROL TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 0:0-0(1999).
EMPL; 1167998; AAR41531.2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; [PR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPre; iPPO01245; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
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                                                                                                                                                                                                                                                                            NCBI_TaxID=382;
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RA Scinct! K., Ecminaton K., Saunders E.D.C., Schenier F., Shen H., RA Sher B.C., Siden Kiamos I., Simpson M., Strong K., Sun E., Spradling A.C., Siaplecon M., Strong K., Sun E., Rad Scincer S., Spradling A.C., Siaplecon M., Strong K., Sun E., Mand A.H., Wang X., RA Scincers E. V. Turnor R., Venter E., Wand A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Yelliams S.M., Woodage T., Worley R., Wurt D., Yang S., Zhu X., Smith H.G., RA Yellos R.A., Myers E.W., Kulin G.M., Venter J.C., Schu X., Smith H.G., RT. The qenome sequence of Drosophila melanogaster."; Science 287:2185-195(2000).

R. Science 287:2185-195(2000).

R. Science 287:2185-2185-2185 (2075).

R. Science 287:2185-2185-2185 (2075).
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NCBL_TayID-566;
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Gaps

Length 598,

8; Mismatches 14; Indels

 $g_{\mathrm{Y}}=1140^{\circ}$  Soulesvorsywopvyhelenhohymenesp $=1223^{\circ}$ 

12; Conservative

Matches

Best Local Similarity

Query Match

314 TQDLETVDDASGKISIRQTAITNLIEHPTQMKPP 347

Dp.

0.66; Score 62; DB 5, 35,3%; Prod No 2 9e+02;

01-0CT-2000 (TrEMBLE), 15, Created) 01-0CT-2000 (TrEMBLE), 15, Last sequence update) 01-0CT-2000 (TrEMBLE), 15, Last annotation update)

HYPOTHETICAL PROTEIN VC2041.

Vibrio cholerae.

SECTIENCE FROM N.A.

PRT; but AA

PRELIMINARY;

Q9KQF7: O9KQF7

٦ V

RESULT 163

Q9KQF7

Caps

0

40, Indels

0.6%; Score ed; Ds 2; 1 25.0%; Pred. No. 2.9e+02;

17; Mismatches

Conservative

Guery Match Best Local Similarity Tothos 19; Conserv

649 AA.

PRELIMINARY; PRT;

P72301; P72301

RESULT 164

P72301

600 AA; 68371 MW; AFEF349F4707943A CRC64;

EMBL; AE004278; AAP95189.1; -. TIGR; VC2041; -.

SECUENCE

Nature 406:477-483(2000).

cholerae.

Fraser C.M.;

 $\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\circ}{\times}\overset{\overset$ 

us-09-603-665-5.rspt

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Yaba monkey tumor virus.
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      SECUENCE FROM N.A.
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                                    STRAIN HB:
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MISSIN R. AINSTONA R. ANDERSON K. Baynes C., Berks M.,

MISSIN R., AINSTONA R., FORMELL M., Copper J., Conjson A.,

Taxton M., Deat S., Du Z., Dutbin R., Favello A., Sulton L.,

Judget A., Shewi F., Baykins I., Hiller M., Johnston L.,

Judget M., Kershew T., Kirston J., Laster N., Latrellle P.,

Lidhalid J., Eloyd C., Memuriay A., Mortimore R., C'Callaghan M.,

Ristons J., Percy C., Milkien L., Shaden R., Showhkeen R.,

A., Shaddon N., Smith A., Sonnhammer E., Shaden R., Sulston J.,

A., Missin M., Wallstock E., Wilkinson Sproat J., Woldman P.;

M., Missin A., Weilnstock E., Wilkinson Sproat J., Woldman P.;

"L. Mo. of contiquents nucleotide sequence from chromosome III of C.
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Phibdilidaen Peloderimaen Caemorhabditis.
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25,0%; Pred. No. c.4e+02;
Use [c. Mismatches 23; Endels
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1269 TITELLOBEKKERSPULIVPILENLESRITEPLPGROOMBYTKOLF 1255
                                                         43 LICORLEDRAPIPPPD/SPALYSLALR/WARREDRPSFSHIPM [ 477
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In Z., chraces I., thoson A.;
"The sequence of Carterbabdilis elements countd (0958.";
Submitted (JUL-1998) to the EMBL Gets. That Israeles
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SEJČENTE – 5 + AAI – 77115, MW. – 912/56/(625/594970) PROGAS
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E MAY Proc (TEMMERE). P. List Sequence update)
F-MAY 2006 (TEMMERE). P. List annotation update)
                                                                                                                                                                                                                                                                                                             of N.V. Fow (TERMILLE), or, Last september update)
01-M.: Zoon (TERMILLE), 19, Last annotation update)
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Bartoric Filmieutes: Barilius/Nostridiam uroup:
Bartilius/Staphylocorus eroup: Staphylocorus.
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Rose Loreal Similarity 25,008
Trebose lay conservative
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                                                                                                                                                                                                                                                 96555
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076555
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Ameno H., Morikawa S., Heda Y., Miyamura T.;
"Nucleotide sequence of the central 50kbp region of Yaba virus DNA.";
satalto-1 (HB 1998) to the FMM Tothars 100kb databases.
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"Libertification and characteristics of the them: How Minase gene of
Yaba virus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viluses, no ENA stade; Foaviridae; Chardopoaviridae;
                                       "Isolation of the Staphylococcus amens ribonaciectide reductuse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :.
©
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 0.6%; Score 62; DH 2; Length 71H; Bost Local Similarity 34.1%; Pred. No. 3.66*82; Matches 14; Conservative 5; Mismatches 18; Indels
                                                                                                   Submitted (MAR 1969) to the EMES, Wishing Titled databases.
EMBC: AJ183495: CAB38642.13 *.
InterProj IPRO00788; *.
                                                                                                                                                                                                                                                                                                      PROSTIE: PSOCORS: RIBORED LARGE, UNKNEWN_1.
SEQUENCE 718 AA, 82163 MW, BR7205520247HE2F CR564;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1993 OFTLNCLYKTELFDTQHFISKERAXALMMPLVDQLENKLGG 2033
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01-WAY-2300 (TrEMBLEEL IS, List sequence aplate)
01-WAK-2301 (TrEMBLEEL IS, List annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAY-2000 (TrEMBLrel. 14, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 QYGLYHAYRLAIAPIQSISYVQNATSSVMPIVDQIERRIYG 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   572 HERKEISTRESERGESYNVENTETETETETE 609
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EMBL: AB015885; HAA88789:1: -.
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                                                                                                                                                                                                                              Plam, PF00317; ribonucleo_rec; 2.
PRINTS; PR01183; RIBORDTASEM1.
Morrissoy J.A., Williams P.,
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01-IIIN-laux (Tremmire) ub, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINF=97410310; PubMcd-9267025;
                                                                                                                                           MEDLINE-98065952; PubMcd:9403694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLyBase, FBgn0021776; miranda.
SEQUENCE 839 AA; 44112 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMHL; AF045771; AAC02621.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.78,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIRA OR MIRANDA OR CG12249.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                               Nature 390-625-629(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 90:449-458(1997).
                                                                                                                                                                                                                                          asymmetric divisions.
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                                                                                            SEQUENCE FROM N.A.
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                                                                                                                      STRAIN-CANTON-S
                                                                                                                                                                                                Matsuzaki F.
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Adams M.D. Celdiker 3.E. H01t R.A. Evans C.A. Gacayue J.D.

Adams M.D. Celdiker 3.E. H01t R.A. Hoskins R.A. Galle F.F.

Adams M.D. Celdiker 3.E. H01t R.A. Hoskins R.A. Galle F.F.

RA Adamstaldor B.C. Scherer S.E. H01t R.A. Hoskins R.A. Galle F.F.

RA Sutten G.G. Wortman J.R. Youthell M.D. Zhong O. Chen L.X..

Ballew R.M. Payle C. Baxter E.G. Hell G. Nelson C.R. Miklos G.L.G.

RA Adayani A. Bayanel A. An H.J. Andrews-Pfannkoch C. Baldwin D.

RA Ballew R.M. Baya R. Bayandale J. Hayarakarodu L. Beasley E.M.,

RA Ballew R.M. Baya R. Bayandale J. Borkstein P. Brokarov S.,

RA Ballew R.M. Baya R. Bayandale J. Borkstein P. Brokarov S.,

RA Borkova D. Botcher A. Bonck J. Brokstein P. Brottier P.

Butis R.C. Busam D.A. Butler H. Cadleu E. Center A. Chandra I.

RA Borkova D. Botcher A., Danke C. Davenport L.B. Dow T., Dietz S.M.,

RA Cherry J.M. Cawley S., Dalike C. Davenport L.B. Davies P.,

RA Cherry J.M. Cawley S., Dalike C. Davenport L.B. Davies P.,

RA Durbin R.J. Byangelista C.C. Forraz C., Forriera S., Fleischmann W.,

RA Bartis N.L. Harvey D., Helman T.J. Hernandez J.R., Flouck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M., Holly B., Joi Z.,

RA Hostin D., Houston K.A., Howland T.J., Wei M., McPherson D.,

RA Minnel B.E., Kodira C.D., Mald M. T., Rayitz S., Hulp B., Joi Z.,

RA Liu X., Mattel B., McIntosh T.G., Morris J. Mscherson D.,

RA Merkulov G. Milshina N.V. Moharry C., Morris J. Mscherson D.,

RA Brisch P., Lof Y., Levilsky A.A., Il J., Il Z., Hand Y., Maller B.,

Radial M., Raish F., Rarpon G. H., Misserom D. P., Horsey M. R.,

Radial M., Malush R., McIntosh T.G., Morris J. Mscherson D.,

RA Brisch P., Mc J. Wayan R. C., Morris M., Strong R., Sinth T.,

RA Brisch R., Nolske R.A., Murphy B., Misserom D. P., Walley S., Sinth T.,

Radia S., Techor C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Brisch R.A., Woodage T., Shang M., Scheeler F., Shen B.,

Radia S., Jacker F. M., Weits R.A., Shang S., Phill B., Weith R. M., Weits R.A., Woodage T., Shang M., Weits R.A., Weit
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                                                            Pterygota; Neoptera; Endoptorygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Eukaryota: Metazoa: Arthropoda: Tracheala; Hexapoda, Insecta;
                       brosophila melanoqaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda: Tracheata, Hexapoda, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 62; DB 5; Length 815;
46.7%; Prod No 4.10+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FHqn0021776; miranda.
SEGGENCE 815 AA, 92677 MW; 537701439FP930F6 CPC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                388 TEQUQAVAKVQQQVESDLESAVEREKSYWR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TFEMBLEEL 06, Created)
01-JUN-1998 (TFEMBLEEL 06, Last sequ
01-MAR-2001 (TFEMBLEEL 16, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003728; AAF55723.1;
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Best Local Similarity 45.7%
Terhos 14; Conservative
     MIRA OR MIRANDA OR CG12249
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                                                                                                                                                                                   SECUENCE FROM N.A.
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RESULT 170 044224

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Prerydota, Reoptera; Endopterygota, Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae, Drosophila.
NCBI_TaxID=7227;
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydronea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               o; daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen C.P., Jan L.Y., Jan Y.N.; "Miranda is required for the asymmetric localization of Prospero during milosis in Drosophila.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .:
O
                                                                                                                                                                                                                                                           "Miranda directs Prospero to a daughter cell during Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           brosophija melanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.6%, Score 62; DB 5; Length 830;
46.7%, Fred. No. 4.2e+02;
ive 4, Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Guery Match
Best Local Similarity 45.78; Pred. No. 4.2e:02;
                                                                                                                                                                                                     Ikeshima-Kataoka H., Skeath J.B., Nabeshima Y., Doe C.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.20:02;
4; Mismutches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shen C.P., Jan L.Y., Jan Y.N.;
Submitted (FEB-1998) to the FMBL/GenBank/FURT dalabases.
                                                                                                                                                                                                                                                                                                                                         ELENT ABOO5661: BAZ4111.1: -.
FYPASS: FBG0021776; miranda.
SEQUENCE Ast AA; 93171 MW; F7AD159AA58F178A CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7ZFROEGA *FEATTRE CRO64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
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01-0CT-2000 (TrEMBLEEL. 15, Created)
01-0CT-2000 (TrEMBLEEL. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              830 AA.
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Cuery Match
Best Local Similarity 43.4%,
Matches 13; Conservative
                                                                                                                                                 Bradyrhizobium japonicum.
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                                                                                                                                                                                                                                                        NCBI_lax1D=375;
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                                      Arabidopsis Thilana (Mouse our cress).
Enkary des Villafiel unlace Enkaryodist inscheopkera: Spennatophyla:
Enkary des Villafiel unlace Enkaryodista inscheopkera: Spennatophyla:
Entasi des Enkaralogist des Villafiels entasiones des Villafiels Enkaryodists (Enkaringer).
Entasi des Enkarsicaceaes de Eddepsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structural northers of Arabadopsis thatiana chromosome 5, XI."; sharing d (JUL 1979) to the EMBL/Checkark/2016* (JUL 19789). EMBL, About MA GOOD I. SELECT HAN A A A STRUCT AND A STRUCT A
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                                                                                                                                                                                                                                                                                                                                                           Kanooko I., Katoh I., Asanizu P., Sato S., Nakanura Y., Kotani H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.5%; Score 62; DR 10; Landth 836;
11.0%; Pred. No. 4.2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unorg Match 0.66; Score 62: 08 14; Length 903; Best Local Similarity (0.05; Fred. No. 4.6e-62;
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EMHID APPS/2005 AAL470-04.11 3
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of off-2000 (FEMBLIE), By Last annotation update)
GENOMICTON, CHROMOSOME T. BAY CHONEFFER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of MAY-20 \alpha (FrEMHirel, 19, last sequence update, of MAY-2000 (TrEMHirel, 14, Last annotation update)
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N°BI_Lavid-4,6-4;
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\$7 \$ \$ d.d 1.74 4.74

PESTILI 174

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P14 4.24 

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Adams M.D. Celniker S.E. Holf R.A. Evans C.A. Gorayne J.D.,
Adams M.D. Celniker S.E. Holf R.A. Evans C.A. Gorayne J.D.,
Adams M.D. Celniker S.E. Li P.W. Hoskins R.A. Galle K.E.,
Adams M.D. Celniker S.E. Li P.W. Hoskins R.A. Galle K.B.,
Adams M.D. Cewer S.E. Li P.W. Hoskins R.A. Galle K.B.,
B. Sutton G.G., Wortman J.E. Yardell M.D. Zhang Q. Chen L.X.,
B. Briddon K.C., Rogers Y. H.C., Blazel R.G., Champe W. Preiffor H.D.,
R.A. Abril J.F., Adbayani A., An H.-J. Andrews-Plannkoch C. Baldwin L.,
B. Ballew R.M., Basu A. Baxmadale J., Raylaktaredia L., Beasley E.M.,
B. Ballew R.M., Bouck J., Bromen B.P., Phandari D., Bolskakov S.,
B. Borkova D., Botchan M.K., Bouck J., Brownport L.H., Lovices P.,
B. Borkova D., Botchan M.K., Buller H., Cadieu E., Center A., Chandra I.,
B. Borkova D., Botchan M.K., Buller H., Cadieu E., Center A., Chandra I.,
B. Borkova D., Botchan M.K., Buller H., Cadieu E., Chief S.M.,
B. Borkova D., Botchan M.K., Buller H., Cadieu E., Chief R.,
B. Borkova D., Botchan M.K., Bouck J., Brownport L.H., Lovices P.,
B. Borkova D., Botchan M.K., Bouck J., Brownport L.H., Lovices P.,
B. Borkova D., Botcher A., Deng Z., Mays A.D., Dew I., Bletz S.M.,
B. Bottis F. L. Boanes P., Buller P., Borrier P.,
B. Bodger R., Gong F., Gerrell J.H., Ga Z., Guan P., Harris M.,
B. Bottis N., Harvey D., Helman T.J., Herrander J.R., Bouck J.,
B. Bottis D., Houston K.A., Howland J.J., Wei M.-H., Ibedwam C.,
B. Ballali M., Kalush F., Kraften G.H., Ke Z., Rennison J.A., Kerebum K.A.,
B. Harris N.L., Harvey C.D., Kraft C., McLeod M.P., Morbherson D.,
B. Kalmmel B.E., Modita C.D., McLeod M.P., Morbherson D.,
B. Lin X., Mattel B., Mchick H., Mchairy C., Morris J., Loi X.,
B. Morkulov G., Milshina N.V., McDairy C., Morris J., Loi W. Mchairy C., Morris J., Loi W. McDairy C., Morris J., Loi W. McDairy C., McLeod M.P., Morbherson D.,
B. Lin X., Morkulov G., Miller M. M., McDairy C., McLeod M. D., Loi J., Loi J., McDairy C., McLeod M. D., Loi J., Loi J., McDairy C., McLeod M. D
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Eukaryyda, Metacka, Arthropyda, Tracheata, Hekapeda, Insecta;
Pteryyda, Neotera, Endopteryacta; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Bradyrhizobium group: Bradyrhizobium.
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"Bradyrhizobium uponioum does not require alpha-ketoulutarate
dehydrogenase for growth on Succinate or malate.";
J. Racteriol. 179:194-201(1957).
EMBL: U74618; AAC44748.1;
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3.3%; Pred. No. 5.1e+02;
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SEQUENCE 985 AA; 110920 MW; C3D4E9TA8EFB4280 CRC64;
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O9WOWZ
O9WAY-2000 (TEMMILE) 13, Created)
01-MAY-2000 (TEMMILE). 15, Lest sequence update)
01-MAK-2001 (TEMMILE). 15, Lest amnotation apdate)
01-MAY-1997 (TrEMBLiel. 03, Last sequence update) 01-MAY-2000 (TrEMBLiel. 13, Last annotation update)
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                                                                                                           ALPHA-KETOGLUTARATE DEHYDROGENASE.
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MEDLINE-97136621; PubMed 8981998;
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TKK PROTEIN (BTB-III PROTEIN).
TKR OR GG2672.
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Mornt S.M., May M., Marphy B., Murphy L., Murny D.M., Nelson D.L., Nelson D.R., Nelson D.R., Nixen K., Nussketh E.B., Parleb J.M., Najazzolo M., Pittman G.S., Pan S., Pollard J., Parl V., Reese M.G., Perincrt K., Beminston K., Sanders B., Scheeler F., Shen H., Shue B.C., Siden-Klamos L., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Stapleton M., Strong R., Sun E., Spradling A.C., Thurer E., Venter F., Wang X., Wang C. Y., Wassartan F.A., Weitscher F., Wang X., Wang C. Y., Wassartan F.A., Weitscher F., Win D., Yang S., Yao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Sheri Y., Sheri M., Zhou M., Zhou X., Zhu S., Zhu X., Shill B.C., Gibbs K.A., Myers E.W., Kubi G.A., Venter G.C., The G., Shill B.C., Gibbs K.A., Myers E.W., Kubi G.A., Venter G.C., The G., Shill B.C., Williams S.M., Weitscher G. M., Kubi G.A., Venter G.C., The G. M., Shill B.C., Gibbs K.A., Myers E.W., Kubi G.A., Venter G.C., The G. M., Shill B.C., Williams G. M., Shill B.C., Gibbs K.A., Myers E.W., Kubi G.A., Venter G.C., The G. M., Shill B.C., Miller G. M., Robert G. M., Shill B.C., Miller G. M., Robert G.
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MEDLINE-95024186; PubMed*7938017;

Zollman 3., Jodt D., Prive 3.6., Coudere J.E., Laski F.A.;

Zollman 5., Jodt D., Prive 3.6., Coudere J.E., Laski F.A.;

Zollman 1., found primarily in zire finger proteins, defines an evolutionarily conserved family that includes several developmentally requiated genes in prosophila.";

From Matl. Acad. Sci. 0.3.A. 91.10717·10721(1994).

EMBL: ALSS2174; CAE64389.1; -.

EMBL: 014400; AAA50835.1; -.
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97Ph4Ph9A744PPE; PPPh4;
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Submitted (DPC-1999) to the EMRE, Georgank /DDRT databases
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-- 112297 MW;
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InterPro: IPR000210; -.
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PROSITE; PS50097; BTB; 1.
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12;
                                                                                            Query Match
Rest Ireal 9
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                                                                                                                                                                                                                                                                                                     C9ENB3
                                                                                                                                                                                                                                                                 RESULT 178
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                     Q9RNB3
                                       Ö
                                         Caps
                                                                                                                                                                                                                                                                                                                                                          Enkaryola: Holasca, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Entheria, Primates, Catarrhini, Hominidae, Homo.
                                       0
Score 52; DB 5; Length 1046;
Pred. No. 5.4e+02;
5; Mismatches 4, Indels
                                                                                                                                                                                                                                                                                     16, Last annotation update)
                                                                                                                                                                                                                                                                   (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                              PKT, 1114 AA.
                                       5; Mismatches
                                                                                                                                                                                                                              Q9H0F1;
01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                            1182 POPMYOURSODLESVORVOOS 1203
                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLEGL 16, Last
HYPOTHETICAL 125.0 KDA PROTEIN.
                                                                                                Owery Match 0.6%;
Best Local Similarity 57.1%;
Matches 12; Conscrutive
                                         Conservative
                                                                                                                                                                                                              PRELIMINARY,
                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                      DKF2P434M1526.
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O9H0F1 RESULT 176 Q9H0F1 AC DT

्र r. NCB1 TaxID: 9606;

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Milson E., Ainsceape E., Anderson K., Paynes C., Porke M.,
Ponfield T. Purren I., Connell M., Copecy T., Cooper J., Coulson A.,
Craxton M., Derris S., Pur Y., Purbin P., Pavello A., Fulton I.,
Jones M., Green P., Hawkins T., Hillier I., Hor M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister I., Herr M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister I., Herr M., Johnston L.,
Parsons M., Rershaw J., Kirsten J., Laister N., Latreille P.,
Smalden M., Smith A., Sonnhammer R., Shaden R., Showheen R.,
Phierry Mich. T., Phiken J., Poppra A., Sandens B., O'Callaghan M.,
Watson A., Weinstonk I., Whithuser Spreat J., Wahlman R.,
Watson A., Weinstonk I., Whithuser Spreat J., Wahlman P.,
Watson A., Weinstonk II., Whithuser Spreat J., Wahlman P.,
                                                                                                                                                                                                            0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pubargeta, Moragoa, Nomatoda, Chromadoroa, Phabditida, Phabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 62; DB 5; Length 1334; ps 5%: Prod No. 7 20+02;
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Similarity 29.2%, Prod. Mc. 5.96:02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; 299169; CAB16307.1; -.
SEQUENCE 1334 AA; 149813 MW; R7CROP44ERDSADRR CPC64;
                                    Wiemann S.;
                                                                                                           PANKOPROPRO19067 CPC64;
                                Ansorge W., Wirkner U., Mewes H.W., Weil B., Wiemann S., Schmiffed (TAN-2000) to the EMHLAtendank/PhRT databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1997) to the RMML/GenBank/DDB1 databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLEEL, 13, Created)
61-MAY-2000 (TrEMBLEEL 13, Last sequence update)
01-MAR-2001 (TrEMBLEEL 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                        12, Created)
12, East sequence update)
12, East annotation update)
                                                                                                                                                                                                                                                1487 FNKSESQEEMLQVFNVETHTSKQLRHFKFLSVSFMSQLL 1525
                                                                                                                                                                                                                                                                                  446 FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESL 484
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                                                                                                                                                                                                                                                                                                                                                                                        PPI; 1334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94150718; PubMed=7906398;
                                                                                                               104953 MM.
                                                                      EMBL; AL136821; CAB66755.1; -.
                                                                                                                                                         Outry Match
Best Local Similarity 28.2%
****Ahos 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conscivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      PPELIMINAPY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 368.32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1888 (TrFMRLrol
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLr⊝)
01-NOV-1999 (TrEMBLr⊝)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                        Hypothetical protein.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPOTENCE PROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C26H9A.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_Tax1D-6239;
                    TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elegans."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Smye R.;
                                                                                                                                                                                                                                                                                                                                                                                                        Q9XTS7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2689A.
                                                                                                                                                                                                                                                                                                                                                                                        28TX60
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                                                                                                                                                                                                                                                                                                                                                                       09XTS7
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 $\mathbf{z}$  is a  $\mathbf{z}$  function of the following  $\mathbf{z}$  and  $\mathbf{z}$  following  $\mathbf{z}$ 

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Eukarpetu Metiser, Tusilakas Studaras Vettebratas Euteleostomis
Amphibla, Battachias Andras Mesobattachias Pipoldeas Pipidaes
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RGLIZInder M., Stiegler E., Remmy E.,
"Closino and sequencial of Pol-Loxes expressed in Xenopus lacets
tected embryos."
Nather Acids es. 18,519-518 (1909).
HMREL VETO', "AXAMAGES."
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26.6%; Pred. Ko. 2.let03;
59: 15; Mismatches 82; Indels
                                                                                                                                                                                                                                                                                                                               The market of a synthesis of the control of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microsystis nerodinosa.
Bastoria: Oyas dasCoria: Chrososcoales: Microsystis.
NOB: LaxID: 1126:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSTEE FEMALE BEREATH INC. THERED. CHRINKE, PERSILE PEMALE, CHRINKE, CHRINKE, CHRINKE, CHRINKE, CHRISTIE, PSAGONO, CHSAST, P. TINKE, WA. J. FROMER, C. S. SOGONO, CHRISTIE, PSAGONO, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIE, CHRISTIA, COLONO WW. 4APPSAGONO AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTIE: FSCOLGOOF AA FRANSFER CLASS († HNKNOMN_1).
PROSTIEF: PSSOLJE; AZE DOMAIN: Z.
FROSTIEF: PSCO14°C; AMP_BINIING: 1.
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Plant Provided by Mar Distance.
Plant Provided by Planther 2, new order, Subdessalting 2.
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Host Local Similarity 26.68,
Matches 17, Conservition 1
                                                                                                                                                                                                                                                                                       Thirt by Notion RAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterProp (PR000954);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterProg [PRecons.]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interferor (PROSES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; Pi45047; LAMIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interfer a DPROvi6ed
                                                                                                                                                                                                   SECHENIE FROM N.A.
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                                                                                                                                                                                                                                               SIRAIN PTC7805;
                                                                                                                                                                                                                                                                                                                                                                            THE PARTY CONTROL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDEPTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1115 PESF 1118
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::
                                                                                                                                                                                                                                                                                                                            0.6%; Score fly DB 14; Detath 114;
3.3%; Pred, No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 61; DB 14; Length 136;
28.1%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                           14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29: Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine respiratory syncytial virus.
Viruses: ssRNA negative strani viruses: Menomedavitales:
Paramyxoviridue: Preumevirinas: Preumevirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses, sseka aedativo strand viruses, Mononegavirales:
Paramykoviidae, Pacamemirinae, Pacamemirus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laisen L.E., Gottshalch E., Blischkrone-Moller M.;
Sulmitted (MAR 1998) to the EMBL/Sochart/Tond Jatabases.
EMBL: AF054666: AAC36672.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Haddiructural protein.
SEQUENCE 136 AA: 15276 MW: IARGAFF7D63HH789 CRC64;
                                                                                                                                                                                                                                                         SEQUENCE 114 AA; 12758 MW; 640924F4866270DD CRO64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NoV-1998 (TERMILE). 08. Created)
01-NoV-1998 (TERMILE). 08. Last sequence update)
01-NoV-1998 (TERMILE). 08. Last annotation update)
NONSTRUCIORAL PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61-MAY-1999 (frEMBLrel. 18, Created)
01-MAY-1999 (frEMBLrel. 10, Last sequence update)
01-MAY-1999 (frEMBLrel. 10, Last annotation update)
MONSINGTURAL PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN 88CVA70, 88LU195;
Larsen i E., Gattsbalch E., Rlivonkrone-Moller M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        622 ATMISKSGIGSLHPLLRGWEEALFNVIKST 651
                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 ALMESERNMORERFELERWENDAFNITOST 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bowine respiratory syncytial virus.
                                                                                                               PRINTS; PRU0028; POUDOMAIN.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00465; P0U_2; 1.
                                                                                                                                                                                                                                                                                                                                                     43.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 28.1%;
Matches 16; Conservative 1
                                                                  Pfam; PFU0045; homeobox; l.
Pfam; PFU0157; pou; l.
                                                                                                                                                                                                                                                                                                                               0.69
Bost Local Similarity 43.39
Matches 13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                   InterPro; IPR000327; -. InterPro; IPR001356; -.
                                                                                                                                                                                                                                 113
                                                                                                                                                                               SMART; SMO0352; Poff; DOR_TER 1
HSSP; P14859; locT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11246;
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Q9YJB7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 091860;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.98160
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Sutaitted (MAE 1998) to the E4BL, Sengank, SISBS databases.

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Bacteria;
           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryona, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta;
Magnoliophyta; Liliopsida, Poales, Poaceae, PACC clade, Panicoldcae;
Andropogoneae, Zea.
                                                                                                                                                        161 IWELIYKOSGVETAKSTELITHTTELESPMDFITSLYTKSVKVPAFYPGSSAQERVEE 217
                                                                                                                                                                           Bacteria: Proteobacteria: gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Marck Eccarzuk M M . Skorupska A M . "Recognition of a gene involved in biosynthesis of miacin in Pseudomonas iluorescens strain 267.";
                                                                                            0.6%; Score 61; DB 14; Length 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.6%; Score 61; DB 2; Longth 163; Hest Local Similarity 40.7%; Pred No. 89; Mismatches 7; Indels Matches 11; Conservative 9; Mismatches 7; Indels
                                                                                                                            Stopul ; PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (APR-2000) to the EMBL/Genbank/Dubi databases.
EMBL: AF257101; AAF72624.1; ".
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHOUENCE 163 AA; 17620 MW; 085E1CC1A255B6F0 CRC64;
                                 Nonstructural protein.
SEGGENCE 136 AA; 15258 MW; AEB6A89D7BFCDD24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TremBLrcl. 16, Last annotation update)
GLUTATHIONE S-TRANSFERASE GST 39 (EC 2.5.1.18).
                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (FrEMBLEEL, 15, Last sequence update)
01-0CT-2000 (FrEMBLEEL, 15, Last annotation update)
OURNOLINIC ACID SYNTHETASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 200 AA.
                                                                                                                                                                                                                                                                          163 AA
                                                                                                                             12, Mismatches
                                                                                                 Query Match
Best Local Similarity 28.1%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           497 LAMNHLKKIMKTSKEGVDESFIKEAVL 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       105 MAMNILERILKSLKEGINEIFVDPALI 131
                                                                                                                                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel: 15, Created)
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                                                                                                                                                                                                                                                                          PRT;
EMBL; AF054665; AAC36669.1; -.
EMBL; AF054664; AAC36666.1; -.
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                                                                                                                                 16; Conservative
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                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas fluorescens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas.
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                                                SEQUENCE
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                                                                                                                                  Matches
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BEDLINE 20150255; PubMod-10684935;
Read T D., Brunham R.C., Shen C., Gill S.R., Heidelborg J.F.,
White O., Hickey E.K., Futerson J., Ulterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouli H., Clavos B., Bowman C., Fodson R.,
Galin M., Kolson W., DeBoy E., Koleny J., Medirity G., Falzberg S.L.,
Fisch J., Frascr C.M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Enkaryota: Metazoa; Chordata: Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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0.6%; Score 61; DB 10; Length 200; 40.0%; Pred. No. 1 le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 39.5%; Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Indels
                                                   7; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN 37 237 PROLACTIN-LIKE PROVEIN.
SEQUENCE 237 AA; 27377 MW; E3B703F17E18BAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAK-2001 (TrEMBLrel. 16, Last annotation apdate)
                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel, 01, Last sequence update)
01-MAY-2000 (TrEMBLrel, 13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                       1094 ELYAGMPTIQITALEKITKPFFAAISDEKV 1123
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                                                                                                                                                      78 ELFAGRPILPTDPYERATARFWAAYADDKL 107
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TISSUE=PLACENTA OF 6 MONTH GESTATION:
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                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15; Conservative
                                    Best Local Similarity 40.04 Matches 12; Conservative
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                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovidae; Bovinae; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
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LM28, 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDITING AND STATES FOR BOARD FOR ARTHUR BY, ARTHUR F.A., Accurding M., Sampson A.J.S., Profitable F.Y., Arthur B., Alara S., Bapilista C.S., Additional B., Mary B. Banda S., Bapilista C.S., Additional B., Bondres I.B., Brother J.M., Bridges M.E.S., Battless M.E.S., Bandario M.B., Carrato D.M., Franco M.B., S., Franco M.S., Franco M.E.S., Franco M.E.S., Franco M.E.S., Franco M.E.S., Comes S.L., Griber A., Britanda J.B., K. Holes J.M., Britanda J.B., K. Holes J.M., Britanda J.B., K. Holes J.M., Gurnes M.V., Britanda J.B., K., Markado J.A., K. Markado J.A., Markado M.C., Markado M.C., Markado J.A., Markado M.C., Markado J.A., Markado M.C., Markado J.A., Markado M.C., Markado J.A., Markado M.C., Markado M.C., Markado J.A., Markado M.C., Markado J.B., Markado M.C., Markado J.B., Markado M.C., Markado M.C., Markado J.B., Markado M.C., Markado J.B., Markado M.C., 
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40.70, Silva Ga W.D., d. P., ca A.B.,
Instit G., fsai S.M., Isriako M.H.,
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Zado M.A., Zatz M., Meidanis J., Setubal J.C.,
"The denome sequence of the plant pathogen Kylella fastidiosa.";
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(Aft. Shore Al.: 58 2) laminh 246;

(Ost Colif Similarity 4504) Frod. No. 1.46002;

Marchas (2) Ansarrative for Mismarches 8; Indels
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27.96; Fred. No. 1.50+02;
12c - 12; Mismatches 50; Indexs
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                                                                                                                          246 AA; 2776° MW; FF7774FB9D077BE7 (3R054;
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                                                                                                                                                                                                                                                                                                 LATA KIRIMKVIJOVNORMVISQIJEPMARGIJEKI 1045
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FIRE: PC0865;
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EMBE AEPO4049, AAPPGOMILE
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                                                                                           InterPres IPRG01440;
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SECUENTE 214 AAS
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Narriour Arids Res.
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Nebt. taxii: 2421;
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Wilson R., Ainscouth R., Adderson K., Baynes C., Berks M., Ronfield J., Burton J., Conneil M., Copsey T., Conger J., Coulson A., Cratton M., Boart S., Da Z., Durbin K., Evyello A., Politon J., Gardener A., Green P., Hawkin T., Hillier L., Jier M., Johnston L., Jones M., Kirston J., Haister N., Latreille P., Callanlan L., Lighthing J., Lloyd C., Mcmuriay A., Mortimore R., O'Callanlan M., Parsons J., Percy C., Ritken I., Roppier A., Sanders D., Showkeen R., Smaldon N., Smith A., Sonnith M., Shaden R., Saladers D., Showkeen R., Thierry-Mica J., Thomas K., Vaudin M., Vaudhan K., Waferston K., Waferston R., Weinsterk I., Wilkinson-Sproat J., Weblidman P.; "2.2 Mb of Contiquous nucleotide sequence from chromesome III of C., eleqans."
Sdro :o
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EMBL: AL396935; CACO0895.lr -
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SEQUENCE 271 AA: 30356 MW: B59E6302D321EFF4 CRC64;
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01-0CT-2000 (TrEMHLrel. 15, Last sequence update)
01-0CT-2000 (TrEMELrel. 15, Last amotation update)
POSSIBLE PROBABLE ECF-FAMILY SIGMA FACIOR (FRAGMENI).
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01-R2V-1999 (TrEMBLECL, 12, Last sequence update)
01-NOV-1999 (TrEMBLECL, 12, Last annotation update)
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36.7%; Pred. No. 1.6e+02;
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MEDLINE=94150718; PubMed=7906:98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 36.79
ws 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N X X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MERKER KENNER KENNER KENNER KAN KENNER KAN KENNER K
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Mature 368:32-38(1994).

POST TAVELIAFEREEFENVISSA IL TAEVISTILALALATAGARSAHESALTIMMATSALINSAR 1754

27.98;

24: Comservative

Mathhes

coval Similarity

EMBL; 281074; CAB03036.1;

SEQUENCE

×

22.48;

Similarity

Ma. Local Sim 15;

Matches

5 a 5

Query Match

Conservative

315 ICERPEP 322

83 VTVSPVP 89

.; O

0; Caps

: NE

PRESENTANTARY,

RESULT 189

Caenorhabditis elegans.

F10G8.7 PROTEIN.

DT DE TQ TQ

SEQUENCE FROM N.A.

Basham V

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Adams Hills 2019 out to the control of the control 
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                                                                                                                                                                                                                                                                                                                   Lee J.S., Kang H.S.;
"So pretex indipsis of i 44Pll fosmil elega of "greenends "ebilis 2M4.";
Submitted (JAN-1999) to the EMBL/GeuBauk/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prerygota; Newpierd, Endoplerygota, Dipiera, Brachycera; Mushamorpha;
Ephydreidea; Drosophilidae; Drosophila.
NCBI_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          657 IGVANQKMIELLADMINLGDPSSMLKMVEDLISVGERESFNLFQKVTFHVI1SVLV 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 TGAFFTFDILLLSEQLQKSGVSALLLPLVSYHALNEDEVFSLYETVSKHVSVPVIV 131
                                 Sartelia, Profesharteria, alpha subdivision: Sphingomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rokaryota, Metagos, Arthropods, Trachesta, Hexapods, Insecta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Bost Local Similarity 28.5%; Prod. No. 1.80×02;
Matches 16; Conservative 15, Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
0AKHSHIC ANHYDEASE (EC 4.2.1.1) (CAFRCHATE PEHYPRATASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3A42C938653F5E11 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRT; 322 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
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PRINTS; PR00146; DHPICSNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           298 AA; 33180 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF13753.1: -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002220;
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                                                                                                                                                                                                                        SPOTENCE FROM N A.
Symomonas mobilis
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                                                                                                                            NCBI_TaxlD=542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBI - AF117351
                                                                                                                                                                                                                                                                                 STRAIN-ZM4;
                                                                                                Zymomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9VD19
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Benfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Grandner A., Green B., Du. Z., Buthin R., Favello A., Fulton J.,
Gardner A., Green P., Bawkinstein L., Jier M., Johnston L.,
Jones M., Kershaw J., Eitsten J., Laister M., Istreille P.,
Lidythning J., Lloyd C., Memerray A., Mottimore B., O'Callaghan M.,
Edythning J., Lloyd C., Memerray A., Mottimore B., O'Callaghan M.,
Smaldon N., Smith A., Sounhammer B., Staden R., Sulsten J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Watersten R.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Watersten R.,
T. 2 Mb. of Cantiguous to Jevilide Seppent J., Wohldman F.;
eleqans.
                                                                                                                                                                                                                                                                                                                                                                   25.0 DYFAATYMITOTISVEVTMENTVASLASQTIFTLIFFITELIEFOLSOLIVELOEGEFES 315
                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nematoda; Chromadoroa; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ci
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                                                                                                                                                                            0.6%; Score 61; DB 5; Length 278; 22.4%; Pred. No. 1.6c.02;
                                                                                                                                                                                                                                                                            39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1532 REVVESSIEDLIPSLEBELLISVI GYTJAVAQBMENARRI 1986-1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEF 1996) to the EMBL/GenBunk/DDBC databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 210 PERALGE CONSTRUCTOR ESTERNATE CONTROL OF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33613 MW; ACHEFSU41218818A CROS4;
                                                278 AA; 30948 MW; 08DIEL9B501F962E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLEEL 13, Created)
01-MAY 2009 (TrEMBLEEL 17, Last sequence update)
01-MAR-2001 (TrEMBLEEL 16, Last annotation update)
DIHYDKODIFICGLINATE SYNTHEWASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FEB-1967 (TrimBirel, 02, Created)
01-JAN-1998 (TrEMBirel, 05, Last sequence update)
01-JUN-2000 (TrEMBirel, 14, Last annotation update)
                                                                                                                                                                                                                                                                        13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khabditidae: Peloderinae: Caenorhabditis.
NCBL_TaxID-6239;
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MEDLINE-94159718; PubMed-7905398;

ξ  $^{\rm KA}_{\rm AA}$ 

SECUENCE FROM N.A.

Nature 368:32 78(1994). EMBL: 280216; CAB02283.1; InterPro; IPR000445; -.

폰 플 포 포

235 AA;

SEQUENCE

EKT:

PRELIMINARY;

Q9RQD0; 0.28000

P 51 52

RESULT 190

õ 20 03KOD0

DAPA.

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Theologis;
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                                               Q9M9T2;
Q9M9T2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               096354;
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                   RESULT 193
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                                 Z T 6 M 6 C
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O
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Spriet E., Sprailling A.C., Stapleton M., Strong E., Sun E., Sylvakas K., Lector C., Lurner K., Venter E., Wand A.H., Wang X., Ward E.Y., Wang S., G.M., Weinstock G.M., Weinstock J., Williams S.M., Woodbar I., Werley K.C., Wu D., Yang S., Yao O.A., Ye L., Yeh K. E., Zaveri J.S., Zhan M., Zhang C., Zhao Q., Zheng L., Zhao K.H., Zhong F.N., Zhong M., Zhou K., Zhao G., Zheng L., Gibbs B.A., Myers E.W., Philia G.M., Venter J.C.; J. Chi N., Smith H.O., Cibbs B.A., Myers E.W., Philia G.M., Venter J.C.; J.
                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliama (Monse ear cross).
Enkaryota, Viriditladiuch Embryphyla. Harboophyla, Sprimatophyla.
Montenboophylar endlestyledons, earc endicots, Rosidae, enrosids 11;
Brassicales, Brassicaeeae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN TV, C. LUMBIA:
Lin X., Karl S., Shea L.E., Pritt C.Y., Shea M., VanAken S.E.,
Barnstead M.E., Masson F.M., Bowman C.L., Ronning C.M., Benito M.,
Cattera A.L., Creasy L.H., Buell C.R., Fown C.D., Nierman W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
©
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; 58 10; Length 335;
Pred, No. 2e:02;
                                                                                                                      Seitere 281:2185 2195(2-0-0).
! FTN:TIAN: PEVERSIBLE HYDRAIATION OF ARRON DIOXIDE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                    Length (22)
                                                                                                                                                                                                                                                                                                                                                                                                               Score 51, 198 5; Length 322
Pred, No. 1.90-02;
5; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Intels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (8184 MW) BOB(4D47FB)8144C CRC64;
                                                                                                                                                                                                                                                                                                                                                                    322 AA: 3720 MW: 107037C7EA2DF619 CRCC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Of N.V. 1999 (FERRENCE), 12, Last sequence update)
of N.V. 1999 (FERRENCE), 12, Last sequence update)
Of MAR-2001 (FERRENCE), 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1259 LSALAALQKVVETLEHFISEYLEGIT.SQVEHL 1789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 VIVLAVLEKVVRSOPEFYGEOTSETESSITHE 214
                                                                                                                                                                                                                                                                                                                                    PROSITE: PSGG162; FHK_COZ_ANHYDRASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 PACK TEWETHERFHIRM SELENTED 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 PROFESEMIMHEYTTH (APPLIANCE), 153
                                                                                                                                                                                                                                                                                                      Hums PF00194; carb_anhydrase; 2.
bridsam: Phydra465; -: 1.
                                                                                                                                                                                                                                                                          FlyBase: FB400038956; edf.479.
                                                                                                                                                                                                                                                                                                                                                                                                                  1. 5
5. 3
2. 7
2. 7
4. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5.6.4
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Best Local Similarity (9,84)
                                                                                                                                                                                                                                                                                                                                                                                                                              toetal Similarity - 43.8%
res - 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C.M., Venter J.
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                                                                                                                                                                                                                                                                                          InterProj IPROULLAB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145, AA;
                                                                                                                                                                                                                                                            HNSFC CA4444 LZNC
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                                                                                                                                                                                                                                                                                                                      Probam: Phorogens
                                                                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                       Lyaser Zine.
SEQUENCE 3
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Best Lereil 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Materbers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFSII, 1-142
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Chin S., Sakdon H., Yu G., Lee J., Lenz C., Pham P., Toriumi M., Chin S., Sakdon H., Choi E., Cunq M., Gonzalez A., Howng B., Liu A., Vaysberq M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A., Hansen M., Johnson Hopson C., Khan S., Kim C., Lam P., Miranda M., Nquyen M., Palm C., Shinn P., Southwick A., Lavis R., Fcker J., Foderspiel N., Theologis A., Razbidopsis thaliana chromosome I."; Submitted (vCT 1994) For the PMRLAN-Grabab-Punkl databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O: Gaps
                                                                                                                                                                                                                                Eukaryota, Viridipiantae: Embryophyta; Iracheophyta; Spermatophyta; Madnoliophyta, cudicotyledons; core endicots; Rosidae; curosids II; Brassicaics, Brassicace, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eufeleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lepidosauria; Squamata; Ignamia; Acrodonta; Agamidae; Agaminae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oacen
Local Similarity 35.5%, Prod. No. 2002
os 15, Conservative 7, Mismarches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AC012188; AAF43929.1;
SEQUENCE 339 AA, 37685 MW; 675AEE017AFBBE07 CRC64;
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01-MAR-2001 (TrEMBLIEL, 16, Last sequence update)
01-MAR-2001 (TrEMBLIEL, 16, Last annotation update)
                                                     01-0CT-2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, List sequence update)
01-0CT-2000 (TrEMBLrel, 15, List annotation update)
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                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
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PKT;
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trapelus sanguinolentus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CV. COLUMBIA;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                           0, Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 265 NELIKQELLILATTIALMSLINLLFYMRIAYLSAMLISPITSISITKWEGGIKÖPNMITT 324
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                                                                                                                                                                                                     Maccy J.R., Schalte J.A. II, Larson A., Ananjeva M.B., Wang Y., Pethiyagoda K., Rastegar Poujani M., Papenfuss T.J.; "Evaluating Trans-Tethys migration: An example using Acrodont lizard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enkarjota, Vildiplantae, Embryobiyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Atylosia.
"Replication slippage may cause parallal evolution in the encodary
structures of mitochondrial transfer RNAs.",
                                                                                           Macey J.R., Schulte J.A. II, Larson A.; "Evolution and information content of the mitochondrial genomic structural features Illustrated with acrodont lizards."; Syst. Biol. 45.257 277(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "intracellular gene transfer in action, bual transcription and multiple silencings of nuclear and mitochondrial cox2 genes in legumes.";
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Adams K.L., Song K., Roessler P.G., Nugent J.M., Doyle J.L.,
Doyle J.J., Palmer J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%, Store 61, DB 10, Length 342,
Fost Local Similarity 37.1%; Pred. No. 2.1e+02;
Matches 13; Conservative 8; Mismatches 14, Indels
                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 0.6%; Score 61: DB 8: Length 341: Best Local Similarity 23.9%; Fred. No. 2.1e+62. Matches 17: Conservative 13. Mismatches 41; Indois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 - 342
342 AA, 38434 MW, UA846A8DD7169330 CRC64;
                                                                                                                                                                                                                                                                                                                                      341 AA; 37661 MW; 1FA6CCC0B3B8550F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAI 2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Nati. Acad. Sci. U.S.A. 96:13863-13868(1999).
EMBL; AF181940; AAF15328.1;
InterPro; IPR001505;
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PROSITE; PS00436; PEROXIDASE_2; UNKNOWN_1.
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                                  Mol. Biol. Evol. 14:30-39(1997).
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                                                                                                                                                                                                                                                                             49:233 256(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         325 LIPTALLSLIA 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCB1_TaxID=109161;
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                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                           SEQUENCE FROM N.A.
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MEDEJNE-26465 / ATCC 700392;
MEDEJNE-97394467; PubMcd 9252385;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White D., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Pleischmann B.D., Kerlavage A.R., Gill S., Dougherty B.A.,
Polsoc P., Quackerbush J., Zhou L., Kirkness B.P., Peterson S.,
Loffus P., Pichardson P., Fordson R., Khalak H.G., Glodek A.,
McKenery K., Pittgerald L.M., Lee N., Adams M.D., Hickey E.K.,
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Alm P.A., Lina L.-S.E., Moir D.T., King B.L., Brown E.D., Dolq P.C.,
Smith D.E., Noonan P., Guild P.C., delong P.L., Carmel G.,
Tummino P.J., Caruso A. Irria-Nickelson M., Mills D.M., Ives C.,
Gibson R., Morberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Generals sequence comparison of two unrelated isolates of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                   Haliochartor pylori 199 (Campylobacter pylori J99).
Bacteria, Protocbacteria, epsilos subdivision; Helicobacter group;
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23.0%; Pred. No. 2 lea03;
ive 17; Mismatches 40; Indels
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Pfam: PF02272: DHHA1; 1.
SEQUENCE 347 AA; 40067 MW: 03FDF6409241F854 CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-0cT-2000 (TrEMBLrel 15, Last annotation update)
1521 MSQLLSSMNPLKKVVESGGPETLKGLEERLLBTVL 1555
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                                    5 MSRFLHTNNFERKLISSGGNESYGHFSKRSYSSLL 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gastric pathogen Helicobacter pylori.";
                                                                                                                                                                                                                        PRT;
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EMBL: APAG1473, AAGG45 1; -.
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es 17; Conservative 1
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Berg B.E., Derayne J.D., Otterback T.R., Peterson J.D., Kelley J.M.,
Noften M.D., Weidman J.M., Pojli C., Bosmon C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Kirp P.D., Smith H.O., Fraser C.M.,
Weiden J.C., Co.
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Enkarpela: Metalea. Meddata, Yranista, Vertebrata, Esteirostomi.
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                                                                                                                                                                                                                                       Cuerty Match 0.10%; Score 61; 196-2; Length 448; Best Local Similarity 23.00%; Pred. No. 2.1e-02; Marches 17; Conservative 17; Mismatches 40; Indels
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Pram: PF 2272; DHHAL; 1.
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Magnoliophyta, endirotyledons, core endicots, kosidae, ennosids 11:
Brassicales; Brassicaceae; Arabidopsis.
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Amphibia, Batrachia, Caudata, Salamandroidea, Salamandridae;
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21.7%; Pred. No. 2.10+02;
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EMBL: AF070733; AAF14029.1: -.
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01-0CT-2000 (TFEMBLE). 15, Tast sequence update)
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4'(2'),5'-HISPHOSPHATE NUCLEYTIDASE.
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"Regulation of Prox 1 during lens regeneration.";
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EMBL; AB019227; BAA96902.1; -.
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SEQUENCE 353 AA; 37956 MW;
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176	176   60   0.6     177   60   0.6     179   60   0.6     180   60   0.6     181   60   0.6     181   60   0.6     182   60   0.6     183   60   0.6     184   60   0.6     185   60   0.6     186   60   0.6     197   60   0.6     198   60   0.6     199   60   0.6     191   60   0.6     194   60   0.6     195   60   0.6     195   60   0.6     196   60   0.6     197   60   0.6     198   60   0.6     199   60   0.6     190   60   0.6     190   60   0.6     190   60   0.6     190   60   0.6     190   60   0.6     190   60   0.6     190   60   0.6     190   0.6     190   0.6     190   0.6     190   0.6     190				r YJL1 petica rences 887: 5 2a Lib regic 76 Seque 76 X8502 X8504 A57; MI equences cquences cquences	36. ative
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A.Reference number: A35435; MUD0:90285165
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A)Cross-references: EMBL:AF055035; NID:95478223; PIDN:AAD43810.1; FID:45478224
A:Experimental source: strain 972
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N;Alternate names: protein L0901; erotein YLL040c
C;Species: Saccharomyces cerevisiae
C;Species: 01-Aug 1995 #scrpuegre_perision 24 May 1996 #revt_change 10-Sep 1998
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       Cracession: 864791; 864792; 814891
Ribuesterhoeff, A.; Floeth, M.; Heiss Neitzel, D.; Hilbert, H.; Merstl, D.
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C;Species: Schizosaccharomyces pombe
C;Date: 21 Jan 2000 *sequence_revision 21 Jan 2000 *text_change 21 Jai
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submitted to the Protein Sequence batabase, May 1996
A;Reference number: 864792
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A:Cross-references: EMBL:273145; MIFS:YLL045c
A:Experimental source: strain S2880
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A;Residues: 2991-3647,'L' <Lom>
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A:Residues: 1095-3144 -WED>
A:C::se references: EMB::27
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A;Recession: 864791
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Antrosameterenees: EMBLALALASAAT FINGHAAIBH72.]: USPEREERUSO67: SPERESPBC24B6.04C
Alforentmental source: strain 972nc; esmid e23E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SPBC23BC.04c - fission yeast (Schizosicharomyces pombe)
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State: Telection and sequence_revision Ostber-1999 #Fext_change US-bec-1999
FAX-resision: LOSA MAND REPORT BAGS FORD A. Schmidt B. Schioll.
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                                                                                                                                                    64 DEBARDES, DARIDERSVUTRAVNRODERNISDE DHILSPYEDLARAMCHEWIJHEPHT 104
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H. LAUVASNIKT VALH BERFUELLIRATI LYNER LAATOON HIT HAAGEALLISOT HERYK AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1965 DB 2: Length 1649; Best Local Stationing (5.5%) Pred. No. 4.5e-16; Marches 19; Connectative 21; Mismatries (7; 15.5e); Annother (7)
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As Status: prediminary: translated from CBZEMBLZCHBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1.24 HOYN, DSELANVOPYHOTELTVRVIQUEKT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 HVKNTEMILLSTINYYQTPVFKRILSTIKL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4,1,18
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A:Accession: 12/864
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A:Map position 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sporty Marott.
Best Local Similarity
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RESTILL

A; Introns: 48

Matches

Caps

Cispecies: Arabidopsis thaliana (mouse-ear cress) CiDate: 14-May-1999 #sequence\_revision 14-May-1999

hypothetical protein T1P17.150 - Arabidopsis thaliana

RESULT

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A;Cross-references: EMBL:AL049730; GSPDB:GN00662; ATSP:T1P17.150 A:Experimental source: cultivar Columbia; BAC close TiP17

A,Reference number: Z15790 A,Accession: T07648

C;Accession: T07648

1-198 FRV

A: Residues:

A; Molecule type: DNA

A;Gene: ATSP-T1P17 150

A; Map position: 4

Gaps

22: Indels

9, Mismutches

Score 76; DB 2; Length 3144; Pred No 13;

0.7%;

Query Match Best Local Similarity 36.79 Matches 18, Conservative

Description: involved in regulation of membrane traffic F;1084-1100/Domain: transmembrane #status predicted <TMM>

:Keywords: transmembrane protein

A; Map position: 12L

1462 SIMNILQYILKLUBEKEETIPKAVSENKSESQPEMIGVENVETHTSKOL 1510 2227 SLL nLAZSKII LEHERPETT PEMPSPINKEDINFSINAPI PERTSEMISSKII. 2275

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A;Title: Human desmin-coding gene, complete nucleotide sequence, characterization and
A;Reference number: JE0063; MUID:89378751
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A. Kesidues. Liu Lie,255 265,274,282,393-191 CP7

C. Comment: There appears to be a single desmin gene in the haploid children myon prodominantly in skoletal, cardiae, and most types of smooth miscle cells during myon cicomment: Desmin intermediate filaments are found in the cytoplasm of cultured myone cing myofibrils to each other and to the plasma membrane from the periphery of the 2 citom myofibrils to each other and to the plasma membrane from the periphery of the 2 citominant. The molecule conduins three sturturally distinct domains the surface-exp. The tailpleer comprises the carboxyl terminal residues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: cytoskeletal keratin
C;Keywords: blocked amino end; coiled coil; intermediate filament; massle: phosphopro
                                                                                                                                                                                                                                                                  R;Kitamura, S., Ando, S., Shibata, M.; Tanabe, K.; Sato, C.; Inaqaki, M. R;Kitamura, S., Ando, S.; Shibata, M.; Tanabe, K.; Sato, C.; Inaqaki, M. A. Talol. Chem. 264, 5674-5678, 1989
A;Title: Protein kinase C phosphorylation of desmin at loar scrine residues within the A;Reference number: As2858; MGID:89174618
R;Geisler, N.; Weber, K.
EMBO 7, 77, 15-20, 1986
A;Title: Phosphorylation of desmin in vitro inhibits formation of intermediate filame
A;Reterence number: $02448, MUID:88196075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Chemical cross-linking indicates a staggered and antiparallel protofilament. A;Keference number. S23189; MUID:92299013
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C.Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 10-Dec-1999
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30.4%; Fred. No. 2.6;
ive 13; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Li, E.; Lillenbaum, A.; Butler-Browne, G.; Paulin, D.
Gene 78, 243-254, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.B.s.idn.s. 10 14,28 42,49 59 3KUT:
R.Gelsler, N.; Schuenemann, J., Weber, K.
Eur, J. Blochem. 206, 841-852, 1992
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Matches 24, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F.133-142/Region: linker 1
F.143 243/Region: coil 1B
F.244-259/Region: linker 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 1-69 <GE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;lo0:467/Domain. rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;345/Region: stutter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: JE0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A32858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S23189
                                                                                                                                                         A;Accession: S02448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 278/Pegion:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type:
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A;Residues: 366-463 <CAP>
A;Cross:tricicucas: 38.K92445; NID:9211727, FIPR AAA48751 1; FIP:9211728
R;Kusubata, M.: Matsuoka, Y.; Tsujimura, K.: Ito, H.; Ando, S.; Kamijo, M.; Yasuda, H.;
Bjochem: Biophys. Res. Commun. 190, 927-934. 1993
A;Title: cdc2 Kinase phosphorylation of desmin at three serine/threonine residues in the
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A;Reference number: A90969, MUID:84207925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 81, 6909-5913, 1984
A,Title: Characterization and regulation in the expression of a gene coding for the into
A,Reference number: A94014; MUID:85063701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R.Bedan, M.; Feters, S.A.; van Staveren, M.; Dirken, W.; Stickoma, W.; Bandroft, I.; Mew
submitted to the Protein Sequence Database, April 1999
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Gaps

15; Indels

14; Mismatches

32.6%;

14; Conservative

Best Local Similarity

Matches

Query Match

723 FPFAIRVFSLLQKKIKKLESVITAVE1PSEWHIELMLDRGIPV 765 

0.7%; score 74; DB 2; Length 408; 32.6%; Pred, No. 2.2;

C.Daro: 18-Dec-1981 #sequence\_revision 12-Apr-1996 #text\_change 10-Dec-1999 C.Accession: A90969; A94014; JC1459; S02448; A22858; S23189; A02957

R;Geisler, N.; Weber, K. EMBO J. 1, 1649-1656, 1982

Ngai, 1; Lazarides, E.

A;Molecule type: protein A;Residues: 1-463 <GET> R;Capetanaki, Y.G.: Ngai,

A;Accession: A94014

A;Accession: A90969

A;Reterence number: JC1459; MUID:93176201 A;Accession: TC1459

A;Molecule type: protein A;Residues, 5-9,16-27,63-67 <KUS.

N'Alternate names: type III intermediate filament C;Species: Gallus qallus (chicken)

desmin - chicken

RESILT

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DMCH

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A;Title: Fungus-specific translation elongation factor ( gene present in Pacumocystis
A;Reterence number: A49204; MUID:94014112
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Vysotskaia, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A.Mcittari Lyper DNA
A.Regidues: 1-1942 *YPMS
A.Cross references. CBAM87665, NIB 4469411; FIDKLANA30789.1; FID:q169412
A.Ncross reference extracted from NCBI Eackbone (NYBIP:114-91)
C.Superfamily: fransistion elongat on factor 4, AIF Einding cassette homelogy
C.Keywords: ATP; nucleotide binding: P-Toop
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CoDate: 14-May 1999 %septembe_fevision 14 May 1999 %text_change 18-Jun-1999 CoAccession: T02139
                                                                                                                                                                                                                                                                                                                                                                                                   Cispecies: Pheumocystis carinii
Cibate, 21 Jan 1994 *sequence_revision, 18 Noc 1994 *text_change 62 Febratori
CiAccession: A49204
Kiyma-Wond, Febrato, W.A.; Sypherd, P.S.
Infect. Annum, 69, 4140-4147, 1992
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Cover 73, 48-2, Length 1127;
Best Local Similarity 21.3%, Frod. No. 9.8;
Matches 19; Conservative 22; Mismatches 48; Indels
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8.685 975/Samain. Air binding cassette baselog, APSE
F.752 769/Kegion. nucleotide binding motif A (F-100p)
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Best Local Similarity
Matches 17, Conserve
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CDANCOSSION BALLON BALLON GLO. Meinstoof T.M. Willer, G. B. C. L. D. D. 1948-10. B. C. D. 1988-10. B. D. 1988-10. B. C. D. 1988-10. B. C. D. 1988-10. B. C.E. gwards: asstylated amino ends soiled soile intermediate filament, moscle, phosphopro
Fig. 469/Profest here: hemein *claims prelieted offine
Fig. 1994/Annaton bad office.
Fig. 448-469/Femalic rad office.
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E77.42 World: 1 '10 plus plus (Ser) (Lab.2) (Ryolf Finas) France predicted
E17.48 Weblifer (True plus plus (Ser) (Lorder) (Ryolf Finas) 2, Ellas predicted
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A; Indrons: 140/3, 2567., 36471, 35571, 3343. 44373. 4542.

A:Map position: | A; Note: F8K4.14

A;Status: translated from GB/EMBL/IDBJ A;Molecule type: DNA A;Residues: 1 553 <VV3>

A;Accession: T02139

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AsMap position. 3
A. Introns: 48,73, 142/1, 343/1, 611/1, 445/2, 71844, 868.3, 1126.3, 1263.3, 1295.3
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A,Residucs: 1-132 -WILD
A,CLOSS Leferences, EMBL,259874; PIDN:CAA96775 1; OSPDB:CN00021; OESP:T08A11.2
A;Experimental source: clone R1084
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A,Cross-references: EMBL.259375, PIDM.CAA99777 1; GSP98-CNA9021- CPSP-TOWALL 2
                                                   A.Class references EMRE Y08097, MID $2791895, PIDM:CAA70201.1; PID:42791896
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C.Dato. 20:May-1994 #sequence_fevisios 10:Nov-1995 #fext_change 21-Jul-2000
C.Aro-ssion S41467, S41463. C72373
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C.Species: Caenorhabditis elegans
C.Bato: 15 oct 1999 #sequenco_rovision 15-oct-1999 #text_change 29-oct-1999
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A,Residues, 11690 <PAD:
Ajchoss notorogous, FMRL,M22695, HTD 4425255 PTBN-MART247 1- PID-4425259
Ajchoss notorogous, FMRL,M22695, HTD 4425255 PTBN-MART247 I-EMBL Data Library, Mar
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                                                                                                                                           Query Match 0.7%; Score 71; DB 2; Length 1307; Best Local Similarity 37 0%; Pred No. 21; Matches 17; Conservative 10; Mismatches 19; Indels
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Best Local Similarity 37.0%; Pred. No. 22;
Matches 17; Conservative 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                     1813 LATTLAPRVILPATEKTYEQIEKNWENHMCPEMSTLQEHIGXMEKE 1858
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A;Reference number: 219922
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A;Accession: $41467
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A;Accession: T24140
A:Molecule type: mRNA
A:Residues: 1-1307 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              T24140
                                                                                                                                                                                                                                                                                                                                                                                             E.Schmidtefarlmann, M.S., Kneeth, S., Kraemer, A.
Mol. Biol. Cell 9, 143-160, 1998
Astrite: Molecular characterization of a novel, widespread nuclear protein that co-local Asterence number: 220921; MUD:9809665
Asteression: T30887
rtz, B.; E.; V.; Falm, C.J.; China, P.; Sun, E.; Davis, P.W.; Feber, T.F., Pederspiel, submitted to the BMBL Data Library, Auqust 1998. Associated to the BMBL Data Library, Auqust 1998. Associated to the BMBL and pidopsis thaliana chromosome 1 BAC 1884 sequence.
Associated number: 214574.
                                                                                                                                                                                                                                                  A,Groos-retermees: EMBL:AC004392; NTD:g3282170; PTDN:AAC28510.1; PTD:g3367525
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A;Reference number: 139709; MUID:95164506
A;Acression: 139711
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Osspecies: Agrobacterium tuMefaciens Ospate: 19-Jul.1996 #sequepre\_remision: 19 hgl 1696 #rext\_change ON-ver-1969

celE protein - Agrobacterium tumefaciens

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K;Matthysse, A.G.; White, S.; Lightfoot, R. J. Bacteriol. 177, 1069-1075, 1995

C; Accession: 139711

Caps

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0.7%; Score 72; DR 1; Length 553, 33.3%; Pred. No. 5.8;

Conservative 10; Mismatches 18, Indels

Best Local Similarity Matches 14; Conserva

Query Match

2100 TVILLPESTPPLAELMEPPCPPVPHQCQKTTQQLFTVLGRPLQ 2141 

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A,Moleculo type: protein
A,Rosiducs. 2-3,'XX',6-20,'X',22-35','X',23-38 <PAW>
P;Nelson, K-P-; Clayton, R.A-; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
                                                                                                                                                                                 C) Aroression, $41467, $41463. 572373
R) Palan, P., Schleper, C., Arnoid-Ammer, I; Holz, I.; Meier, T.; Lottspeich, F.; Zill
R) Rollick Acids Res. 21, 4944.4998, 1993
A; Fille: The DNA-dependent RNA-polymerase of Thermotoga maritima; characterisation of
DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Thermotoga maritima (strain MS
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30; Indels

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Hest Local Similarity 29.3% Matches 17; Conservative

Ouery Match

A;Gene: celE

C; Genetics:

0.7%; Score 72; DB 2; Length 1189; 29.3%; Pred. No. 14;

2008 GHE ESKERAXALMMITTVEGLENPT OFFERFØEPVTKHILPY TAGESVAMAFFISTMKPL 2065 

A; Cross-references: GB:L38609; NID:q716486; FIDN:AAC41432.1; FID:q710489

Asstatus; preliminary, translated from GB/EMBL/ADBJ

A;Molecule type: DNA A;Residues: 1-1189 <RES>

C.Species: Xenopus laevis (African clawed frog) 7.5atc. 22.5ct 1999 #sequence\_relision 22.0ct 1999 #text\_change 21 Jul-2000

146D nuclear protein - African clawed frog

RESULT 14

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T30887

C; Accession: 130887

ApAccession: 130887 Apstates preliminary, translated from CR/PMBL/DDBJ

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Ayauthors: Foulder, D.; Fritz, C.; Philita, M.; Philita, Y.; Fuma, S.; Cadizzi, A.; Callech, J.; Harwood, C.R.; Homant, K.; Hilbert, H.; Holsappel, S.; Hosson, S.; Holle, M. Koetter, P.; Keningstein, G.; Erok, S.; Keningstein, G.; Erok, S.; Keningstein, G.; Erok, S.; Kening, Levine, A.; Layles, A.; Lardino, A.; Cadarer, G.; Cadarer, V.; Kening, Levine, A.; Liu, H.; Masoda, S.; Marier, Y. M.; Cadava, K.; Oriwara, A.; Ouseda, B.; Park, S.H.; Parto, V.; Pobl, J.M.; Portete Kieper, M.; Rivolta, C.; Rocha, H.; Roche, B.; Park, S.H.; Parto, V.; Pobl, J.M.; Portete Kieper, M.; Handrosh, A.; Satroneter, E.; Soffon, F.; Soffon, J.; Sadaie, Y.; Sato, J.; Sofani, J.; Minters, P.; Wipper, A.; Tanakoshi, A.; Tanako
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December of the bamater desmin gene: expression and formation of dos A.Reference number: A24783; MOID:85079506.
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CoAccession: 152469
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AjCross-references: EMBL:X73524; NIB:a452778; PHDN:cAA51920.1; PHD:a452779
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Best Local Similarity 29.3%, Pred. No. 8.8;
Matches 22; Conservative 19; Mismarches 46; Indels
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17; Conservative 9; Mismatches 21; Indels
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A.Title: Rat desmin acne structure and expression.
A;Reterence number: 152469; MUID:94114564.
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Almi Albeni, Gi, Azevedo, Vi, Berter
1 : Bran Si, Brintlet, Si, Brusial, T.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
A : Ebrit Co, Silo; Emperiodo (Lilie Entino K.D.) Enthaten, J.; Pabret, C.; Perrari, B.
Natare (90, 24) 256, 1997
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Righta W.; Sin der Heurel, R.; Ethetts, W.V.; Jona Desker, T.; Etheradal, H.
Fric, Mill. Acres 1, 51, 513, A. M.; Sofie Sofa, 1984
Alletter Intermediate thinmen of CNAS from PHR-21 cells: domestration of distinct agnes
Albertere inners: Acres, MillorBiolites
                                Burnett, M.M., Stewart, A.M., Outon, M.D., Praft, M.S., Phillips, C.A., Richardson, D.,
                                                                                                                                                                Natures (1957), and (257), 1999.
Applicable Broblems Lot (1999al) notes transfer between Archaes, and Bacteria Troncationne see
Arberteries manager: AZZLOG, MIDIO 0220316.
ADAPOSSI 01: 07233
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6.24; Fred, No. 25;
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Asiessislaes: 1 total AANA
Asitoss retreterences: 14eAF et/24th 18
AsEXperiment to source: 31eAfm MSRM
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res 14, Conservative
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A;Reference number: A86141; Muldisides
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C;Species Treponema pailidum subsp. pallidum (syphilis spirochete)
C;Date: z4-uul-i598 #sequence_tevision 24 Jul 1998 #text_chruge "F.Nev-1999
C;Accession: D71372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown protein F5A18.7 [imported] - Arabidopsis thaliana
C,Species: Arabidopsis thaliana (mouse-ear cress)
C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2067 YOLLLKTEDSSPKVRFAALITVLALAEKLKENYIVLLPESIPPLAELMEDECEEVEHQOQ 2126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        u.b%; Score 69; DB 2; Longth 749;
Conscryative 21; Mismatches 33; Loderic
                                                                          A,Status, preliminary; not compared with conceptual translation A,Molecule type: mRNA A,Residues: 1-571 <HEM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.68; Score 69, DB 2; Length 571; 22.28; Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: phosphoprotein phosphatase 65K regulatory chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches
                                                                                                                                                                                                                                     Ajornes references ob-M65254; NID:q189429
A; Reference number: A34541; MUID: 90241887
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Best Local Similarity 22.2%
Matches 16; Conservative
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329 SVIMGESTILGK 340
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nes 17; Conscrv
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                                                 A;Accession: B34541
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PyHemmins BAA, Adams-Prarson, C.: Maurer, F.; Mueller, P.; Goris, J.; Merlevede, W.;
Biochemistry 29, 3166-3173, 1990
Ayrithe: Alpha- and beta-forms of the 65-Kbs subunit of protein phosphatase 2A hare a si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Late: 02 Any 1994 #Sequence_revision 92-Avg-1944 #Foxt_change 19-Apr-1996 C, Accession: A54104; S31404 C, Accession: A54104; S31404 B: Li, H.; Choudhary, S.K.; Milner, D.J.; Munir, M.L.; Kuisk, I.R.; Capetanaki, Y. J. Cell Biol. 124, 827-841 1994 A; Tille: Inhibition of desmin expression blocks myoblast fusion and interferes with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RTLL B.; Capetanaki, Y. submitted to the DMBL Library, December 1992. Astrogreption: Regulation of the Mouse Desmin Gene: Transactivation by MyoD, Myoqunia, Astrogrene number: 831404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phosphoprotein phosphatase 2-beta requiatory chain - human N.Alternate mames: phosphoprotein phosphatase 2A-beta 65K requiatory chain C.Species: Homo sapiens (man) (man
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 193 TQFETQUREFARNNLAAFRADVDAFLARIDJERKIESINGETAFLKKVHEBETRELQAQ 252
                                                                          A;Molecule type: DNA
A;Residues: 1-469 <QUA>
A;Cross-references: GB:M12104; NID:q191360; PIDN:AAA37072.1; PID:g387071
                                                                                                                                                                                                                                     Authorne, 1927, 112/3, 114/3, 208,3, 940.3, 114/1, 419/1, 45/2, 0.Supertamily: cytoskeletal keratin
Cykeywords: coiled coil
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ellarity 29:3%; Prod. No 8 8;
conservative 13: Mismatches 40; Indels
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C;Supertamily: cytoskeletal keratin
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Best Local Similarity 29.4%;
Matches 22; Censervative 1
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A;Cross-references: GB:L22550
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A;Molecule type: mPNA
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Query Match

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Azauthors: Foulger, D.: Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Hultor, M.; Marthors: Ended and a control of the control
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C;Superfamily; cell division inhibitor related protein; terrodoxin 2[4Fe-48] homolody
F;62-118/Domain; ferredoxin 2[4Fe-48] homolody <FER.
                                                                                                                                                                                                                                                                                                                                                                                                     Ajdross references, dB AJD18287, GB.AL096836, NID.af458367, FIDA.MAB49776, http://db.AjExperimental.source: strain Orsay
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C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errinaton, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORF MSV194 ALL motif qene family protein - Meianoplus sanguinipes outen-poyeitas
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C.Date. D.Can DSSQ #sequene-nestrian 21 Jan 2000 #1-41_dange 21 Jal 2000
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Cybate: 05-Dec 1997 Esequence_revision 05 ion 1997 Minal Change 20-Jun 20
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RATORISMO CLL, Tulmann, E.R.: Lu, &:r.:mma, E.: Kutish, G.F.: Fork, L.L.
I. Virol, 73, 5.45-552, 199
A.T.H.: The prome of Melan plus prinisher of meg citrus.
A.Keference annuler: 200484; Müllisher of meg citrus.
A.Reference annuler: 200484; Müllisher of meg citrus.
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9 Mismatches 47; Indels
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Best Local Similarity 27.3%;
Matches 21; Conservative
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A:Reference number: A75001
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A;Residues: 1-409 <AFO>
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A. Accession: 1845.4
A. A. Catton, B. Catton, M. B. Catton, B
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AERSPORTMONTH SOURCE SECLIE NICHSES
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A: Penome: plasmid
A:Note: this stible 58 kilobase pair plasmid is also designated BCL (large extrachromose
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                                                     Science 241, 475 488, 1998.
As fitter Vomplers departe sequence of Freperienca pullidoum, the syphilis spirochete.
As fitter Vomplers A71250; MTD59842770.
As Asvession: D71472.
As Startus: persimitary: nocleic acid sequence not shown; translation not shown A5 Medicule; persimitary.
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Rest Corol Similarity 28,28; Pred, No. 7,3;
Marches 20: Conservative 14: Mismarches 89; Indels
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A;Reference number: A69580; MUID:98044033 A;Accession: D69859

A; Residues: 1-454 <KUN>

A; Molecule type: DNA

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Pithologis, A. Berker, d. F. Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K., Gonn, L.; Conway, A.B.; Conway, A.B.; Creasy, T.H.; Dawar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
Nature 408, 816-820, 2000
Aduthors: Hunter, J.L.; Jenkins, J.; Johnson Hopson, C.; Khan, S.; Khaybir, F.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X., Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maill, F.; Marzia Rinco, M.; Boeney, T.; Pewley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, Wu, D.; Yu, G.; Etastr, C.M.; Vedler, J.C.; Davis, R.W.
A.Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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Mol. Gan Ganat 262, 633-642, 1999
Ajfitle: Isolation and characterization of AtMLH1, a Muth homologue from Arabidopsis
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A; Ornss : p. (p. chines | GR : NC_061268; NID: 97267557; PIDN: CAB78038.1; GSPDR : GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA mismatch repair protein MLH1 (imported) - Arabidopsis thaliana (fragment)
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Late. 62 Mai-2001 #Sequence_revision 62-Mar 2001 #*ext_change 31-Mar-2001
C;Acression: C86201
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C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 03-Nov-2000
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Pred. No. 27;
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5; Mismatches
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C,Superfamily: mismatch repair protein MLH1
                                                                                                                                            C:Superfamily mismatch repair protein MLH1
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Best Local Similarity 43.8%;
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43.88;
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Matches 14; Conservative
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A; Residues: 1 819 <STO>
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                                                                             A;Gene: AT4909140
                                                                                                                  A; Map position: 4
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                                                   C;Genetics:
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Article: Sequence and analysis of chromosome 4 of the plant Arabidopsis thallana.
Arketerence number, A85001, MUID, 2008/9488
Arketersion: F85092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cidecession: A42020
Richen, J.D.; Chan, C.S.; Pirrotta, V.
Mol. Cell. Biol. 12, 598-608, 1992
A;Tille: Conserved DNA binding and self-association domains of the Drosophila zeste prot
A;Reference mimber. A42020; MUD:92123185
A;Accession: A42020
                                                                                                                                                                                                                                                                                                                                                                  Algene: ykoH
Lisuperfamily: hypothetical protein H11707, sensor histidine kinasc homology
C;keywords: autophosphorylation; phosphobistidine; phosphoprotein
File? 417, Londin. sensor Listidine Finasc Lamelogy Suff
Fjel/Alading site: phosphate (His) (royalent) (by autophosphorylation) #status predicte
                                                                                                                                                                                                                                    Apotoss inferences, dB.250116, dB.AE000126, NIS.92622472, PIPN.CABIAPA I; PIDN-gomanna
AjBypejjmental source: strain 168
           AyAuthors. Foshikawa, H.F., Ecumetrin, E., Yoshikawa, H., Danchin, A.
AyTitle: The complete genome sequence of the Gram-positive bacterium Bacillus subtills
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                                                                                                                                               Asstatus; preliminary, nucleic acid sequence not shown, translation not shown
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C;Date: To Fcb.2001 Macquence_terision 16 Fcb.2661 Mt.xt_rhange A2 Mar-20A1
C;Areession: F85092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 68; Db 2; Langth ei8; 37.1%; Pred. No. 22;
Live 8; Mismatches 14; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Owery Match 0.6%; Score 68; DB 2; Length 454; Best Local Similarity 21.3%; Pred. No. 16; Matches 13, Conservative 22, Minmorches 26; Indels
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regulatory protein zeste - fruit fly (Drosophila virilis)

Drosophila virilis

C:Speries:

RESULT 29

A42020

5 **Q**  1173 PLGTVQQKRRQKMQQKESQFFFESVQFVFGSYWQFV 1207 517. PTGAQQQQQQQQQQQQQQQQQQQQQAXYEERT 551

Local Similarity 37.19 os 13; Conservative

Matches

22

Ouery Match

A;Cross-references: FlyBase:FBqn0013149

A;Gene: FlyBase:Dvir/z

C;Geneties:

A;Cross-references: GB:M76700

A; Residues: 1-bi8 <CHE>

A;Status: preliminary A;Molecule type: DNA

MLH1 protein [imported] - Arabidopsis thaliana

RESULT

A;Status: preliminary A:Molecule type: DNA A;Residues: 1-737 <STO>

: -

75; Indels

23: Mismatches

Fred. No.

13.4%;

gmery Mareb Best Local Similarity Matches - 25: Conserval

25; Conservative

0.6%; SCATE 58; DB Z: Length 819; 3.4%; Fred: No. 41;

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C.Species: Xenopus laevis (Arrican clawed troa)
C.bate. 01thec 1992 msequence_revision 01 two 1992 mixt change 14 Angel999
C.Accession: A43554
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TVLALAEKLIENY I VILLPESTIP FLAFILMEDEN EEVEHQ 2124
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29.3%; Pred. No. 21;
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Best Local Similarity 29.3%; Pred. No. 21;
Matches 22; Conservative 12; Mismatches
                                                                                  25, Mismatches
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18.18; Pred. No.
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Development 105, 299-307, 1989
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A;Cross-references: EMBL:AL391144
Hest Local Similarity 18.1%
Matches 15, Conservative
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                 A;Status: preliminary
A;Molecule type: mkNA
A;Residues: 1 458 <HDK>
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A; Accession: T51409
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Actitle: ANLI-ANLE, an Arabidopsis gene lambly with similarity to floral homeotic and transferences number: A 95.44 MHD194164981
A Accession: B 979-44
A Medecule of the part of the Analysis of 
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distiputionily: franscription factor squar serum response factor DNA-binding domain homo
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                                                                                    C.Species: Arabidopsis thaliana (monse-car cress)
C:Date: 17.dal [992 #sequence_revision 17.dai-1992 #text_change 24-Sep-1999
                                                                                                                                                                                                                                                                                                                                           1109 KIIRPFFAAISHEKVYYSELLPMLFILLIVNOKMSHTAGIVSSVFKGISVMAEQVRIFIEPP 1169
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11. olivija - 13. olivija -
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March Condition C.64; Store 67; DB 2; Length 246; Local Similarity 18,94; Prod. No. 19; es 14; Sarorative 26; Mismarches 5; Indeis

CHOTY Match Bost Local S

Mathematica

N:Alternate names: flora; homeotic profein AGLZ

MADS box protein Add.

RESULT 54

ij

R:Ma, H.; Yanotsky, M.F.; Meyerowitz, E.M.

C.A. Cession: Bess 44

Arabidopsis thatland

Rishna, S.K.; An. G.
Submitted to the EMBL bata Library, July 1998
Atheremee counter; 21863
Atheresistan; 1724
Atheresistan; 1724
Atheresistan; 1724
Atheresistan; 1724
Atheresistan; 1724
Atheremee Type: mRNA
Atheresistan; 1724
Atheremee Type: mRNA
Atheremental Source: PMB Therefore, 1000
C.Function:

ctSpecies: Malus damestroa (appre tree)
cyfafr. 15 ant last #schade.jecished

C.Accession: 117524

apple tree

MAUS box protein 1

REGULT

ACH YALASTERN 677

-5 Sir Indels

serum response actor GNA binding domain homology «SRF»

Theyworks: INA bindings society transcription regulation by \$12.577 whats its second response actor but binding domain how

8.869 | Shiring 4.75 | 149 | 25 | Length 2485

CHAILS MARCH

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A. Brinds, 677, 867, 1197-148, 1717-1517.
A:Note: F14F8_180
C:Superfamily: transcription factor squa; serum response factor DNA-binding domain bo
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A,Reterence number: A43554: MUID:90012404
N:Alternate names: protein F14F8_Lto
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Late: 18-Auq-2000 #sequence_texision 18-Auq-2000 #trat_change 02 Sep-2000
C;Accrossion: 171409
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Rato, T.; Asamira, F.; Kotani, H.; Tabuta, S.;
submitted to the Protein Sequence Database, August 2003
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C.Species: chloroplast Chlorella vulgaris

- Sate, 14 May 1999 sergices - Levisies 14 May 1999 #Fext_charts 21 - 51 - 2000

C.Accession: 107208

P.Wakasuqi, T.: Nagai, T.: Kapror, M.: Suqita, M.: Tho, M.: Ho. S.: Tsudzuki, J.: Na Proc. Natl. Acad. Sci. U.S.A. 94, 5967-5972, 1997

A.Tille: Complete nucleotide sequence of the chloroplast genome from the green alga C.A.Reference number: 215985; MUID:97203241
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A, Fitte: AGLI AGLE, an Arabidopsis gone family with similarity to floral homeotic and A; Peference number: A39534.
A, Accession: D39534.
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NyAlternate names: kinase-related transforming protein (bmk)
CySpecies. Mus musculus (house mouse)
CySpecies. Bot 1989 Esequence_revision 31-per 1989 #fext_change 28-tan-2000
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CySpecies: Arabidopsis thaliana (mouse-ear cress)
Cypate, 17 Jul 1992 #sequence_revision 17-Jul+1992 #text_change 24-Sep-1999
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A,chosamphoropas, on MSSSS, NID g166592: FIDM AAAR2734 1 FID g166594
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F;2-57/Domain: setum tesponse factor DNA-binding domain homology <SPF>
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Matches 16, Conservation
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R.Klemsz, M.J.; McKercher, S.R.; Maki, R.A.
Nucleic Acids Res. 15, 9600, 1987
A;Title: Nucleotide sequence of the mouse hck gene.
A, Reference number: A27282; MUID:88067781
A, Accession: A27282
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Bost Local Similarity - 44.89
Matches - 13; Conservative
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A;Molecule type: DNA
A;Pesidues: 1-68 <WAK>
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Asfintnomm (2013) 144, 1, 165, 1, 148, 3, 1, 163, 3, 199, 2, 145, 3, 148, 3, 1419, 3, 19173, 3, 2023, 103
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A;Gross-references: EMBLAL021172, PIDH.CAA16299.1, GSFDB.GN06023; CESP.Y17F7R.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein 17707B.; Cachorhabditis elegans
O:Species. Cachorhabditis elegans
O:Date: 15:oct:1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
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CiDate: 20∙Sep-1999 #sequence_revision 20∙Sep 1999 #text_changv 2v Sep 1 vev
CiAccession: Ti5963
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23.8%; Prod. No. 23;
Live 14, Mismatches 16; Indels
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833 FEMMUNGADAVHFRVLMKGFTKVHGEDVFQGERFCSVDWTYG 874

Ouery Match
Rest Local Similarity 23.55.
Thus 16, Conservative

A:Introns: 42, L. 80, 1, 103, 3, L03, 3, L40, 3, L72, E, 525, E

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type.

A,Reference number: 220222 A,Accession: T26483

A, Experimental source: clone Y17D78

A;Gene: CESP:Y17D7B.1

A;Map position: 5

R;Kershaw, J. Submitted to the EMBL\_Data\_Library, January 1948

Accession, T26483

RESULT 47

D.

126483

270 FRAVIGGEMERFOLIVETELMISSTEVITICQIVANES 311

hypothetical protein F07F6.4 - Caenorhabditis elegans

RESULT

Q C

5

Richissoe, S. submitted to the EMBL Data Library, July 1995 Appearintion: The sequence of C. elegans cosmid FO7F6. A:Reference number: 218438 A:Accession: T15963

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA

1009 SCPSYTANDIMKYLQGVNGEMYLSULLEMARQLIERTQKRPT 1050

250 ELLGKKKSDUAAALUKLSAKFAMUULAQEKGMEAKVAKDPI 301

hypothetical protein 68 - Chlorella vulgaris chloroplast

RESULT 39

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FLEE - KLE -

A: Residues:

TREE PER MINE (PERMISSING PERMISSING PER FILE) PER (PROPER)

U. 58; Seester 56; FB 1; Tength 503;

pred, No. 42;
{4; Mismutible 21, 10.8.1s

Bost Local Similarity 23.0%; Matches II; conservative :

CONTY Match

:74

1219 (LEGALARIPERE PSE, LIVE LENGES POR PORCE CHARACTER LL 1255 443 VISALEGICTAMPERONTELLINIAIR WENEFERFIELILISVI, 488

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Asstatus: prelimming: not compared with conceptual translation

A:Medievation types mkNA A:Postaless 1-5-4 - Heli-A: Accession: Acted

A: Fees achies:

At Year's references:

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ArMolecule type: DNA
ArResidues: 1-1316 <-2012
Arress references: GB:275972; GB:ALI24456; HIB:47249; FHR:CARCG489:1; PID:G-41918
A:Experimental source: strain H3782
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A,Title: Deciphering the biology of Myrobacterium tuberculosis from the complete acno-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, November 1996
A.Reference number: 219888
A.Zavence number: 219888
A.Zavence to the EMBL 219888
A.Zavence type: DNA
A.Residees: 1-1231 "WIL>
A.Gross references: EMBLIZE2127, FICHTYARGEE 90.1, CSEMBLORGECORD TESPERMANTA
A.Experimental source: clone T04A11
C.Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                 Cisperies: Caenorhabditis elegans
Cibate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #fext_change 15 oct-1999
C:Accession: T24415
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36.78; Pred. No. 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
1734 PSLMPSLLTTM 1744
                                                                                                1138 KEITPNYVFIV 1148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1156 LUSDPGFF 1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asgene: CESP:T04All.6
AsMap position: 4
Aslerense Anger: 1503
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C'Species: Gallus quilis (chicken)
C'Species: Gallus quilis (chicken)
C'Species: Gallus quilis (chicken)
C'Acter (4 Mar 1974 *September of recision 15-Acter (5)7 *Heat_s charge to September (5)7
C'Acter (6)7
C'Acter 
                                                                                Appress reterences: CBCYOLGB7: NID.G51209; PIDN.CAACB544.1; PID.G51210
ETH-UTZMAIN D.A.: Yook, W.D.; Dunn, A.K.
Thori, Natl. Area, Sci. US.A. H.H. 8425-8429, 1987
A.H.P. Area and Sci. US.A. H.H. 8425-8429, 1987
A.H.P. Sci. Balaren and Sci. US.A. H.B. 88068587
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Fill-Mikhowain, SH2 beam-down verge.
Fill-Mikhowain, protein Kinse harding motified.
Fill-Mikhowain, protein Kinse Affe-binding motified.
Fill-Mikhowain street may respect to a mine oud (BH2) (in mathure term) metatus predicted.
Fill-Mikhowain street palmilate (Cys) (covalent) metatus predicted.
Fill-Mikhowain street Mys metatus predicted.
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COPP.yr TAS, ACE, and plu offset, Latino, Kima F. Camin, and. Tip gr. Polic, suprintibution, pl.
F262 T10/Demnin: SH3 homology asH45
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Ackersion: Skr740
Ackersion: preliminary
Ackersion: Type: akka
Ackersion: 1-885,7 (887-121 - 285)
Ackersion: 1-885,7 (887-121 - 285)
Ackersion: Preferences: EMBL:Xv.2681; NID:q6357; PID:q6358
Ackersion: Matallens in this gene allect morphysics of both limbs and kidneys.
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15.24 LIKLLCKNEGAENIOFFVEVEXTAVKLTAPERREERNVLGSALLCTAFVESTFFALALPQC 17.33 THEFT IS THE TOTAL SERVICE FROM THE SERVICE FOR THE TOTAL SERVICE FROM THE 
40: 12:4018

14; Mismatohas

Comservative

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Georg March (1984) (1984) Score (6) (1984) Longth 1219; Best Local Similarity (25,4%) Prod. No. 89;

Aprilement 1d C:Reywords: nucleus

Connet ics.

Submitted to the EMBE bata Library, Auqust 1991

IP3 receptor, XIP3R - African clawed frog

A40743

; Accession: A40743

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methyl-accepting chemotaxis protein mcpA (imported) - Bacillus halodurans (strain C )
C,Species: Bacillus halodurans
C,Date, 01 Dec. 2000 #Sequence_fernsion 01 per 2000 #15xt_charac 01 Der-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RyTakami, H.: Nakasone, K.; Takaki, Y.; Maeno, G.; Susaki, R., Masui, N.; Fuji, F.; H. Nacleie Arids Res. 28, 4312-433, 2000
Ayritle: Complete genome sequence of the aikaliphilic bacterium Bacillus halodurans a Aykeference number. A83650; MULD:20263314
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P;62-118/Domain: ferredoxin 2[4Fe-48] homology <FEP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P;Kawarnbayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohluku, Y.; Funanashi, T.; Lanaka, i.; Kudoh, Y.; Namazaki, J.; Rushida, H.; Oqu
DNA Pes. 5, 55-76, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71040; MG1D:98344137
A;Accession: A71090
                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: transcription factor squa: serum response factor DNA-binding domain ho C;Reywords: DNA binding; transcription factor, transcription regulation F;2-57/Domain: serum response factor DNA binding domain homology <8RF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2049 TAGESVAMADDSLWKPLNYQILLKTRDSSPKVRFAALITVLALAEKLKENYTVLLPESTP 2108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1846 STLQEHIGXMRKEELTSHQSQLTAFFLEALDFRAGHSINDLEFVGKTFNCLTIXLVAMVV 1905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Pyrococcus horikoshii
C,Spate: 10-Sep-1999 #sequence_rovision 10-Sep 1999 #text_change 21-Jul 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 LADLDVEAPNDHILLGVFLQNFREVHQFMPKFNYSKGIKGYRKCAEAGEEHAIVTLRUSTF 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 65; DH 1; Length 286; 26.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Scole 65, DB 2, Length 203;
25.0%; Pred. No. 18;
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                                                                                                                                                        A;Cross-relerences: EMBL:L40404; NID.9655316; FID:9695317
A;Experimental source: CV. Scania; petals
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein PH0982 - Pyrococcus horikoshii
                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule Lype: mRNA
A;Fesidos 1,233 :BAD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 25.0%;
nes 16; Conservative 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C:Accession: H84120
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A; Accession: 110714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: PH0982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                 A;Gene: CMB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
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                                                                                                                                                                                                                                                                                                                                 A/Title: The Xenopus 1P3 receptor, structure, function, and localization in occytes and A/Reference number: A40743; MJID:93258819
                                                                                                                                                                                                                                             R:Kume, S.: Muto, A.; Aruqa, J.; Nakaqawa, T.; Michikawa, T.; Furuichi, T.; Nakade,
Rell 73, 555-570, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: DDBJ:AP000062; NID:g5105244; PILN:BAA80820.1; PID:g5105507
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Cjspories: Dianthus curyopbyllus (clove pink)
Cjbate: 16-Jul-1999 #sequence_revision 16 Jul-1999 #Lext_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Aeropyrum pernix
C;Judto: 25 Aug 1959 #sequence_revision 20-Aug-1000 #fox! ohange 20-Jun-2000
C;Aecession: G72566
                                                                                                              O.Species: Xenopus Laevis (African clawed frog)
C.Date: 03-Mar-1944 #sequence_recision 18 Nec-1944 #fext_change 20-Tun-29A0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 VIKSVAVEALYMISSAQLAVLIJAFVASTIVSALVAAEDVSDNIJAKLPPYIQKOLKESEP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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AjGross-references: GB:D14400; NID:q464219; PIDN.BAAG3304.1: P3D:g464220
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// Match 0.6%; Score 66; DB 2; Langth 2693, Local Similarity 47 4%; Pred. No. 2.36:92;

2110 LABLMEDECERVERGCORTIQUEFTVEGEPLOS 2142 Db 2456 (AQV) REFERERETTL MCTVTVISHGLKS 2488

14; Conservative

Matches

Š

Query Match

hypothetical protein APE1817 - Aeropyrum pernix (strain K1)

RESULT 46

7; Mismatches 12; Indels

A;Status: preliminary; not compared with conceptual translation

A; Molecule type: mkNA

A; Accession: A40743

A.Baperimental source cocytes and eggs A.Note: sequence extracted from NCBI backbone (NCBIP:131713)

C; Superfamily: inesite larisphosphate receptor

Guery Match 0.6%; Score 65; DB 2; Length 113; Best Loral Similarity 24.6%; Pred. No. ? ?; Mest Loral Similarity 13; Mismatches 36; Indels Matches 16; Conservative 13; Mismatches 36; Indels

Query Match Best Local S

256 DYRAA 260

<u>a</u>

95 AHAAS 99

RESULT 47

F10714

R;Baudinette, S.C.: Savin, K.W. submitted to the BMBL Data Library, March 1995 A;Description: Carnafion MADS box genes. A;Reterence number: 217094

T10714

C. ACCESSIOE:

C;Superfamily: Aeropyrum pernix hypothetical protein APE1817

A; Experimental source: strain Kl

A; Gene: APE1817

A;Molecule type: DNA A;Residues: 1 113 <KAW> A;Status: preliminary

A; Residues.

A;Accession: G72566

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A.Residues: 1-152, M. 154-331, 12, 333-1044 soln.
A.Cross-references: EMBL:J05197; NID:4174213; FIBN:AAA.5232.1; FID:q174214
E.Sanduaken, M.G., Lapisella, J.A., Dibamente, E., Thakiaturity, E.
J. Biol. Chem. 265, 15838-15844, 1990
A.Title, Protein synthesis in yeas. Structural and tenctional analysis of the dence A.Reference number: A38376; MUID:90368801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Affective type: DNA
Affection 1-1044 -1048
Affections reterences: EMBL:020865; MID:4652-40; PIDM:AAB67491.1; Fib:4662445; OSPUB:0No
Affection acceptance: Strain SAR8C (AB972)
B;Qin, S.; Xie, A.; Bonato, M.C.M.; McLaughlin, C.S.
J. Biol. Chem. 265, 1903-1912, 199)
A;Title: Sequence analysis of the 'ranslational clonation factor of from Savcharomyre-A;Reterence number: A45027; MUID:90130446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation elongation factor eEF i yeast (Saccharomyces cerecisiae)
N.Allernate names: protein 19625.5; protein YLR249w
S.Speries: assertatempress correctsiae
C.Speries: assertatempress correctsiae
C.Dafer: 41-December 90 #sequence_revision 24 Feb-1996 #rext_change 19 Jan 27 el
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N.Alternate names: hypothetical protein N2846
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                                                                0.6%; Score 65; 108 2; Length Leist
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34.3%; Pred. No. length
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A; Reterence number: 859386
A; Aeression: 859395
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F;917-921/Kegion: cuelectide-binding motif B
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submirted to the EMHL Data Library, February 1995
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A;Cross-reterences: S3D:S0004249; MIPS:YLR249w
A;Map position: 12R
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Although M. C. Stoil, Immercol. 154, 125-155, 1900.
Although M. C. Stoil, Immercol. 155-155, 1900.
Although 
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ArExperimental source: strain C+525
Commetics:
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Fisher, M.S., Burkier, A.F.; Eack, S.; Bubai, P.; Brown, C.M.; Cerny, P.; Borsnell, T.;
M.; Barrell, B.S.
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A:Pesitaes: 1 a41
A:Tross refredence: EMBGLXI/Te o NIDA$959); FIDNOMA-6871.1; FIDA1780865
A:Note: this sequence wis submitted to the EMBG bata Library, December 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 AVIMSELSKIABNSABSV_CIARRAMA_VXQIABLVQBPMBFSP_SSMPWVFILAR
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time 17; Mismatches 45; Indels
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A:N te: hos' Bame Saprens (mar)
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hypothermon, provolusing 4-4482(23)
hypothermon, provolusing (acto)
185-670-83; Hancompletes (acto)
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Rose Connection
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C. Species: Saccharomyces cerevisiae

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R;Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, K.
Nucleir Acids Res 24, 4420-4449, 1996
A;Tilie: Complete sequence analysis of the geneme of the bacterium Mycoplasma pneumon A;Frier complete sequence analysis of the Accession: $73777
A;Accession: $73777
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A)Note: the nucleotide sequence was submitted to the EMRL Data Library. November 1996
C)Genetics:
                                                                                                                                                                                                                                                                                          R,Audersson, S.G.E., Domorodipour, A.; Andersson, J.C.; Sinberitz-Poston, T.: Alemark
Nature 246, 123-140, 1998
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Albasitefetenes, GRAT235270, GRAT235260, NIPqaakus72; PibnerAA14609.1; PID:q386
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                                                                                                         dna-directed RRA polymerase beta prime chain (spcC) PP141 Picketisia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21 M.y 1998 #sequence_recisios 21 % v 1998 #rost elagrae 03 Nov 2000
C;Accession: B71724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C)bate: 27-Fcb-1997 #sequence_remision 35 April997 #foxt_change 17-Mar-2000
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NATIONAL norms - hypothectical profess Pillorf229
Cispecies: Mycoplasma promociae
Alvarioty: APCC 29442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 64; DB 2; Length 229; 27.1%, Fred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Malch 66, 28, 28, 28, 28, 2, Lenath 1972
Best Local Similarity 40 08, Prod No 1 46:02;
Matches 12; Conscruative 11; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \mathfrak{S}_{0} particles and \mathfrak{S}_{0} controlled and \mathfrak{S}_{0} decomposite kinase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 RVINRNNELKKLIESKAPDIIVPNFKPMIQ 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Experimental source, strain Madrid E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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Matches 19; Conservative 1
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Residues 1 220 FPTM
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Cysuperfoaming Lactob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Cross references. EMBL.AC004176, RID.43184270, Fib.43181283
A)Experimental source: cuitivar Columbia
R)Elin, X.; Kaul, S.; Kounsley, S.D., Shear T.P., Benito, M.T., Town, C.D., Fujii, C.Y.; M.Y., Kaul, S.; Kaul, S.; Surangerein, L.A.; Shon, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Biocn, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ayini rons: 12,5, 65,0, 138,5, 131,7, 137,0, 777,3, 318,0, 667,5, 386,3, 414,2, 445/37 47
                                                                                                                                                                                                                                                                                                                  Ajkosidues: 111044 <AND>
Ajdross references: EMBL:271296, NIB.41391835, FIDR.CAA95874-1, PIP-91301836, MIPS-YNIOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)fitle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliand A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross references: GB,AE902093; NFC-g2184299; PIDN-AAC18930 1; GSPDR-GNO0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: translation elongation factor 3, ATF binding cassette homology
C;Reywords: ATP; nucleotide binding; P-loop; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1688 PEVPVLXTAVKLIAPERKEEKNVLGSALLCIAEVTSTLEALAIPQLPSLMPSLLTTMKN 1746
blate: 27-Apr-1996 #sequence_revision 03-May 1996 #text_change 02-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chaccession: $62926
R;Andre, B.; Iraqui Houssaini, L.; Urrestarazu, L.A.; Vissers, S.
submitted to the Protein Sequence Database, April 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Store 65; DB 2; Length 1217;
28.8%; Pred: No. 1.2e+92;
.ive | 11; Mismatches | 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%, Sepre US, DB D, Length 1044;
33.3%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.235-25[Shemain Transmembrane #status prodicted (iM) -
F.358-374/Lomain: transmembrane #status predicted (IMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig. 615, boundin. ACF binding cassette homology *ABCl. Pids.4 0.VRegion: nucleotide binding motif & (P-loop) Pids.4 0.VRegion. nucleotide assette homology *ABCC. Pids.4 0.0 ionain. Alf-tinding tassette homology *ABCC. Pi701-708/Region: nucleotide-binding motif & (P-loop)
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A;Molecule type: DNA
A;Residues: 1 1217 <ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: strain $2880
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Best Local Similarity 28.8%
Matches 17; Conservative
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                                                                                                                                                                                 A;Reference number: $62920
A;Accession: $62926
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Best Local Similarity
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A;Residues: 1-1217 <STO>
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                                                                                                                                                                                                                                                                            A; Molecule type: DNA
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PrHeiderherg, J.F.; Fisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Landson, F. chardson, D.; Ennolaver, M.D.; Vamathevan, J.; Bass, S.; Oliv, H.; Irradoi, L.; Sellers, J.; F. F.; Newtonnes, J.J.; Venter, J.G.; Fraser, G.M.; Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Cross-reterences: GB.AE004198: OB:AE004852; NH :09675474; FIDN:AAF94447.1; -SRIGK-SN
A.Experimental source: serogroup :: , strain N16961; biotype El To
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                                                                                                          C.Aeression: 148128
E.Bibermendal, H., Quax, W., Guax druken, Y.: Dedomont. H.; Komarekers, F.; Donla, L.;
E.Bibermendal, H., Quax, W., Guax, B., Sanden, Y.: Dedomont. H.; Komarekers, F.; Donla, L.;
A.Titte, Organization and expression of the vimentin deno.
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A,tertos 45; 124; 784; 200; 201; 201; 00;
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Fiducing processing the second of the selections.
Figure 2 State and additional expectation of the second                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 H. LRETALLER ELEMEPASI, STANKY, PELANCHISTMI STAUDLANVELLAMMULER FMF S (77
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Post Local Similarity (28.1%) Prod. No. 43, Marticles 19, Caserrofee 12, Mismarches

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2121 VEHÇCQKFIQQLETVLCEP 2139

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227 LOAQIQEQHVQIDVDVSKP 245

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C.Species. Homo sapiens (man)
C.Date. 30-Jun 1988 #sequence_revision 10 May-1996 #text_change 13-Aug-1999
C.Datession: 813115, A55074, J10234; 808487; 154056
R.Honore, B.; Madsen, P.; Fasse, R.; Andersen, A.; Malbum, E.; Celis, J.E.; Leffers, Nucleic Acids Res. 18, 6692, 1990
Affilies Nucleic Acids respected of STNA Several Actions of the Estate of the Estate Nucleic number: $13115; MUID:91067467
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A;Beterence number: $08487; MHID:89303836
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A;Residues, 141,0°,43-441,7°,443 466 sTRE
A;Cross deferences, GR M4144, NID g140218, FIDH:AAA£1279.1; FID:g340219
B;Perreau, 7.: Eillenbaum, A.: Vasseur, M.: Paulin, D.
Gene 62, 7-16, 1988
A;Fille: Nucleotide sequence of the human vimentin gene and regulation of its transcr
A;Feference number, J70234; MU10:88226018
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A; Residues 11% 200, 24, 202 244, 57, 266.277, 77, 779.466 ZPPEN
A; Note: the authors Lianslated the codon GCG for residue 287 as Asp
B: Sommers, 7 L.; Malker Gones, D.; Heckfold, S.E.; Warland, P.; Valverius, P.; Clark,
Pancer Res 49, 4258-4263, 1989
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                                                                                                                Fil/Modified site: acctylated amino end (Ser) #status predicted F_{\rm c}(1/1) = 1/1/10 phosphate (Ser) (covalent) (by ede2 kinase) #status predicted F_{\rm c}(1/1) = 1/10/10 phosphate (Ser) (covalent) (by ede2 kinase) #status experimenta
                     C;Reywords: acetylated amino end; coiled coil; intermediate tilament; phosphoprotein F:411-464/Domain: tail <TLE>
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5.3%; Pred. No. 54;
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A;Molecule type: mRNA
A;Residues 167 466 PESS
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A,Acression: 154056
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Gene 86, 303-304, 1990
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Best Local Similarity 25.3%
Matches 20; Conservative
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A; Residues: 1-112,'F'
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R;Chou, Y.H.; Ngai, K.L.; Goldman, R.
J. Biol. Chem. 266, 7225-7328, 1991
A;Fitle: The mydolation of intermediate filament reorganization in mitosis. p34(edc2) p3
A;Reterence number: A39731; MUD:91216232
A;Aereession: A39731
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A.Molecule type, protein
A.Mosci Marian
A.Mosci May be 41.74.42-47.77.78.48.49.50-62.63.57 cmp.
A.Mosci May be 41-Set; nacheic acid seque
C.Comment: The initiator Met is not shown.
C.Comment: The initiator Met is not shown.
C.Comment: Vimentin occurs in intermediate-sixed filaments in various nonepithelial cell
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A. Fordinia of the general sequence and jone organization of the general of a hyper-thermophillic a A. Reterence number: A71000; MUID:98344137
A. Accession, G71135
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Robax-Jenken, Y.E.F.M.; Guax, W. J.; R16mmendal, H.
Proc. Natl. Acad. Sci. U.S.A. 80; 3548-3552, 1983
A)Title: Primary and secondary structure of hamster vimentin predicted from the nucleoti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A) Note: this accession replaces an interim accession for a sequence tuplaced by GenBunk
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                                                                                                                                                                                                                                                                                                                                                                           probable fmu protein - Pyrococeus horikoshii
G:Species: Pyrococeus horikoshii
G:Dutc: 14 Aug 1998 #seqeence_recicion 14-Aug-1998 #text_change 21-1n1-2000
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    167 LEEKLJULMILJERAKSI DJUFFJI VININSI ABIDI PERVESI (PETAF) PYLIIDEFUQE I DO
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C;Space: 19 Feb. 1984 #sequence_revision 27 Nov 1985 #text_change 22-Jun-1*
C;Arcression: A90842; A93953; A39731; A39559
R;Ouax, W.; Eqberts, W.V.; Hendriks, W.; Quax-Jeuken, Y.; Bioemendal, H.
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A, Molecule - Lypo: MRNA
A, Residucs: 'FPHI,EFAG', 25-40,'A',42-113,'E',115-180,'77',182-464 - 42'2>
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25.6%; Fred. No. 52;
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25.00.00

Query Match Best Local Similarity

13; Conservative

Matches

C;Superfamily, hypothetical protein H10624

A;Gene: PHO851

A; Experimental source: strain OT3

-450 <KAW>

A: Molecule type: DNA

A; Residues:

C;Accession. G71135

Cell 35, 215 223, 1983 A;Title: The structure of the vimentin gene.

vimentin - golden hamster

RESULT 63

qq

5

A,Reference numbor: A90842; MUID:84026520 A,Accession: A90842

A; Molecule type: DNA A; Residues; 1 464 <QUI>

A,keference number: A93953; MÖID:83221633 A,Accession: A94953

C;Geneties.

vimentin .

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F)264-282/Region: coil 2A
F)29-41//Region: coil 2B
F)7.23/30.51,66/Minding site: phosphate (Ger) (covalent) (By cAME depinding Kinase an
F)7.0,21,25.55/44/42/Dinding site: phosphate (Ser) (covalent) (by prodein Kinase C) wor
F)47/Minding site: phosphate (Ser) (covalent) (By cAME dependent linere) #F1 the exten
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A-Experimental source: prostatic timor; cell line bunning R-3427; strain Fischer Coperation and College Brockers, M.J.G.; Verhaeqh, G.W.C.L.; Van Bekhoven, A.: Debruyne, F.M.J.; Schalk Brockers, Biochyns, Res. Commun. 182, 1254, 1259, 1992
A.Hitle: Differential expression of Vineelin in rat prostatic tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EgBussemakers, M.J.G. Verhaeqh, G.C.W., van Broken, A., Debruyne, F.M.J., Schalken, submitted to the EMBL Data Library, october 1991
Appearantein differential expressions of vimentin in rat prostatic fumors: complete A.Reterence number: $22119
A.Reterence number: $22119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 64; DB Z; Length 466;
25.3%; Pred. No. 54;
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25.38; Pred. No. 54;
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N:Alternate names: major heat shock protein dnak homolog
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Nucleic Acids Res. 15, 3923, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A)Cross-references: EMBL:X62953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservative
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                F:104-138/Region: coil lA
                                                                                                              F.147 247/Region: coil 18
F.264-282/Region: coil 2A
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A Moreovier Types (DAA)

A forest retreatments (EMELSZZZZZZZ) MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZZZZ MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZZZZ MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZZZZ MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZZZ MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZZ MIREGISTROP PHARCAABOZIII: PIDIJZZZZZZZ MIREGISTROP PHARCAABOZIII: PARCABOZIII: PARC
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Cidares [2 Feb ] Oct #scharm, gent [ ] to D.E. 1964 #CAT. [ Langer 27 J.B. 2007
Cherossion Address 248420 [ SH2A11 S1274] S144265 Av1951; B419515 842627
Disher name: You Kisk, To Perhidben Kin Statters S.
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Atlateons: lead, 17 eff of 17 of 17 of 18 of 17 of 17 of 17 of 17 of 17 of 18 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            214 SLARLIGERKVESLOBELANTERFERORIOA LORONVOLLOVIASED 200
                                                                                                                                                                                                                                                             0.00%; Shore 64; DB 2; Length 466; 82.0%; Ered. No. 54;
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Albestription: Upstream region of the mouse vimentin gene.
A Petrosocie manher: 842627
A A Treasfour: Standa
A Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                12: Mismatches
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AcAmpession: R4195)
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16; Chaserrative
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A:Weleculer types: mRNA
A:Best Less: 1 456 + CAP
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A;Gene: spo[IlE

A; Title: MucLeutide sequence of a Bacillus megaterium gene homologous to the dnaK gene

A; Molecule type:

RESULT 68

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G71409

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Riffser, C.M.; Casjens, S., Huang, W.M., Sutton, G.G., Clayton, P.: Lathiyra, P.; Wh son, D., Peterson, J.; Kerlavage, A.R.; Quackenbush, T. Salzberg, S.; Hanson, M.; Vu ; Bowman, C.; Garland, S.; Fujli, C.; Cotton, M.D.; Hotsl, K.; Roberts, K.; Hatch, B. A. Haure 390, 580-586, 1997
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Aptrossmeterences, GR Agonthaa, OktAbonotes: Nibrazobbalzo, ElbN.AAbotk21.1. Flb:q268
A.Experimental source: strain B31
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Ajexperimental sources strain Rl
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Aritle: Genome Sequence of the radioresistant bacterium Deinococcus radiodurans RI. A.Reference number: A75250; XULD:20036896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preliminary; nucleic acid sequence not shown; translation not shown
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CySpecies, Boirelia burgdorferi (Cyme discase spirochete)
CyDate: 13:Feb_1998 #sequence_revision 13:Feb-1998 #text_change OR-Owt-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Deinococcus radiodurans
C.Date: 65 Lec-1953 #sequence_terision 03 Dec 1999 #text_change 17-Mar-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 0.6%; Score 64; DB 2; Lenath 790; Best Local Similarity 34.0%; Prod No. le+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
                                                    0.6%; Score 64; DB 2; Length 789;
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                                                                                                                        18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SFEQFEAPLFSQLAKTLERSVQTKAVNKQLDENISLFLIHL 101
                                                                                                                                                                                       1470 LLKLPEEKEETIPKAVSFNKSESQEEMLQVFNVETHTSK 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.6%; Score 64; DB 2; I
Best Local Similarity 34.1%; Pred. No. 1.3e+02;
Matches 14; Conservative 9; Mismatches 18
                                                                                                                                                                                                                                                          323 LLKI,PNNPNQSMEKRIJJHKNAEKLKKTLESFGVKAHVSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Mismatches
                                                                                                                        8; Mismatches
                                                                                           Pred. No.
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A, Accession: D70128
                                                            Query Match
Best Local Similarity 33.3%;
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                                                                                                                               13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: DR1629
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Nucleic Acids Res. 28, 4317-4331, 2000
Agritle: Complete genome sequence of the alkaliphilic bacterium Bucillus halodurans and
AgReference number: A83650; MUID:20263314
                                                                                                                                                                                                                Arbescription: involved in protein folding and assembling/disassembling of protein completionally; heat shock protein 70
C.Superfamily; heat shock protein 70
C.Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Authors: Muclier-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech
erhott, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis that
A;Reference number: A71400; MUID:98121113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RiBevan, M., Bandroft, I., Bent, E.; Lovo, K.; Geodman, H., Dean, C., Bergkamp, R.; Di
P.; Wedler, H.; Wedler, E.; Kambatt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Glavanagh, T., Hompel, S., Kotter, P.; Entlan, R.D.; Pieger, M.; Schaeffer, M.; Funk, R.
Nature 391, 485-488, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 0::we-2600 #lext_champ= 0::Dec 2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CjDato: ถึง-Aug-1990 #soquence revision ถึง-Aug-1990 #1คx/_chande 65-Dec-1998
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                                                                                                                                                                      A, Cross reterences: GB:M31338; NID:q39628; PIDN:CAA68348.1; PID:g39629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 PTTEKTLKDLEGKVERAEVTKANFAKDALKAATERNIY EFTKAKKDFLORTV 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 PSSEVTISNIENI POPAPISENTEWYRVIETAADITLIKEETISEMOOLSNOV 599
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                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 64; DB 2; Length 605;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable replication control protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
A;Variety: columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Mismatches 13;
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Hest Local Similarity 32.7%; Pred; No. 73;
Matches 17, Conservative 12; Mismatches
A;Reterence number: 139837; MDID:87231083
A;Accession: 139837
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Best Local Similarity
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A;Residues: 1 771 <BEV>
                                                                                                                                         A; Residues: 1-605 < RES>
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                                                                                                                 DNA
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Proc. Natl. Acad. Sci. U.S.A. 92, 869%-8699, 1955
A/Tikle: Human latty acid synthasc: properties and molecular cloning.
A/Reference number: A57788; MUID:96004605
A/Accession: A57788
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C:Superiamily, rat latty arid synthase, 3 oxeacyl (acyl varrier protein) synthase 1 h
ydrolase bemology: 8port chain alcohol dehydrosenase hamolody; (acyl carrier protein)
C.Keywords, acyltransferase, carbon oxygen lyase, carrier protein; coenzyme A: tatty
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N.Contains, 3-hydroxypulmitoyl (acyl carrier protein) debythitase (FC 1.1.1.0), 4.18
oyl (acyl carrier protein) reductase (NADH, 8 specific) (EC 1.3.1.10); obcoyl lacyl
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A.Cross references: EMBL-U26644, NID-41049652, FILM.AMT6259.1: PID:4114-614
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C.Species: Homo sapiens (mun)
C.Date: 23-Feb-1996 #sequence_revision 10-Jui-1998 #text_change 05-May-2000
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H77KV)
C.Species: Mycobacterium tuberculosis
C.Date, 17 Jul 1998 Wsequence_revision 17 Jul 1998 Meat_bhange 20 Jun 2000
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30.6%; Pred. No. 3.8e.02;
ive 9; Mismatches 34; Indels
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A.Molecule type: mkNA
A.Residues: 1 1297, TPTQDASSLSYGOVA', ESTA -2504 -3AYz -
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Hivo 9; Mismatches
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Matches 19; Conservative
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A. Actorience confident; MCDD:99021743
A.Setters Series 271625
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A;Molecure type: EMA A;Residues: 1-64,187,66-1-76,747,10/8=1089 +480+ Actoss-references: EMHL211538; NID:q4245; PID:q4246

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P,Tabami, H.; Nakaseer, K.; Jakaki, Y.; Marenn, C.; Stanki, P.; Masni, N.; Fuli, F.; H. Nucleic Acids Res. 28, 4337-4331, 2000.
Aprille Complete genome sequence of the alkaliphilic bacterium Bacillus balodurans a Aprille Masse, Mullo-20263314.
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A)Experimental source, strain C-125
C)Genetics:
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Cispecies: Bacillus halodurans
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C.Speries: phage T3
C.Date: 30-Sep-1991 #sequence_revision 30 Sep-1991 #text_change 20 Sep-1999
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22.9%; Pred. No. 83;
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J. Mol. Biol. 210, 687-701, 1989
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C;Superfamily: phage T7 head-to-tail joining protein
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                                                     A)Map position: 5
A)Extracts 1471, 7572, 25471
C)Superfamily: human fibrillarin
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A; Regidues: 1 522 <89
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                       A; Gene: CESP:10103.7
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C; Genetics:
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Nucleic Acids Ros. 17, 9783-9796, 1989
A;Title: Cioning, characterization and heterologous expression of the Smal restriction of
                                                                                                                                                                                                                                                                                                                                                                               Ajūross references. SB.255436, GR.AL123456, Albu-43261770, FIDA.CAD68846 1, FID güldfefa
AjExperimental source: strain H37Rv
                                                                                                                                                         A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
                          Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R., Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajundream, M.A.; Rogers, J.; Kutter, S., Sceger, K., Skeiton, S.; Squares, S. Nature 335, 547-544, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  type II site-specific deoxycibonaclease (EC 3.1.21.4) Smai · Serialla marceadens
N.A.Lernate names; restriction enzyme Smal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: Serratia marcescens type I; site specific deoxyribonuclease Smal
C:Reywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residnes: 1-552 vWIL:
Cross-references: EMBL:Z78413, PIDN:CAB01657.1; GSPUB:CNG00023; CESP:T0103.7
A;Experimental source: clone T0103
                                                                                                                                                                                                                                                                                            A, Status: preliminary, nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Cabrorhabditis elegans
C.Date: 15-001-1999 #sequence_remision 15-001-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C,Species: Serratia marcescens
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O: Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross references: GB:X16458; NED:947262, PIDN:CAA34478.1; PID:947264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ے
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 63; DB 2; Length 211; 32.4%; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score 63; DB 2; Length 247;
34.0%; Pred; No. 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AVNKQLDENISLELIHESFYFILKFAQKCLEMLIHNFHIHLYNQDSI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein T0103.7 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1834 BENWENHMOLEMSTLUGGEGAAMENET FEHUSADE 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 FRNWJGYFIPAMSVLKNRVGARTHAELRDARNDL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                         A;Reference number: A70500; MUÍD:98295987
A;Accession: B70563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Reference number, S00035, MULD:50058643
A.Aeression: S06035
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A;Accession: T24279
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C;Accession: S06035

PESULT 76

Query Matich

Matches

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C; Geneties: A;Gene: fic A;Gene: smalk

G:Genetics:

Query Match

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C; Accession: 124279

R; Wild, A.

RESULT 77

T24279

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A;Molecule type: DNA
A;Residues: 1-1017 - RJOS
A;Cross-reterences. EMBL,272729, NiD;q1322831; P10R;CAA96013.1; P10:q1622832; GSPJ650
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Proc. Natl. Acad. Sci. U.S.A. 91, 7435-7439, 1994
A.Fille, Human cylopidamic isolencyi URNA synthetase, scheetive diverdence of the ant
A.Reterence number: [59314; MUID:94329529
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A; Reference number: 225394
A; Actession: TS1491
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Cospecies: Arabidopsis thaliana (mouse-ear cress)
C.Date: 18 Aug 2000 #sequence_revision 18 Aug 2000 #text_change 18-Ang 20-o
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CiDate, 8 May 1996 #Sequence_forMelon 8 May 1996 #text_change 24 Nov 1999
CiAccession: 159814
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Ambleonic type: mRNA
A:Residice: 1-1246 (RES
Autross reference: GB:Duat72) MID:9551621: PIDM:PAA058(5.1): PID:4551622
Autross reference: GB:Duat72) MID:9551621: PIDM:PAA058(5.1): PID:4551622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FVNDSTUPPCOPLOTIVISATINEMPSINEPAPSEX SEALNBURKVIDAVTORIVERAE 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Superfamily, yeast replication licensina factor MCMC, HTM homology C.Keywords: cell cycle control; DNA replication; nucleus P;275-8su/Domain: MCM homology - MCMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Guery Match 0.6%; Acore 63: DB E: Length 1017; Best Local Similarity 29.1%; red, N. 1.80.02; Matches 16: Conservative 10: Mismatches 29: Indexs
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Bost Local Similarity 25.4%, Fred. Bo. 2:2e-02;
Matches 17; Conservative 16; Mismatches 34; Indels
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Asinthons (7,1 119,1 177,3, 118,9 17
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Abbleche type: UNA
Asstatues: 1-1189 sSAT>
A.Cross references: EMBLAL991148
                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: SGD:MCM6; MIPS:YGL201c
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       A.Arression, 354219
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A. Miller, An analyzin related dense (unev-44) is necessary for proper axonal quidance in Cad. A. Betterener nomber: AC282; MIID195264664
A. A. Cossenor: LOTZAZ
A. Struss, preimment at MIZZAZ
A. Struss, preimment at MIZZAZ
A. Miller, The Miller, MIX.
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Sed21)
Pepiratron iioensing lactor MOMS——yeast (Saccharomyors reterisiae)
NSAlternate bampes: Dypotratival provine 31256; hypothetical protein YGLZOICE minichromom
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Cisperies: careachanditis elegans
(Cisperies)
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NATH ordane anness hypotherists, protein YMH021.14
"Species: Succentingers corevision of Sep 1995 #text_change 05 Nov 1999
Citates of Jul 1995 #sequence_revision of Sep 1995 #text_change 05 Nov 1999
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1551 LETVIORISAVAVOMERNAISKIIVETWEALLINASSLALAVAALLASILLISILLI LEVIRILN 1508
                                                                                                                 44 TEAPLSYAPMINSAVORIGHRAVIAEETRYVASELEDITENAVISTISQELQIPTARVILL 405
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0.6%; Source 63; D8 2; Length 834; 51.6%; Pred, No. 1.46+02;

Sourty Match Best Local Similarity 25.0%; Matches 11; Conservative 1

14: Mismatches 19: Indels

1157 NABLVETEERFORARFETTVOLKEPROEMBORRSELLEVOLVET 120

RESHUL 41 States

0.6\*; Score 64; DB-2; Length 971; 34.8\*; Prod. No. 1.7e+02;

Eyeski 449,75 mmain. Fransmombrane metatus prodicted  $\pm m_{\rm e}$  Ey722778 Zhododin: fransmombrane Estatus prodicted  $\pm 102$  .

A) bone: MIESSYMELBOW A:Map position: 148 ?/Keywords: Transmembrane profein

7; Mismatches 24; indels

Matches 16, Causervative Chery Mutch Best Local Similarity

TRIX DATIOAPPVOUPATRETYRUTERINGUMENHMOTHMETTQEH-COMMMET 1958 

Projection, A.U., McRopadilla, A.B.K., Writh: E.E. substited to the Protein Sequence Latabase, May 1996 Algebreice manhor: Sed.14

A; Cross - references: GDB:384085; OMIM:600709 A; Map position: 9q21-9q21 C; Superfamily: isoleucine--tRNA liqase

A; Gene: GDB: IARS; ILRS

C;Superfamily: isol C;Keywords: ligase

Matches 15; Conservative

õ 9 RESULT 85

Best Local Similarity

Query Match

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Pithcologis, A : Ecker, J P : Paim, C.J : Enderspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L., Comway, A.B., Conway, A.E., Creusy, T.H.; Dewar, ansen, N.F.; Hudbes, B.; Huizar, L. Analone, B.; Huizar, L. A. A. Huizar, E. A. A. Huizar, E. A. A. Huizar, E. A. A. Huizar, E. A. A. Huizar, J.E., Jenkins, J., Johnson Hopson, C.; Khan, S.; Ebaykin, F.; Kim, P. A. Hi, J. H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Piron, M.; Ponchy, T.; Powley, P.; Sakano, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shins, P . Southwick, A M.; Sun, H.; Tallo
                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable protein gipsy/Ty3 signer polyprotein [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cispecies: Arabidopsis thaliana (mouse-ear cress)
Cipate, 02 Mar.2001 #serpeter-revision 02 Mar.2001 #fext channel 31-Mar.2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-1447 <STO>
A;Cluss:trfereness: GR-AE005172, HID:q11034946; PIDN:AAG27103.1; GSPUR-GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ajcross-references: EMBL:292569; PIDN:CAB16467.1; GSPDB:GN00020; CESP:W1006.1
AjExperimental source: clone W1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  c;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #fext_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,A,15,13 S,115,14, S,1., Schwirtz, T.F., Shinn, P., Scuthwick, A.M., S. ker, M.: Wu, D.: Yu, G.: Fraser, C.M.: Venter, J.C.: Davis, R.W. A,Titie. Sequence and analysis of chromosome 1 of the plant Arabidopsis. A,Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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A, Anterns, i egye (dayz) old/2: greak, clines (1945) (Leneth 129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 63; DB 2; Length 1461; 34.4%; Prod. No. 2.8e+02; ive 7; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 63; DB 2; Length 1447; Bost Local Similarity 28.6%; Pred. No. 2 7 \times 0.2; Matches 14; Conservative 14; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 351 LPHLVVSIIHHVTGEETECMPGQIYKPHLEAILTKISLKNNLDHLLASLL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352 MPQISVNAVSGISGYKIMGVKGTV()*PPILFILLIDSGSTHNFIDSTVAAKL 401
19; Indels
                                                                                                                                                                            428 LSAWETAMEBTIERVEDKEIKMIKOSALLKTFADGI,NVGAP 468
                                                                                                    637 LKGWEEALENVIKSTKPGKLIGVANQKMIELLADNINLGDP 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothefical protein W1006 1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary, translated from GM/EMMH/7DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, September 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1879 AQBREND EFVORTENCIIDCLVAMVVKLSEVT 1911
10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136 AETTRKNLLERGKHEPCVVDCVDAAFVMKSG1T 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 43
           12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 39 43
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Reference number: 220199
A;Accession: T26327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: G86474
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: CESP:W10C6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Ainscough, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 89
                                                                                                                                                                                                                                                                                                                                                                               87
                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΩD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORA directed RRA polymerase (EC 2.7.7.5) beta' chain - Mycobartorium loprao
Cyspecies: Mycobacterium reprae
Cybate. 30 Sep 1553 Resquence_revision 30 Sup 1553 Rext_change 18 Aug 2000
Cyacession. 33146
Refference Signal Superior S.; Chanteau, S.; Doucet Populaire, F.; Eiglmeier, K.; Gazuier, T.;
del, P.R.; Sitisombut, N.; Wurfunter, S.; Cole, S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Nucleotide Sequence of the first cosmid from the Mycobacterium leprae genome pr
A;Reference number: $31143; MUID:93188701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959, 1959
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A)Gross-references: EMBL.014211, BLD.q14282; P1DN.CAA78659.1; PLP.g581338
A)Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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A,Experimental source: clone E0362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein E0932.2 Generhabditis elegans
C.Species: Gaenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15 Oct-1999 #text_change 18-Fcb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OB PERSOLANTERANÇINAVINÇERINLSERTEREPAĞKOLEMETEK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 PLEDYFLKCKENGAFTVLVDNYVKEEEGTSVVEQAPTFCAEDYRVCMDFNTIR 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 63; DB 2; Length 1316;
33.3%; Pred. Mc. 2.4e<sup>,</sup>02;
ive 13; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%; Score 63; DB 2; Length 1398;
29.3%; Pred. No. 2.6e±02;
                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 63; DR 2; Longth 1266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asstatus: nucleic acid sequence not shown, translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                       28.3%; Fred. No. 2.3e+02;
tive 10; Mismatches 28; Indels
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Best Local Similarity 33.3%; Fred. No. 2.4c Matches 10; Conservative 13; Mismatches 1523 QLLSSKNILLKEVVESGGPEILFOLFFFITF 1552 346 RVINRAMREKREIDEGAPDIIVNNEKRMEQ 375

Query Match

5

A; Molecule type: DNA A; Accession: S31146

A;Start codon: G1G

A;Gene: rpoC

Genetics:

A;Reterence number: Z19275 A;Accession: T20434

C; Accession: T20434

RESULT 86

T20434

R;McMurray,

A;Moiecure type, bNA A;Residues: 1 1398 <WIL>

A,Gene: CESP:E03G2.2

A; Map position: X

Onery Match Best Local Similarity

alpha tetoprofein enhancer binding profein - human

N:Alternate names: AIBEL protein

A; Accession: A41948

Appenent obstaturel

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A, Cross references, EMBL, US0071, NID. 41268871, PID. 4120×877, PIDR: AAAY 447.11 (ESE) FP
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A:Experimental source: Lissue-type etiolated hypocotyls
                                                                                                                                                                            A:Cross references: EMBL:064854; ilDN:AAB18418.1; GSP:04:GN:00024; CESF:unc-68
A:Experimental source, strain bilatol NZ, clone NIIC4
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C:Date: 20:Sep:1909 #soquence_revision 20 (ap. 1909 #:ext_change 20:Sep:1939
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C;Species: Lycopersicon esculentum (fomato)
C;Date: 23:Apr-1999 #sequence_revision 23 Apr 1999 #fext_change 20-Apa-1999
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Best Local Similarity 25.0%; Pred. No. 1.2e+04;
Matches 11; Conservative 14; Mismatches 19; Indels
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R:Nebentuellr A.; Lomax, T.L.
submitted to the EMRL Data Library, September 1997
submitted to the EMRL Data Library, September 1997
A:Beference number: 215303
A:Reference number: 215303
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A.Molecule type: mRNA
A.Residues: 1-75 <NEB>
Asstatus: preliminary, translated from ChysMas /DDBJ
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R;Gattung, S.
Submitted to the EMBL Data Library, Pebruary 1996
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A, Accession: T15448
                                                         A;Molecule type: DNA
A;Residues: 1-5107 <PAU>
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A, Littels: 27 : 54 4
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A;Gene: CESP:B0350.1
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A: Fifter A buman diplarite toporting enhancer bonding protecting Aibbi, contains four homes. A; Reperence nomber, Adivide Mineral 1988.
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A,Residnes: 1-27k3 - MeR-
Azitess references: GHECTO25er GHEDGO35; NEGGIS42c. PIDN.BAAG1935.1. PID.G219430
Azitess references: GHECTO26er GHEDGO35; NEGGIS42c. (PUBLN.G627), BEHELG527c)
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A:Map postfion: Peq2s.4 [6q2s.]
A:Map postfion: Peq2s.4 [6q2s.]
C:Seperfounity: alpha-reperiorism enhance: tinding protein; Lomeobox Formalony
C:Seperfounity: Dam-obox, no leus, transcription requiation; zinc finger
E:72-94/Region: zinc finger diffi motif
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Ottabe: Newel 1999 #sequence_regis.or 18 ect+1999 #rext_change 31 Jan 2000
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Figure 958/Reqion: alutamine r.ch.

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Fig. 11. 21.47Restion: Aire tinger O'HH motifi Fig. 55eegbestion: Aire tinger O'HH motifi Fig. 55eegbestion: Aire Aire Aire Aire

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11,5%; Score 64; DB 1; Length 2784; 27,5%; Prod N. 5 96+50;

13: Mismatches

7

Substy Match Rest Local Similarity 27,000 Matches 19, Conservative

PASS COUNTRY LASS 47) 1ETLECA 437

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46; Indels

Estauloy, A.s Saffund, S. Soffwiller, Duly 1996. Astronomy and the EMML batt Library, July 1996. Astronomy from the Sequence of C. elequis cosmid Kilet, A.Accession: L2944.

'remerhabditis elemans

partial 758 PESOL:1 129144

": Accession: [29]44

C, Superfamily: auxin-induced protein aux28

0.6%; Score 62; DB 2; Length 75; 38.2%; Pred. No. 12;

6; Mismatches

Best Local Similarity 38.29 Matches 13; Conservative

Query Match

992 SHQKLSELLENLLSCVYSCPSYTAKDIMKVLQGV 1025

35 SYOKLINALENMFTCLTICNSQSESKLMDLTNGV 68

90

hypothetical protein yrrD - Bacillus subtilis

RESULT 93

Nature 390, 249-256, 1997

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C.Este: 20-Aug 1999 #Sequence_revision 20-Aug-1869 #Lext.related 24 Sep-1999 C.Accession: H72465
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A;Molecule type: DNA
A;Cross:refelances: BURE.X65128, NID-940649; PJPN-CAA46919.1; PJD:940700
A;Experimental source: serotype B
A;Accossion: $28664
A;Molecule type: DNA
A;Molecu
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E)152-197,ccmain: HKBP-1ype peptidy)projyl (semerise homology cPP):
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DB 2; Length 232;
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                                                                                                                                     7; Indels
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P.Lundemose, A. Ar Pata Data Dibrary, June 1992
Submitted for the PMRI Data Dibrary, June 1992
       0.6%; Score 62;
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Best Local Similarity 31.2%
Matches 15, Conservative
       Query Match 0.6%
Best Local Similarity 42.9%
Matches 12; Conservative
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A;Accession: S28638
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A,Residucs. 1:243 -AFN>
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P.Experimental Source: strain 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyperes: Barrillus subtilis
Cybate: 05-bec:1997 #sequence_revision 05-bec 1997 #fext_change 20-Jun-2060
Cyacession: Boy979
Ryknust, 20-gasawara, R.: Moszer, L., Albertin:, A.M., Alloni, G., Areveta, V.: Bortor
Ryknust, S.: Brouillet, S.: Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
C.; Bron, S.: Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Erriugton, J.; Fabret, C.; Ferrari, B.
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C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-oct-1999
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A)Cross-references: GB:AE001328; GB:AE001273; NID.93329015, P1DB:AA/58178 1, F1: 933236
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0.6%; Score 62; DB 2; Length 174, 44.0%; Pred. No. 31;

6; Mismatches

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11; Conservative

Query Match Best Local Similarity

A; Experimental source: serotype D, strain UW-3/Cx

A;Gene: lcrH\_1

A; Reference number: A71570; MUID:99000809 A; Accession: B71497

C;Accession: B71497

A;Status: preliminary A; Molecule type: DNA

A;Gene: yrrD C;Superfamily: Bacillus subtilis hypothetical protein yllD

A.Reference number: A69580; MuID:98044033 A.Accession: B69979

A; Molecule type: DNA

B; Indels

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A,Title. Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero A,Reference number: A72450; MUID:99310339
A,Accession: H72465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В,Камагабауакі, У., Нібо, У., Нотіважа, В.; Узшатакі, В.; Наібажа У. Люпол К.; Та
ама, Н.; Такашіуа, М.; Маsuda, S.; Fundhashi, Т.; Tanaka, Т.; Kudob, Y.; Vamazaki, J.
DNA Pos. 6, 83-101, 1999
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AjExperjmental sentite: serctype D. strain UM-37Cx
probable fktp-type poptidyl-prolyl els-trans isomerase - Chlamydia trachomatis (serot NyAlternate names: mip-like protein Cyspecias: Chlamydia trachomatis (cyspecias: Chlamydia trachomatis Cyate: 17-Apr 1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999 cynoresion. $228639, $228639, $71503
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0.3%; Score 62; DB Z; Length 245; 29.3%; Pred. No. 47;

99 Mismatches 24; Indels

14) Conservative

Matches

poery Match Best Local Similarity

15 (a) REVVELLO TELLA MERCE CITAL DE L'AVAÇERILE SALALUARIAN. 1006

30 FEVEVEREBURE SLEDNIVE SIMBLE SEAAGELL I DADAF KAKSING 130

M79 profesio a rice.

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A:Title: Genomic sequence comparison of two unrelated isolates of the human qustric p. A:Reference number: A71800; MUID:99120557
A:Aecession: B71964
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R:Halin, L.: Jaurequiberry, G.
Bur. J. Biochem. 228, 86-91, 1995
A;Tille: Molecular characterisatio) of the ADP/ATP-transporter cDNA from the human ma
A;Reterence number: $68943; MUID:43188418
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P[7-189/Domain: short-chain alcohol dehydrevenase broclogy (SAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross references: GB:AE001456, GB:AE001439: NID: q4154689; PIDN:AAD05765.1; PID: q415
                                                                                                                                                                                                                                                                                                                                          RyAlm, R.A.) Ling, L.S.L.; Moir, E.L.; King, B.L.; Brown, E.L.; Loig, E.T.; Smith, Javes, C.; Gibson, R.; Merberg, E.; Mills, S.D.; Jiang, O.; Taylor, C.E.; Vovis, O
Nature 397, 176-180, 1999
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C)Superfamily: ADP,ATP carrier pro ein; AEP,ATP carrier protein repeat homology
                                                                                                                                                                                                                                            A.Varicty. strain J99
C.Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #fext_change 21-Jan-2000
C.Accession: B71964
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Cispecies: 97-May 1995 #sequence_revision 01 Sep 1995 #text_change 09 Jun 2000
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                                                                                                                                                                              m.... starter priori (strain 199)
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F6-102/Domain: ADP,ATP carrier protein repeat homology APP1>
F:112-203/Domain: ADP,ATP carrier protein repeat homology APP2>
F:209-301/Domain: ADP,ATP carrier protein repeat homology APP2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 52; DB 2; Length 275;
38.5%; Pred. No. 54;
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39 VINCERSEVPILLEPIYUPPAYNEDVMSILLOOPIKKKPFSR1 81
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C.speries, Caenorbabditis elegans
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Ojspecies: Helicobactor pylori
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Matches 15, Conservative
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A:Molecule type: DNA
A:Residues: 1-275 <ARN>
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                                                                                                         RESULT
                                                                                                                                             B71964
       9
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J. Gen. Vicol. 74, 1847 1897, 1993
A.Filler, Health Control on and expression of the Euman herpesvirus 6 alycoprotein H and int
A:Performer number: Jozies, M.Dr.9386943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *. Superfamily: transcription factor spur, serum response factor bNA-binding domain home.
E. 2. 57/Bomain: serum response factor bNA-binding domain homelogy sSFFs.
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Cibute: 24 April 99 #sequence revision 23 April 999 #Lext_change 20-Jun-2000
CiAreession: 104-09
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Cibute: JR-Feb 1994 #sequence_revision ok-Peb 1994 #foxt_change 28-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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# Marth. 0.6%; Score 62; 68 2; Length 249; Loral Similarity 21.8%; Pred. No. 48;

48; Indels

20: Mismatches

19; Canservative

Matches

Querry Materl.

T CWOF

AtExperimental sources subsp. (aponies, ev. Thonaha P.

A. Serner M79

A:Residnes: 1-249 - gul. A:Cross-reterences: EMBL:Y15008: PIDN:GAA75241.1

submitted to the EMBL Data Library, September 1997 A.Arression, 104.07 A.Stression, 104.07 A.Stotoner, preliminary, translated from GB/FMRG/AGRIA A.Molecile type: mKNA

A; Residues - 1 gan attm. Artossareterenees: dB:X84413; NID:4853961; PION:CAA59331.1; PID:4854060

Additional Source: strain Uliuz

Aprilentiers off,

A) Acression Juzien | A) Melecule Type: DNA | Access 1 950 etc.

digroprofein at precursor - human horposylius 6

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CIAMPOSSI OIL TQLI65

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Cykeywords; alymopratein F1 To/Tomatic Stand Separate #status predicted - SIG-F11 Z50; - 4. F1 E12 F1 Co. 4. F1 F1 F2 F2 E13 F2 E14 F2 E25 F156/Biadini site; carbebydiate (Asn) (covalent) #status predicted

0.6%; Score 62; 08-2; Length 250;

21; Indels

99 THES TANDERSHIVED VSTVENCE CONNECTED OF A MILLION THREE

Goral Similarity 25.6%; Prod. No. 48: es 11: Classicative 11: Mismatches

Dipory March Bost Local

Matches

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-364 <WIL>

A; Molecule type: DNA

submitted to the EMBL Data Library, October 1996 A;Reference number: Z19984 A;Accession: T25124

C; Accession: T25124

R;Smye, R.

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P.Heridelberg, T.F.; Fisen, J.A.; Nolson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I. P.P.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Peference unimber AR2035: MIID:20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyster family and yield line receptor.

Cykeywords: glycoprotein; for channel; neurotransmitter receptor; postsynaptic membra cyteowords: glycoprotein; for channel; neurotransmitter receptor; postsynaptic membra cyt. Cyt. Domain: signal sequence #status predicted <200.

Fig. 52.7 broader; interfinity and ylebellor receptor dipartitle chain #status predicted F22. 240/bonain; extracellular #status predicted.
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C;Species- Vibrio cholerae
C;Satu. 18 Aug.1306 #sequence_recision 20 Aug.2000 #frx!_change 02 Pob-2001
C,Accession: C8116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nicotinic acetylcholine receptor alpha-1 chain precursor – fruit ily (Drosophila mela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Applile: Gessivation of neural nicotinic acetylcholine receptors from Drosophila to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CiSpecies: Drosophila melanogaster
CiSpecies: 3: Pet-1991 *seppender_rovision 31 Dec-1991 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                               1342 PHPPLPH UQLUPPLCARRELWILLTILEPROYVERTVLAAAYGEKDAILEADTEFWESUC 1451
                                                                                                                                                                                                                                                                                                                                                             188 EHSRLPISLQISVIPDEKALLIFLINIVETVEVVNTLNNVINAELDIYYDLFTEEVCKLC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sabs
                                                                                                                                                                                                                                               Gaps
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Fig86-325/bomain, transmembrane #status predicted CTM7>
Fig86-513/bomain: intracellular #status predicted CTM7>
Fig814-532/bomain: transmembrane #status predicted CTM4>
Fig85-233/binding site: catellydade (Asn) (escalen) #status predicted Fig81-233/binding site: catellydade (Asn) (escalen) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: mRNA
A,Eosiducs: 1 %67 %PO2
A,Cross-references: EMBL.X07194, NID:q7575; FIDN:CAA30172.1: PID:q7576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Grossinn: A38801
A;Accession: A38801
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41.2%, Prod No. 1.20:02;
Live 8; Mismatches 12; Indels
                                                                                                                                                           Score 62; DB 2; Length 443;
Pred. No. 93;
                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map Position, 3P 96A
A,Introns, 64/3, 79/3, 116/2, 176/3, 330/2, 401,1, 493,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;246-264/Towals: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1641 FLKLVPDILATVQPKKFEGEREQAINRQTALYTL 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 PIQILDRALLCIERPRAKEEPEREDQPPEVLTDVYHL 378
                                                                                                                                                                                                                                           9; Mismatches
A, Experimental source: strain HST; pop, variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: $00381; MULD: 88283626
A; Accession: $00381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.Cross-references: FlyRase-FRgn000036
A.Mar Fosition, 3R 96A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.; Spierer, P.
                                                                                                                                                                          0.6%;
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                                                                                                                                                                                                                                                      18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: S00381; A38801
                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bossy, B.; Ballivet, M.
EMRO 1 7, 611-618, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: FlyBase:nAcR&agr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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                                                                                                                                                                              Query Match
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C, Genetics:
                                         C; Genetics:
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K.Isaqawa, Y. Makai, T., Nakana, K., Kagawa, M.; Chon, T.; Mori, Y.; Sunagawa, T.; Kawa
J. Viroi, 73, 8033-8063, 1999
A.Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and
A.Reterence number: 222/32, M010:99412319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               iste Agrono 57, INTO garox (100), Priote AACD6/12: 1. Priote 04 (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribeckert, G.; Warren, P.V.; Caasterland, T.; Young, W.G.; Lenox, A.L.; Graham, B.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: The complete genome of the hyperthermophilic bacterium Aquifex acolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Cross-reterences: EMBL:AB021506; NID:g4995977; PIDN-BAA76125 1; FID-94995932
                                                                                                                                                                                                                                                                                                               A)CLOSSTRECTEMBERS, EMBL.481127, FIFH.CAPG3388.1, GENDA CNOOD23, GPSP.T22G5/3
A)Experimental source: clone T22G5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Applicates, preliminary, machele acid sequence not shown, translation not shown Applicate type; DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Spreies. Aquitex aeolicus
C.bate: 10 Sep 1999 #sequence_revision 16 Sep 1999 #text_change 21.Jul 2000
C.Arcession: E70341
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C.Aecession: F43964
       C;Date: 15-oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Species: human herpesvirus 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 6.04; Scote 62, DB L, Length 376, Best Local Similarity 46.2%; Fred. No. 76; Matches 12; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; Score 62; DB 2; Length 364;
35.1%; Fred. No. 74,
.ive 7; Mismatches 17; Indels
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conserved hypothetical protein aq\_454 - Aquifex acolicus

E70341

CGenetics: AGene: 4454 GSuperfamily: conserved hypothetical protein yodg

A; Experimental source: strain VF5 A)Residues: 1-370 <AOF>
A, 1108S references GR AEGODA + 0.

5

A; Variety: strain HST

RESULT 103

A,Reference numbet: A70300, MUID:98195555 A:Accession: E70341

Nature 392, 353-358, 1998

A:Status, preliminary, translated from GB/EMRL/DDBJ A;Molecule type: DNA A;Residues: 1-443 <1SE>

A; Accession: T43964

TIES CISVNARQVPIPIPPPPPARFICTVQGEPPQMQQPR 1189

Best Local Similarity 35.19 Matches 13, Conservative

Query Match

A;Map position: 5 A;Introns: 25,2; 102,2; 295,2

A; Gene: CESP:T22G5.3

C: Genetics:

â 5

A: Map possition: Appendix Volume

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Liberty Material Bosst Lovert

PESHLI List

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Cjoute, L. Currendo Recquence_rectain. L. Current_change 28 Jul-2000
CjAccession: T44153
Friveninter; G.: Cambuadh, L.K.; Stamey, F.K.; Dewhorst, S.; Inoue, N.; Pellett, P.E.
J. Virol. 73, 8040-8052, 1959
A:Title: Human herpesvirus 6B genome sequence: coding content and comparison with hum
A:Reterence number: 222734; MUDE:93412318
                                                                                                                                          C.Krywords, autophosphorylation, «lycoprotein; phosphoprorein
E19,65,187,223,224,250,611,660/Birdinq Site: carbohydrate (Asn) (covalent) #Status pr
E19744/Birding Site: phosphate (Tyr) (covalent) (by antophosphorylation) #Status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Fitle: Miranda directs Prospero to a daughter cell during prosophila asymmetric div
A:Reference number: 214067; MOID:98065952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A.Residuas: 1-840 <1KE>
A.Cross-references. EMBLAB005661; MID.92749776, PIDN.BAA24111.11; PID:447777
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Nature 390, 625-629, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22 Jan 1999 #sepector_recisi s 22 'i. 1999 #1004_dunde 17 Not 2000
Sion: 100029
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C.Species: human herpesvirus 6
A.Variety: strain 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.6%; Score 62; DB 2; Laugth 903;
Best Local Similarity 30.0%; Pred. No. 2.1e-02;
Matches 18; Conservative 9 Mismatches 33; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 0.6%; Score 62; DB 2; Length 830; Hest Local Similarity 46.7%; Pred: No. 1.9e-02; Matches 14; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Onery Match 0.6%; Score 52: DB 2; Lougth 753; Best Local Similarity 57.1%; Pred. No. 1.7\alpha-02; Matches 12; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Miranda protein – fruit fly (broscphila meianogaster)
C:Species: brosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Asstatus: preliminary, translated trum GB/EMPL,/DDBJ
AsMolecule type: mRNA
AsResidues: 1-830 c1KE>
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ArMolecule type: DNA
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A;Cross-references: EMBL:AF157706; PIDN:AAD49634.1
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A:Map position: 92B-C
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A; Status: preliminary

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A; Residues: 1440, ***, 432-83, ***, 365-907, ***, 969-2296-3512>
A; Residues: P440, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83, ***, 432-83
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A)Experimental Source. strain Sabin variants P(V)-son/37
A)Note: the strain Sabin Vaccine P3/Leou/37 is the progenitor of the strain Sabin vaccine P3/Leou/37 is the progenitor of the strain Sabin vaccine P3/Leou/37 is the progenitor of the strain Sabin vaccine P3/Leou/37 is the progenitor of the strain Sabin vac A)Note: the authors trainslated the codon 3A0 for residue 497 as 31% Rountford, R.C.; Ryshamway, G.: Cann, A.J.; Hauphmann, R.; Hughes, P.; Clarke, L.D.; Mountford, R.C.; Nucleic Acids Res. 11, 5629-5643, 1983
C)Accession. A93987, A93484, S42524; A03900 Known, P.; Minor, P.P. Schild, G.C.; A stanway, G., Hujbas, P.J. Machillad R.C.; A Proc. Natl. Acad. Sci. U.S.A. 81, 1539-1543, 1984
Aprille: Comparison of the complete nucleotide sequences of the genomes of the neurow A;Reference number: A93987; MUID:84170338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C)bate. 3) Sep. 1908 #sequence_restston 07 Sep. 1998 #foxt_shange 26-Ang-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        573. QSALPQGI EDLI SEVAQGALI GSEFKQQDSI ITDI KASGI MESRI VEAL I AVETTATNITLA 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493 PVPILAMNHLKKIMKTSKEGVDESFIKEAVLARLGDDNIDVVLSAISAFEIFKEHFSSEV 552
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N:Contains: coat protein VP1; coat protein VP2; coat protein VP3; coat protein P3-4a; protein P3-6a; protein P3-6b, protein E7-9; protein P3-6b; Species; human poliovirus 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Residues. 579-878 SIA:
A,Cross-reterences: EMBL:VUI>40; NIU:951154; FIDN.CAAE4780.1, FID.4929811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;1543/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: genemic RNA A;Residues: 1 2206 /8T1>
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                                                                                                                                                                                                                                                                                                                                                                            A;Accession: A93987
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NJOontains: coat Frotein VP1; evel protein VP2; coat protein VP3; coat protein VP4; core
otein P3 1b, protein P3-2; RNA-directed RNA polymenase (PC 2 7 7 48) P3-4b
Cysperies; buman policytrus 3
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A;Note: the publication sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: valine--tENA ligase
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Yamada, M.: Yasuda
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AyIntrons: 135,0; Tokyo, 202,0 (001,0), 200,0 (006.0), 469.0; 604.73, 588.71, 619,73, 638,73-
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O, K., Obsmeta, S., Stompe, S.: Takenchi, C.: Wada, T.: Watanake, A., Yamada, M.: Yas
DNA pec. 3, 104-136, 1996
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A)Experimental source: clone C26H9A
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C.Spate: 15-Oct-1949 #sequence_revision 15-Oct-1999 #text change 15 Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.Species: Sylechocystis Sp.
A:Variety, FSC 5833
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text change 20-Jun-2000
                                                                   1392 PHERLD ULVOLVETLOAFRE WILLILL FROYVERTVLAAAYGEKDAILEADTEFWESVC 1451
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                                                                                                                                       987 EKKLKSHQKLSETLKNELSCVTSCPSYTAKDLMKVLGGVNGEMVLSQLLFMARQLL 194J
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23.2%; Pred Mc ? 254.0?
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Matches 13: Conservative 16, Mismatches 27; Indels
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hypothetical protein C26H9A 2 - Caenorhabditis elegans

RESULT 111

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T19493

A;Status: preliminary; translated from GB/EMBL/DDBJ

submitted to the EMBL Data Library, September 1997

C; Accession: T19493

R:Smyc.

A;Reterence number: 219131 A;Accession: T19493

A; Residues: 1-1334 <WILE

A:Molecule type: DNA

A;Gene: CESP:C26H9A.2

GNNY4P

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C; Genetics:

F.154 (Bunding sites plosphory) kwa (Fyr) (covalent) #status predicted

submitted to the EMBL outs library. April 1985

A: Malecule type: denomic RNA

A: Reference ranbor: 8 4 629

A:Accession: St4320

April 88 Interestions: EMBL: Xoofot

A.Account of the SARALL A.Molecules Types (epiconic PNA A.Bostdoes) | Lack + P.Y.

CACCOSSION: S04822; S04920

0.08; Score 62; DB 2; Length 2206;

State 52, Pred, No. 60002; Tradition 73, Indels

Matries 20 Conservative 27; Mismatches

Sporty March Rost Local Similarity 17.8%;

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C;Accession: S14722

E;Tanaka, M.; Mihosta, H.; Ushiro, H.; Nakashima, K.

E;Tanaka, M.; Mihosta, H.; Ushiro, H.; Nakashima, K.

Ejtanaka, M.; Mihosta, 1988, 185-389, 1991

A;Tilli, A most | offMa close, caseding a production like profession that the two core A; Note the number: S14722; MG10:91198142

A;Accession: S14722
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, C.; Ledsen, F.; Swinn, M.; Melser, W.; Ferey, F.; Folonay, J.; Mediarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Title: Genome sequences of Chiamvdia trachomatis MoFn and Chiamydia pheumoniae Ak<sup>49</sup>
A;Reference number: AB1500; MUD:20150255
A;Accession: DB1655
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A:Experimental source: strain Nigg (MoPn)
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Nature 406, 151-157, 2000
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Resimpson, A.J. G., Rehnach, F.G.; Arruda, P.; Abreu, F.A.; Arencio, M.; Alvarena, F.
Hriones, M.R.S.; Bueno, M.R.P.; Camardo, A.A.; Camardo, J.E.A.; Carrer, D.M.; Currer
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
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Nibato, 18-Aug 2002 Facquence-rothing 20-Aug 2009 First, charac 02-30-2000
Chaccession: A82577.
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CiDate: 31-Mari20600 Macquenco_revision 31 Ma: 2000 #feat_chanae 11 May 2000
CiAceession: D81655
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A,Reference number: A82515; MUIB120465177
A,Note: for a complete list of authors see reference number A59428 below
                                                                                                                                                                                                                                                                                                    A.Residies, 1-237 (TAN)
A.Gross references: GB:X59504; NID:4561; PIDN:CAA42092.1; PID:4562
C.Supertamily: prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PB 2; Lenath 246;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 LLICOGNSCPSCCPDVSD1PLDLLXELFLNATLLSQST 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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Octob: Section 6.1

Host Local Similarity 19.5%; Prod. No. 61;
Matches 15; Conservative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N. Superfamily: polizzinas aenome polyprotein.
O. Kepwords: aenome linkel prefeit; porteetid; trusterase: prosphoprotein; polypratein.
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CrSqFort.melly: transcription tactor out-1: home-doox bazed epy: P-0 domain homology
CrSqFort.melly: CNA birdings homo-dooy; craciery: transcript bes peopletion
PST-4974-medic: F-00 domain.homo-dooy; (transcription besonder): PST-4974-medic: B-00 domain.homo-dooy; (transcription):
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Cisperies: Kenepos incris (Attican clawed froq)
Cipate: 21 Nor Port #septemee_perision 10-New-1995 #text_change 15 cet 1999
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C:Accession: S12184

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0.04; Scott 61; 108 z; Length 114; Rest Local Similarity 44,48; Pred. No. 26;

11, 11,4013

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5.2 AIYEEKSTE SCHPEENMEEALENVIKSE 651 28 AUNUSEENMERERULERWINDARHIDEL 55

FESSIO 119 81472a hypotheticai protein - bovine

Conservation

Materials 14:

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Query Match 0.6%
Best Local Similarity 22.4%
Matches 15; Conservative
      Ajornss-references: GR:M58706
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A;Accession: T21639
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Atthors: Forreira, V.C.A.; Ferro, J.A.; Frada, J.S.; Franca, S.C.; Franco, M.C.; Frober J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, E.; Kuraman, F.P.; Laigr Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.M.F.; Matshawar, A.Y.; W.F.; M.C.F.M.; Miracca, E.C.; M.Y.; Martins, E.M.F.; Matshawar, A.Y.; W.F., Y.C.F.M.; Miracca, E.C.; M.Y.; Miracca, E.C.; M.Y.; C.Y.; F.G.; Numes, E.R.; Girckia, M.A.; de Oliveira, M.C.; de Lirodia, P.C.; Filmieri, E.Y.; Filmieri, M.A.; Filmieri, M.A.; Verjevski Almeida, S.; Vettore, A.L.; A.K.; Filmieri, A.S.; Vettore, A.L.;
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R:Alternate names: 6-hydroxymetBy1-7.9 dibydroptocin pyropbospbokinisso; 7.8-dibydro-6-hy
N:Contains, 2 amiso 4-hydroxym ( SydroxymetBy1dibydroptociding pyropbospbokinase (PC 2-7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Cochliobolus heterostrophus, Bipolaris maydis
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1695 TAVKLIAPBEKREEKNVLGSALLCIAFVTSTIFALAIPQIDGIMPSILUTMKNTSELVSSE 1754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL; X74455; NID: g437988; PIDN: CAA52464.1; PID: 9437989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 TAAALQLMEQSEPRORIXRALSPIRBETOFILIDOPPALSLITVNALTAADSVIVENOCE 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Parkinson, C.; Luo, H.; Knight, A.; Ahlquist, J.; Perlin, M.H. submitted to the EMBL Data Library, August 1993
A:Description: Phylogenetic analyses using the gamma tubulin gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%, Store 61, DB 2, Length 264, 27.9%, Pred. No. 69;
tive 12; Mismatches 50; Indels
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Hest Local Similarity 28.00.
New 14, Conservative
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A; Accession: $40209
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Best Local Similarity
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A:Molecule type: DNA
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Rytopez, P.; Greenberg, B.; Lacks, S.A. J. Bacteriol, 172, 478-4774, 1990 A.Fitle: DNA sequence of folate biosynthesis gene saib, encoding hydroxymethyldihydrogue A.Reference number: A36704; MOID:90368525

A;Residues: 1-270 <LOP>

A: Molecule type: DNA

Asstatus: preliminary

A; Accession: A36704

C;Date: 10-Sep-1999 #sequence\_revision 10-Sep 1999 #text\_change 10-Sep-1999

C;Species: Strephococous pheumoniae

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C; Accession: A46704

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F.2-119 Domain. Seasono et algebraye by the cyme by dibyde precision py: ple apply 85.75 and in... py: ple apply 85.85.75 and py: ple apply 85.85 and py: ple a
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A,Experimental source: clone F10G8
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A,Closs-teferences. EMBL.281074, FIDN.CAR03336.1, GSFOR.GN09022; FFSPEFF2B6.5
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F3286.5 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15 Oct-1999 #text_change 20 Jun-2000
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G;Superfamily, Cucnorhabditis elegans hypothetical pretain P32R6
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                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 61; DB 1; Length 270; 35.3%; Pred. No. 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16, indels
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A,Accession, 720726
A,Status: preliminary; translated from GR/EMRU,DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1747 TSELVSSEVYLLSALAALQKVVETLPHFISPYLE 1780
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submitted to the FMRL Data Library, October 1996
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Cispectes: Helicobacter pylori
Cibate: 09-Aug-1957 #sequence_revision 09-Aug-1997 #text_change 08 oct-1999
Ciracession: B646450 O.; Kerlavage, A.K.; Clayton, P.A.; Suffon, G.G.; Ficischmann, P. Peterson, S.; Loffus, H.; Richardson, D.; Lodson, F.; Kialak, H.G.; Sledek, A.; McKe son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthery, Nature 388, 549-547, 1997
Arathers: Wallin, F.; Hayes, W.S.; Horrdensky, M.; Karpy, P.D.; Smith, H.O.; Frasci, Arathers: number: Ad520; Muji0:97.49467
Araterence number: A64520; Muji0:97.49467
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A;Accession: D71937.
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A)Cross-references: GB:AE001473; GB:AE001449: NID:04154910; PIDN:AAD05945,1; PID:0415
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Nature 397, 176-180, 1999
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                                                                                                                                                                                                                                                                                                                                                                             hypotherical preveln jhp6482 - Helicobacter pylori (strain J99)
C.Species: Helicobacter pylori
A.Variety: strain J99
C.Date: 12 Feb 1999 #sequence_rovision 12-Feb-1999 #text_change UB-Oct-1999
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62 SEPANDALVNI,SOKCELAKKMI CMGILIKVAMDMILIKPE 99
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A;Residues: 1-348 <ToM>
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Altitude J.Z., Pul-Pen, 1979.
A.Pritterence transfer and analysis of chromosome z of the piant Arabidopsis thaliana.
A.Porterence transfer: A64420; M. Higgine 8487.
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A.A.* Peror maker: As6141; MRID:21046719
A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* Perol Mainor; A.A.* P
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Chemitics:
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CAP-ession: (M467)
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26.7%; Pred. No. 79;
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A;Residues: 1 440 <ROU> A;Cross-reterences: EMBL:ACG04165; NID:93150x90; Pib.43153435

A; Status: translated from GB/EMBL/DDBJ

A; Accession: T00583

A; Molecule type: DNA

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Gene 113, 275-280, 1992 A,Title: The genomic locus of the human hemopoietic specific cell protein tyresine ki
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                                                                                                                                                                                          Rjókano, Y.; Sugimeto, Y.; Fukueka, M.; Matsui, A.; Nadata, K.; Nozawa, Y.
Biochem. Biophys. Res. Commun. 181, 1137-1144, 1991
Agritus. Identification of rat cDMA exceding hok tyriging Finian from monskyrgovytes.
Agreforence number: 191321; MHTD:92109719
                                                        protein tyrosine kinase (EG 2.7.1.112) hok - rat
CySpecies. Rattus norvegicus (Norway rat)
2.59-eius. Rattus norvegicus (norway rat)
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R:Hradetzky, D., Strekhardt, K.; Rumbsamen-Waigmann, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: GB.S74141; NID.4241436, FIDM:AAD20754.1; PID:4241437
A,Experimental source: megakaryosyte
P:Rema, V.; Swarup, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNÅ
A;Residuos: 1 50,7V7,52-204.7R7,206-305,7T7,307-503-<REM>
A;Closs-tefetences. EMBL,X62345, NID.957581, PIDH.CAA44218.1; PIP-357582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the FMBL Data Library, December 1991
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                                                                                                                                                                          C;Accession: J01321; S18974
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A; Rusidues: 1 505 <QUI>
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A. Residues: 1 502 70KA>
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Gene 113, 275-280,
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Mol. Cell. Biol. 11, 4448-4454, 1991
Aptrille: Dilfrential requiation of glucose transporter isoforms by the src oncodence in A;Reference number: A41264; MUID:91342545
A;Accession: A41264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.Experimental source: cultivar Columbia
Rtin, X.; Kaul, S.; Rounsiey, S.D.; Shea, T.P., Benits, M.L.; Town, C.D.; Fujii, C.Y.,
M.; Koo, H.; Moffat, K.S., Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, E.
enss, D.; Nichman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
probable indole-3-acetate beta-qlucosyltranslerase T27El3.11 - Arabidopsis thaliana
                                                                                                                                         Rikounsley, 3.D., Lin, X., kutchum, k.A., Crosk, M.F., Brandon, F.C., Sykos, S.M., Submitted to the EMBL Data Library, May 1998
Asbescription: Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence.
Asketerence number: Z14178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402, 761-768, 1999
AyTitle: Sequence and analysis of chromosome 2 of the plant Arabidepsis thaliana.
AyReference number: A84420, MUTD.20083487
A:Accession: B84705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross references: GB: AE002093: NIP: 43150445; PIDN : AAT16457 1: GSPDR : GNO0139
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C;Joure: 28 Huy 1992 #sequence_revision 28 May-1992 #tox*_change 04-Sep-1998
C;Accession: A41264
                            Species: Arabidopsis thatiana (mouse-rar cress)
Spate: 01-Peb-1999 #sequence_revision 01 Peb 1999 #text_change 23-Mai-zour
Spacession: T00583; B84705
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0.6%; Score 61; DB 2; Length 440;

CySuperfamily: flamoned on-qlumosyltransferase

A; Gene: At2g 30150; T27E13.11

A; Map position: 2 A; Introns: 149/1

1.440 <SIO>

A;Status: preliminary

A; Molecule type: DNA

A; Residues. : Genetics: 28.3%; Pred. No. 1.3e+02; tive 13; Mismatches 29;

13, Conscruative

Matches

ò 90

Best Local Similarity

Query Match

20; indels

1028 EMVLSQLLPMAEQLLEKIQKEPTAVLKDEAMVLHITIGKYNEFSVS 1073

glucose transport protein 3 - chicken

RESULT 127 A41264

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Approximate in the modes of S.M16591
Approximate the modes given for 3-Cys (TCG) is inconsistent with the authors' franslution
Bizingler, S.F.; Marth, J.D.; Lewis, D.B.; Perfmutter, R.M.
Moi. Coll. Biol. 7, 2276-22285, 1987
Approximately production gravity blues, grav. (bek) protected by expressed in cells of Approximate modes. Approximate Mull: 87257943
Cypecies: Homo sapiens (EC 2.7.1.112) hrk - human Cyspecies: Homo sapiens (man)
Cyspecies: Homo sapiens (man)
Cybete: 31-pec-1989 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
Cybete: 31-pec-1989; #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
Cybete: 31-pec-1989; #sequence_revision 1.38268; $31103
Rejuintreil, N.; Lebo, R.; Varmus, H.; Bishop, J.M.; Pettenati, M.J.; Le Beau, M.M.;
Mol. Cell. Biol. 7, 2267 2275, 1987
A;Title: identification of a human yene (HCK) that encodes a protein-tyrosine kinaso A;Reference number. A27811, MUID:87257942
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0.68; Secure 61; DB 2; Tempth 496; 24:18; Pred. No. 1.40:52; 24:18, Pred. No. 1.40:52; Elve 16; Mismatches 44: Indels

0.69 Best Local Similarity 24.19 Matches 19; Conservative

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9

C;Superfamily: glucose transport protein C;Keywords: transmembrane protein

A;Cross-references: GB:M37785

A; Residues: 1-496 <WHL>

A; Status: preliminary

A: Molecule type: mRNA

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submitted to the EMBL Data Library. July 1994
A;Description: Plasmodium falciparum: recombination within the C-terminal region of m
A;Reterence number: $47262
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                                                                                                                                                                          merozoite surface antigen 1 - mala:ia parasite (Plasmodium falciparum) (strain Po 71)
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C.Dato: 14:Pb-1962 #sequence_revision 14 Feb 1992 #text_change 15 Fep 2009
C.Dato: 14:Pb-1962 #sequence_revision 14 folds
C.Accession: A39223, S30094: T39660: T40139
R.Wanq, Y.; Xu, H.P.; Riqqs, M.; Rodqers, L.; Wiqler, M.
Mol. Coll. Bloot. 11, $554-5583, 1901
A.Title: Dyrz, a Schizosaccharomyces pembe gene encoding a protein kinase capable of
A.Reference number: A39723; MULD:99260705
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Experimental source: strain 9724:: c.samid cHz?
K:Wood, V.: Rajandroum, M.A.; Retroll. H.G.; Skelton, J.: Charcher, C.M.
submitted to the EMBL Data Library, June 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Molecule type: DNA
A:Residues, 298 659 -WOZ:
A:Cross-references: BMBL:297211: PTDR:CABIC)50.11: OSPUB:GNGCOC7: SPDE:STBC-FTZ:O1
A:Experimental source: strain 972h : cosmid c2F12
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                                                                                                                                                                                                                                           CySpecies: Plasmodium falciparum
AyVariety: strain Re-71
CyDate: 06-Jan-1995 #soquence_povision 76-38]-1996 #foxt_change 09-Jun 2008
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A)Experimental source: strain Ro-7;
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R;Styrkarsdottir, U.: Eqel, R.; Nielsen, O.
Mol. Cen. Genet. 235: 122-130, 1992
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A)Cross references: EMBL:X68851; NID:q5106; PHAN:CAA4κ731.1: PHL:q51u?
R)Wood, V.: Rajandream, M.A.; Barrell, B.G.; Skelton, J.: Churcher, C.M.
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translated from OP, EMPL, 1008J
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Act chas 16, Consultative 19 Nishatches
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P;Tolle, P ; Bujard, B ; Cooper, J.A.
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A;Accession: T40139
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A;Residues: 1-659 <WAN>
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F.24/257/ped. s. project Kinase Arritation activity.
F.24/257/ped. s. project William (Charles and Charles activity) astatus predicted
F.2/Medified site; painning (Cys) (covalent) #status predicted
F.20/Active site; Lys #status predicted
F.00/Khether activity presplate (Tyr) (covalent) (ky artephosphorylation) #status predict
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myristylation; phosper to formal transfer to the formal transfer formal transfer to the formal transfer                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prinn, X.; Kard. S.; Rodrakey, S.D.; Shea, U.P.; Benito, M.L.; Town, C.D.; Enjil, C.Y.; M.; Kor, H.; Mellat, R.S.; Treale, L.A.; Shen, M.; VunAken, S.E.; Umayam, L.; Tallen, L., euss, D.; Niemmo, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nitare doz. 761-768.
Axiocompore number: F114 or MILLO 224150 or Axiocompore 191149

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AAPENESSION: F84471
A.Strible: Performancy
A.Boricoule Type: DNA
A.Roschdos: ['80 - Sive.
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                                                                                                                          1246 LEPS PER PER PER STREET PARTICIPAL STANSFER HEITALL LATVAGE 1314
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0.74; Score 61: 148-1; Lorath 505; Bost Local Similarity 21.78; Pred. No. 1.50-02; Matches 10: Conservative 15; Mismatches 21; Indels
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22.4%; Pred; No; 1.7e+02;
15; Mingatcher 25;
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A) Consist references; other 10 GOC OMINE 142 870
A) Mapping position; 20411 20412
A) Mapping position; 20411 20412
C) Futer four;
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CiSperios: Arabidopsis thailan (monso-ear cress)
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Best Local Similarity
Matches (1) of gravity
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ArMap position: 2
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FR4471
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RESULT 137
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A:Experimental source: strain S288G
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         C.Superitudii; protein klidase Lyiž, protein klidase hotology, SAM Lomening C.Superitudii; protein klidase C.Keywords: ATP: phosphotransionase; serine/threoning-specific protein klidase Flifo-fromain: SAM Lomening sAM Lomening Klidase homology 2KIN2 F130-408/Region, protein klidase ATP-binding motif
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Ajerosa references. GB.AF661576, MILLy3452316, FIDM.AAC3285411, Filesy3452337
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C,Datē: 05-Peh-1999 #sequence_revision 05-Peh-1999 #rext_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein Yoldilw - yeast (Saccharomyees cerevisiae)
NyAlternate names: hypothetical protein 02321
Cisperies: Saccharomyees cerevisiae
Cibate: 12 Jul-1996 #sequence_revision 12-Jul-1996 #text_change 05-Nov-1999
Cibatesion: S66699
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                                                                                                                                                                                                                                                                                                                                                                                                                   170 AALSSOSSLSPELSSVLPTSTOKRSVPSNNAKPFKSVQKTPGFLINSKL 218
                                                                                                                                                                                                                                       0.6%; Score 61; DB 1; Length 659;
                                                                                                                                                                                                                                                                                                 23; Indels
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ER;Tomarev, S.L.: Zimovieva, E.D.: Chary, R.; Hawes, N.E.
Blochem, Ricphys Res Commun. 248, red-ried, 1998
A;Title: Characterization of the mouse Prox1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RiHughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A; Reference number: $66685
                                                                                                                                                                                                                                                                 Best Local Similarity 30.6%, Fred. No. 2c:02;
Matches 15, Conservative 11; Mismatches
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A,Accession: JEUZ69
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A;Introns: 575/3: 611/3: 676/3
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A;Residues: 1-714 <HUG>
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A; Map position: 2
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                                                                                                                                                                                                                                          Query Match
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A,Title, Sequence of the fourth gene of Luman rotarizases recommend from asymptomatic A,Reference number: A28839; MUID:88275070
A.Accession: C28839
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                                                                                                                                                                                                                                                                                             C. Accession: T48463 April 2000 Buysshaert, C. Passeville, R.; De Clerek, R.; Ewes, H.W., Rudd, S., Lemcke, K.; Mayor, K.P.X.
Ewes, H.W., Rudd, S., Lemcke, K.; Mayor, K.P.X.
Ewes, H.W., Rudd, S., Lemcke, K.; Mayor, K.P.X.
A. Reference number: 224491
A. Accession: T48463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Outer layer protein VP3 - hyman rotavirus A (sorotype 3 strain P)
N;Alternate names: hemagqlutinin
N;Contains: outer capsid protein VP5; outer capsid protein VP8
C;Species: human rotavirus A
C;Species: human rotavirus A
                                                                                                                                                                                                                                                               ejSpheies: Arābidopsis thaliana (mouse-ear cress)
C,Late: 10 Apr 1009u #segueuce_terisien 20 Apr 2000
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C)Keywords: cápsid protein; coat protein; glycoprotein; hemagalutinin
P:1-440/Product: outer capsid protein VPB #saturus predicted «VPB»
P:241-246/Region: clasayage provessing #status predicted
F;247-775/Product: outer capsid protein VPS #status predicted «VPS»
F;25,50,97,129,120,120,294,689,589,599,998,800 proling site canb hydrate
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1472 KIPPERBETTPKAVSPNKSESOPEMLØVPNVETHTSKOLRHFK 1514
                                 A, Experimenta, source: cultivar Columbia; BAC clone IlE3
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                                                                                                                                                                                                                      hypothetical protein T1E3.30 - Arabidopsis thaliana
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A;Note: T1E3.30
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A; Residues. 1 775 <60K>
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A;Molecule type: DNA
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R;Gorciglia, M.; Gre
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Tission yeast (Schillosan harenyes peaker)

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Erillon, K.; Harris, L.; Barrell, B.J.; Kajandream, M.A.; Wood, V. sephiniriod to the EMBL lata Library, Auqust 1995.
A.Retricov number: Z2179.2
A.Retricov number: Z2179.2

Abstatos, prefiminary: translated from 38/RMBL/DDBC AbM certie type: DNA

A: Residues: 1 B63 col.1.

Archert SPLB: SPA 7.181, o 40

Continue 1.3s.

A:Map position: 1

2071 LKTROSSPRVMFAALITVLALAFMI KENYTVIT PESTPFLAELMEDPSE 2119 606 MOTAPROSVAHELVIJAIGAMMUSLEBOFBVYVPSFVPFIJSSALSNEOR 654

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protable practing Kinase (imported). Anabidopsis thaliana

"Accession: 1096558

coery Match 0.0%; Score fit 146.2; Langth 863; Best Local Similarity 26.5%; Pred, No. 2.70+02; Matches 14; Conservative 12; Mismatches 24; Endels

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R;Read, F.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, L.F.; White, -.; Hicker, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, K.; Kolonay, J.; McClarity, S.; Salzbernucleic Acids Res. 28, 1397-1406, 2000
AJTILLE: Genome sequences of Chlamydia trachomatis Moduland Chiamydia promobiae ARPS A;Reterence number: AB1500; MUID:20150255
A;Accession: H81683
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A)Srows references: OB(ABC02329; CB(ABC01162) NID(47190640; FILM(AAFC01011) FIL(1719-
A)Experimental source, strain Nigg (MoPn)
C)Geneties:
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                                                                                                                                               A.Cross-references: DMBL:035022; NID:04584536; PID:04584547
C.Fundrion:
A.Description: is part of a cis-Goldi matrix and has a role in maintaining cis Goldi
C.Keywords: Goldi apparatus
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A,Reference number: A75250; MUID:20036896
A,Accession: F75461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.White, G., Eisen, J.A., Heidelbelq, J.F., Hickey, E.K.: Peterson, J.D.: Dodson, J.M.: Shen, M.: Vennehevan, J.J.: Jam. P.: McDonald, L.: Utterback, T.: Zahewski, S.: Smith, B.O.: Venter, J.C.: Fraser, G.M.Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-directed RNA polymerase, beta' sabunit Tehnomoreus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Dato; 03-Dec 1999 #sequence_revision 03 Dec 1999 #text_change 18-Aug-Zoun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 helicase, probable 19962 [Emported] - Chlamydia muridarum (strain Nica)
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31 Mar 2000 #segaencc_revisio, 31:Mar-2000 #text_chanae 11 May 2050
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C;Superfamily: Escherichia coli DNA-directed RNA polymerase beta' chain
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Best Local Similarity 24.1%; Pred. No. 3.2e+02;
Matches 14, Conservative 15, Mismatches 29, indels
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                                                                                                             A. Kesidues, 1 786 - MAK
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Asstatus: preliminary:
AsMolecule type: mRNA
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Asherestone number: Advisor District M. S. A.; Arcession, 196588
Asherestone number: Advisor Distribution of the plant Arabidopsis.
Asherestone type: LNA
Asherest H. C. Schuller, M. M. G.; Phys. M. C.; Phys. Asherestone to the context of the contex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archessireferences: EMBLANESS Ang FIRMATABBIRSAN, METER MAGNEG, STDELSPACIBLOSS ArExperimental scarrer strain 972h-; cosmid elbl
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                                        Cyspectes: Schizosarchatomyces pumice
Cibite: 04 Dec-1999 #sequence_regision 64 Dec-1999 #text_change 64 Dec-1999
Cycression: Fe005
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Cibate: uz Mar 2001 #aespecre_recisios 02 Mar 2001 #text_change 31-Mar-2001
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Cilate: 16-Tai-1999 #seepaleee_revision 16-Jal-1999 #text_champ 16-Tal-1999
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0.68; Score 61; DB 2; Langth 1546;

Query Match

submitted to the EMBG Gata Library, April 1999

C; Accession: F10754

R; Nakamura, N.

A; keterence comber: 217120 A; A; cossion: 11:754

cis doldi mathix protein SMM to - rat

RESULT 139 [16754

3

Length 876

Prod. No. 2.86+02; 9: Mismatches 15; Indels

0.6%; Score 61; DB 2; 33.3%; Pred, No. 2.8e+02

. \* . . .

Matches 12: Conservative

Query Match Best Local Similarity

ApMap position: 1

12.9 THEYNQUSELIACVEPPETFIFVRVIQLEKINNSKH 158 145 HPCRQDHGQTTDWTGETTPFISSLEERFINNNIY 180

DNA-directed RNA polymerase (EC 2.7.7.5) beta' chain - Aquifex aeolicus

0;

8; Indels

; Pred. No. 5.4e+02; 11; Mismatches 8

36.78;

Rest Local Similarity

Conservative

1523 OLLSSNAPLKKVVPSGGPPTLPGT PPPLLP 1552 563 RUINKNNRLKKUMSQCAPDMIIRNEKRMLQ 592

> S 9

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A.Molecule type: DNA
A.Residues. 1104-1726 (MEB2)
A.Cross-references: EMBLY303331
A.Cross-references: EMBLY303331
C.Comment. The detoculte stayes of different strains have strain-specific surface ant
C.Comment. The detoculte strains of an inferior of an diameter. The
C.Superfamily; major merosoite surface antiqen. tandem repeat
C.Superfamily; major merosoite, surface antiqen. tandem repeat
C.Superfamily; major merosoite, surface antiqen. tandem repeat
E.J.-19700main: siqual sequence #status predicted <SIC>
E.J.-19700main: siqual sequence #status predicted <MAT>
E.J.-19700main: 3-residue repeats (F-6-1)
E.J.-19700main: 3-residue repeats (F-6-1)
E.J.-19700main: 3-residue repeats (F-6-1)
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A/Title: Piasmodium falciparum. Gene structure and hydropathy profile of the major me A;Reference number: A45948; MUID:89005525
CyDate: 36-Sep 1987 #Sequence_revision 31 Mar 1991 #Lext_change 99:Jun-2000 CyAccession: A23386; S06361
RyWeber, J.L.; Leininger, W.M.; Lyon, J.A.
Nucleic Acids Res. 14, 3311-3323, 1986
Ayfitle: Variation in the gene encoding a major metozoite surface attigen of the huma Ayfeference number: A23386; MBID:86205236
                                                                                                                                                                                                                                                                                                                                                                                                                 A, Title: Merozolte surface protein sequence from the Camp strain of the human malaria A, Reference number: $06361; MUID:88143999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              major merozoite surface antigen precursor - malaria parasite (Plasmodium Talciparum)
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C;Date: 15:Oct.1999 #sequence_revision 15 (at.1392) #taxt_charar 21 Jan-2000
C;Accession: T29140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Date. 38 Sep 1993 #sequence_revision 30-sep-1983 #****_rhange 69 Jun-2000
C; Accession: A45948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1726;
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30.2%; Pred. No. 6.1e+02;
Mismatches 27; Indels
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hypothetical protein K11C4.3 - Cacnorhabditis elegans
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A;Cross-references: GB:M37213
C;Superfamily: major merozoite surface antigen
                                                                                                                                                                                                                                                                                                                                                              Sim, B.K.L.; Lyon, J.A.; Wolff,
                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X03831
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                1 1104 <WEB1>
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Matches 16; Conserv
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Nucleic Acids Pes
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N;Alternate names: 195% 41/coprotein
C;Species: Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum) (is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribeckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.P.; Od
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references, GR,AEG06764, HfD;G2984196; FIDN:AAC67724.1, FTF ;C984193, GR APO^0665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apritle: The complete genome of the hyporthormophilic bacterium Aquifex agolicus.
Apreference number: A70300: MHD-98196666
Abacession: G70466
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C:Species: Plasmodium falciparum
C:Date: 28 Oct-1994 #sequence_revision 28-Set-1994 #text_chang= 69 Uun-2009
C:Accession: A54498
                                                                                                                                                                                                                                                                                                                                                                                                                 C.Species: Aquifex abolicus
C.Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 18-Jun-1999
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C;Superfamily: major merozoite surface antigen
C;Reywords: surface antigen
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0.6%; Score 61; DB 2; Length 1574, 33 3%; Pred No. 5.5e+02;

C; Keywords: nucleotidyltransferase; transcription

A, Experimental source: strain VF5

A; Gene: rpoC

C; Genetics:

A;Residues: 1-1574 <AQE>

A; Molecule type: DNA

Nature 392, 353-358, 1998

G70456

C;Accession:

RESULT 142

12; Mismatches 16; Indels

11; Conservative

Matches

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Best Local Similarity

Query Match

0.6%; Score 61; DB 2; Length 1701; 30.2%: Pred. No. 6e-02;

Local similarity 30.2%: Pred. No. 66402 es. 16. Conservative 10: Mismatches

Omery Match

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RESULT 144

A; Residues: 1-1701 <PET>

A;Status: preliminary A; Molecule type: DNA

A; Accession: A54498

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Alchess references: EMBL:728902; NIU:42286312; FIUN:AAC49817.1; FID:42286313
Allapetimental source, strain M201
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A;Residues: 1-248 <KAN>
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A:Introns: 105,''
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RiMerchant, S.; Rogorad, L. J. M. Williams, 1987. J. M. M. M. M. M. M. Williams, 262, 9952-9967, 1987. Affitte. The Gittl. Prepressible plastidic extochrome c. Cloning and sequence of a commune for exterence number: A27113; MUID:87259547. A; Meterssion: A27113.
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A.Criss refered is S. SP. 92774, BIT 177407, FIRELAAAKOBLEE PHOSIDE 2407
A.Criss refered is Sequence, including the amino end of the matoric protein, were defined by R.H.L. Li, H.H., Singer, J., Morchant, S.
B.HILL, K.L., Li, H.H., Singer, J., Morchant, S.
J. Bridle, Chem. 266, 15060-15067, 1991
A.Title: Isolation and structural characterization of the Chlamydomenas reinheadtil quantities.
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A)Chosa references: 08M67448; NILca167414; Film)AABOU7.29.1; PID:a167415
C)Superfamily: cycofrome 65. cyrolrome 65. homology
C)Reywords: chloroplast; chromoprofein; electron transter; hemo: iron; metalloprofein.
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Molecules and Cells 7, 559-566, 1997
A.H.He; Characterization of Lwo rice Mass Few genes that control flowering times.
A.Kererence number: 215254; Müllo:97479823
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Fig. 118 Preduct Type brown of metal secretimental MAF.
Fig. 118 Preduction of homology (SYS).
Fig. 175 Tabusian repreduction (Shorology (SYS))
Fig. 75, 48 Each of Co. (Sys) (Sy
                                                                                                                                                                                                                                                                                                                         1241 ESARPETANEGRAPPRENGAMETAFSQAVERGEPRENGELER EPROFEVER 1500
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C.Dafe: 29-Sep-1999 #seppence_register 20 Sep 1999 #fext_change 21-Jul-zoon
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Species: Chlampdomonas reinhardtii
7 Lat. 37 St. 1962 #8. perceit [2] n. 67 c. 1967 #10 ct. hande oceMuticos
Charcession: A27113; A39341
        Length 4574
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25.88; Pred, No. 48;
                                                                                                                                                                47; Indels
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0.68; Score 51; 186-2; 25.88; Pred, No. 1.90+34; live 12; Misharthes 57
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Best Local Similarity 25.8%: Pred. No. 48:
Matches 11, Omeerwaline 11, Hismatches
                Query Match
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C; Genetics:

Gaps

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A)CIVAS IEFERENCES. GB:AF001508, GB.BA903004, NID:410172890; PIDN:EAE04042.1; GSPDB:G
A)Experimental source: strain C-125
C)Genetics:
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A.Tilia: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A; Peference condet. A83650, MHTD.20263314
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R.Tomb, J.F.; White, O.; Kerlaruge, A.P.; Clayton, P.A.; Sutton, G.G.; Fleischmann, R. Peterson, S.; Loftus, B.; Pichardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKelson, J.D.; Kelley, J.M.; Culton, M.D.; Weidman, J.M.; Fujji, C.; Bowman, C., Watthey, Nature 388, 539-547, 1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cnoyl [acyl-currier-protein] reductase (NADH) (FC 1 3 1 9) - Holicobacter pylori (str N;Alternate names: enoyl-ACP reductase, short-chain alcohol dehydroqenase homolog env C;Species: Helicobacter pylori
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Matches 14; Conservative 8; Mismatches 17:
DB 2, Length 263;
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                                                                                                7; Mismatches 17;
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                                                                                                                                                                                                1857 KEELTSHQSQLTAFFLEALDFPAQHSENDFFFVGKTF 1893
                                                                                                                                                                                                                                                                                           121 KQFLASHSHFNALFLGKCEEEAEKSEFTLQDIDSTD 157
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     0.6%; Score 60,
35.1%; Prod. No
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A) Residues: 1-278 <STO>
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A;Residues: 1 275 (TOM)
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A;Introns: 38,7 = 60.4, 19274- 17471- 22473
C;Superfamilty: Caencrhabdilis clesats hgpertalistic to dein PS256-7; Pet demain homebegy
P:91-195/Londin: POZ domain homebogy <POZz
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A;Title: Comparison of the complete DNA sequences of human herposvirus 6 variants A and A; Reference number: 222732, MOLD.99412339
A; Accession: 144041
                         A;Gene: MADS8
C;Superfamily: transcription factor squar setum response factor DNA-binding domain homol
F;2-57/bomain: setum response factor DNA-binding domain homology <SPES
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J. Virol. 73, 8053-8063, 1995
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A;Residues: 1-263 <WAM>
A;Cross-references. EMBL.AF343645; FIEN.AAB94975,1; GSPDR-GNORD20; CESP-F5206 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ς.
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A)Cross-references: BMBL:AB021506; HID:94995977; PIDN:PAA78302 1; PID:94996069
A)Experimental source: strain HST; pop. variant R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Species: Caenorhabditis elegans
C,Date. 23:00t 1999 #sequence_resision 29:00t 1999 #text_change 28-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qiyroprotein L [imported] - human herpesvirus 6 (strain HST)
N;Allernate names, q}ycoprotein H accessory protein
C;Sporeis: human herpesvirus 6
A;Variety: strain HST
C;Date: 21 Jan 2000 #Sequence_revision 21 Jan 2000 #text_change 21-Tn1-2000
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Best Local Similarity 25.6%; Pred. No. 88;
Matchas II, Conservatire 10; Mismatches 22; Indels
                                                                                                                                                                                                                                                        Guist Match 6.6%, Score 60; EB 2, Length 248, Best Local Similarity 20.5%; Pred. No. 87;
Matches 18; Conservative 21; Mismatches 49; Indels
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A;Reference number: 221226
A;Accession: T32802
A;Status: preliminary; +ranslated from GR/FMH./DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GBzEMBL/iJUbJ
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submitted to the EMBL Data Library, December 1997
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C;Genetics: A; Note: U82

RESULT 151 F44041

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RESULT 152

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RESULT 153

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Nature 490, 249-255, 1997
A.Authors: Foulder, D.; Fritz, C.; Polita, M.; Fajita, Y.; Fuma, S.; Gaileri, A.; Gaileri, A.; Gaileri, D.; Fritz, C.; Polita, M.; Fajita, Y.; Fuma, S.; Gaileri, A.; Garteri, B.; Moseno, S.; Hullo, M.; Korita, K.; Lapidos, A.; Hardino, A.; Authors: Lauber, J.; Lazarevic, V.; Ice, S.M.; Levine, A.; Liu, H.; Masuda, S.; Man A.; M.; Ogawa, K.; Ogiwara, A.; Oudeqa, B.; Park, S.H.; Parto, V.; Polh, T.M.; Porteto Pleger, M.; Pivolta, C.; Pocha, E.; Pocha, R.; Posto, M.; Sadono, Y.; Safor, T.; Scaul, A.Authors: Schiebin, S.; Schieber, E.; Pocha, M.; Sadono, Y.; Safor, T.; Scaul, A. Authors: Poshikawa, H.F.; Zumscho, H.; Yoshikawa, H.; Danchin, A.; Tosato, V.; Ushiya, A.; Authors: Yoshikawa, H.F.; Zumscho, H.; Yoshikawa, H.; Danchin, A.; Authors: Sequence of the Gram positive bacterium Bacillus subtili
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A) Orosa references: GREVOATTI: GREATQUATZG: NTE-47633695 FIRM:CABLEVP7.1: FIRSTAN A) Experimental source: strain 168
R:Yanouri, A.; Daniel, R.A.: Errintton, J.; Buchanan, C.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Title: Cloning and sequencing of the cell division gene papa, which encudes penici;
A:Reference number, A53292, MOID:94004553
A:Accession: A53292
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A:Reference number: A81250; MUID:24456912
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Fetrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Math. J. Math. Str. Brandship Leads in Al-Mar. P. Mich., Stat., State 17, Math. 2000.
CACCESSION: BRIZ53
Kyperthill. J. Wern, B.W.: Mungall, K.: Ketley, J.M.: Churcher, G.: Basham, D.: Ch. C.W.: Quall, M.: Rajandream, M.A.: Rutherford, K.M.: VanVilet, A.: Whitehead, S.: Nature 403, 665-668, 2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-311 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: L09703; NID: q404162; PIDN: AAC44845.1; PID: q404144
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32.3%; Pred. No. 1.16+02;
Mammarches 11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A69580; MIID: 98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175, 7604-7616, 1993
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Matches 10; Conservative
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A;Residues: 108-311 <YAN>
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Tispectors: Barrillas subtitis
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Cravession: Pérdad: Affica.
Extract: F.: Outsaward N.: Moszer, L.: Albertini, A.M.: Alloni, G.: Azevedo, V.: Berter
C.: Bren. S.: Brouillet. S.: Bruschi, C.V.: Gaidwell, B.; Capuano, V.: Garter, N.M.: Gid
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Nature 40s, 189-264, 2000
ArFiller Complete quenomes sequence of Psycadomonas aeruginosa PA01, an opportunistic paths
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sebmitted to the EMBS Lata Library, Rockett 1995. Atterbrace number: 219817. Atterbrace number: 219817. Atterbrace number: 729919. Atterbrace trom one/EMBsL/DDBJ A.Status: pre-laminary, translated trom one/EMBsL/DDBJ

Caenorhabditis elegans

124919 hypotherical profess ReSASO.8

R. Matthews, L.

0.0%) Shore 6.0 108.2; Length 405; (8.0%) Pred. No. 1.10.02; (1.0%) 7; Mismatches 15; Indels

Local Similarity (8.9) PS 14, Conservative

Party Matrix Best Local S

A. Reference number: A82950; MOID: 20437337

A:Accession: H84502 A:Status: preliminary

A: Molectale Type: DNA

A:Experimental source: strain PAOl C:Genetics:

Application PAII45

915 ISSPVVISILINDISPVKEVPRAALO/ILQALS/3VAS 950

Agricology of the contradities of course hypothesical protein K06H6

AsExperimental sources econe E05Alo

A) Map position: 4 A) Map position: 4 A) Intra. (4) (1)

0.2%; Score 60; DB 2; Length 304; 4.8%; Pred. No. 1.16902; ve. 8; Mismatches 8; Indels

Substy Match Best Local Similarity 44.8%;

13; Conservative

Matehes

yib" profein bome baryixA - Ramillus suprilis N:A. efforte names: pope Correction hypothetical protein B

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C.Accession: G96738

RESULT 159

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A;Reference number: A86141; MUID:21016/19

1-384 <STO>

A;Status: preliminary

A;Accession: G96738

A; Molecule type: DNA

A; Residues:

C; Genetics

A; Map position: 1 A; Gene: F14023.4

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C,Accession: T48708
R,Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatu
submitted to the Protein Sequence Database, April 2000
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C;Reywords: transferase
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infert Immin 61, 2172-2181, 1993
A;Title: An aromatic-dependent mutant of the fish pathogen Aeromonas salmonicida is
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C.Species: Neurospora crassa
C.Species: 05-Maj-2000 #sequence_revision 05-Maj 2000 #fext_change 05-May-2000
                                                                                                                                                                                                                                                           C;Species: Aeromonas salmonīcidā
C;Date. 19 Jul 1996 #sequence_revision 19-Jul-1996 #text_change 18-Jun-1999
C;Arresaion: 19959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Status previously translated from GRZPMDL/DDBJ
A Melecule type. DNA
A Postbace: 1 426 PPRS
A CLOSSIDE FOR STOPE OF THE STATE PIDNEARANTEST TO PID G141872
C) Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
O
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Prod No 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Cross references: EMBL:AL353817; GSPOB:GN00112; NCSP:1A9.120
A:Experimental source, cosmid contig 1A9; strain 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h_T^{*}pothetical protein 1A9.120 [imported] - Neurospora crassa
79 AGYIGSHAALRIKESYRVTIVDNLSRGNLAAVRILQELFP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human herpesvirus 1 (strain 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.6e+02;
4; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 60; DR 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Reference number: 139539; MUID:93239331
A,Accession: [39539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2028 ENPLOCHERFORPVTKHLIPCIA 2050
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26.7%;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 DANLQSLLPPSFRKN 228
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A;Accession: T48708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A: Molecule type: DNA
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A;Introns: 54/3
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                                                                                                                                                 RESULT 161
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Nature 408, 816-820, 2000
A; Authors, Huller, J.L.; Jen, X.; Liu, S.X.; Liu, Z.A.; Lucos, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, B.; Marziali, Rizco, M.; Rochey, T.; Rowley, D.; Sakano, H.
A;Authors, Salleberg, S.L.; Schwarte, I.P.; Shins, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Actions assured as a constant of the constant 
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_regision 02-Mar 2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                    hypotherical protein F14023.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-car cress)
C;Date: 02 Mar-2001 #sequence_revision 02 Mar-2001 #1ext_cbingc 23 Mar-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 60; DB 2; Length 419; 41.5%; Pred. No. 1.6e+02;
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Best Local Similarity 41.5% Matches 17; Conservative

Query Match

A; Residues: 1 419 <STO> A;Status: preliminary

A; Map position: 1

A: Molecule type: DNA

A; Accession: E86431

C; Accession: E8643i

RESULT 160

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E86441

A:Note: host Home sapiens (man)

Comment: This protein is required for replication of viral BNA.

variociti zoster virus qene 16 profein

Casupertumbly, varietin abster virus gene Obergeords, CMA binding, CMA bioayorbasis

0.8%; Shore 50; DB 1; Length 488; 52.0%; Pred. No. 1.90-02; 1720 4; Mismatches 5; Indels

101 USPYFILERFAUETLENIE 119 (4) VSAVFLLFFLFR 11.14 | 1 | 4.7

Ė 5

Matches 11: Jonservalive

Similarity

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ABC transporter, permease protein WMB2026 [imported] - Neisseria meningilidis (strain C)Species: Neisseria meningitidis
C)Species: Neisseria meningitidis
C)Bate. 31 Mar 2009 #sequence_terision 31 Mar 2000 #text_change 19 Jan 2001
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A;Authors: Grandi, G.; Sun, L.; Smith, H.D.; Fraser, C.M.; Moxon, E.K.; Rappuoli, R.; A;Attlerse, counder; A81000; Mull:20175755
A;Accession: E81015
probable permease NMA444 [imported] - Neisseria menitalidis (Strain 2249) sereatou, C.Species: Neisseria menitalidis C.Species: Neisseria menitalidis C.Date. 85 May 2000 #sequence_revision 05 May 2000 #sequence_revision May 2000 #sequence_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Cross-references: GB:AL162753; GB:AL157359; NID:q7379120; PIDN:CAR83713.1; FID:q737
A:Experimental source: serogroup A, strain Z2491
C:Geneties:
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A;Experimental source: serodroup B. strain MC58
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(imported) - Chlamydopila parumeni
C;Species: Chlamydophila purumeniae, Chlamydia purumeniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menialfidis 2249)
A;Reference number: A81775, MOID:20222556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clais, 23 Apr 1/20 msequence colision 23 Apr 1/20 mistichange 19 May 2000 C; Accession: P72051; B81615 Marathe, E.; Lammel, C.; Fan, J.; Olimett, L.; Orimwood. Nature denet. 21, 385-389, 1996 Marathe comparative genomes of clamydia pheumoniae and C. trachomatis. A;Reference number: A72000; MULD:99206606
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36.5%; Pred. No. 2.1e+02;
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                         Alithe: The complete DNA sequence of the long unique region in the genome of herpes sim Alforensian Fronta
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about S. Yosh, Y.: Brody, L.L.: Foulter, S.N.: Folger, K.R.: Kas, A.: Larbid, K.: Lim,
A.: Poly, S.: Clson, M.V.
Nature 408, 959-964, 2000
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Asterence number: Ae2950; MLID:20437347
Asterence number: Ae213
Asterence type: DNA
Asterence type
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J. Gen. Virol. 69, 1541-1574, 1988
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POCADE Mainte debydrouenase (acceptor) (EC 1.1.99.16) PA3452 [imported] - Pseudomonas probables: Pseudomonas actuairosa

C. Spendies: Pseudomonas actuairos

C. Spendies: Pseudomonas a
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        Judies vo Junchara #separadre_revision 80 Junchara #text_change 16 Junc2000
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FrMichardt, 5.3: Dalippiple, M.A., Bolan, A., Rokab, B., Perry, E.J., Taylor,
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PRVEDLISVGERES FULRERVIE - 204
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0.6%; Score 50; DB 2; Length 523;

A:Experimental source: strain PAcl

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Accidence Baptara PAN452

// Pred. No. z.le+02;
// Mismatches 43; Indels

Rest Local Similarity 29.5%; Matches 18, Conservative 1

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A; Residues: 1 541 <ARN>

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C;Superfamily; unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
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                                                                                                        Query Match 0.68; Score 60; DR 2: Longth 544; Post Focal Similarity 27.98; Prod. No. 2.2c+02; Matches 17; Conservative 10; Mismatches 34; Indels
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Bost Local Similarity 23.1%; Pred; No 2:30+02;
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C.Date, 22.Apr.1993 #sequence_rev
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A:Kesidues: 1 569 :FOS:
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Satus (2014 #sequence_resision 02 Mar-2001 #sext_change 02-Mar-2001
C;Accession: B66572
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
A;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; IS
A;Title: Comparison of whole qenome sequences of chlamydia pneumoniae J138.
A;Reterence number: A86441; MILD:20130149
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AJExperimental source: strain AR39, HL cells
                                                    A;Cross-references: GB:AE001548, GB:AE001363; NID:94376946; FIDN:AAD18792.1; PID:9437699
                                                                                 A.Experimental source: Strain CWL029
Rikead, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, C., BickGy, C.; Lowlson, B.; Gwinn, M.; M. Ison, W.; DeBoy, R., Kolonay, C.; McClarty, G., Salrberg, Nucleic Acids Res. 28, 1977-1406, 2000
A.Jille: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A.Keference number: A81500; MUID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ryoliver, K., Barris, D., Bandley, S.D., Parkhill, J., Barrell, R.G., Pajandrenm, M.A.
submitted to the EMBL Data Library, April 1999
A;Reterence number: 221573
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274 MENTEVNSLASQIIKTLTEIESLIKESI SCLIVIIQEQR 312 74 LSDQY1GKLIYLVWLTLITTISVLFSGPSGLIVAIVPQK 112

RESULT 168 B86572

a š

Ouery Match 0.6%; Score 60; DB 2; Hest Local Similarity 33.3%; Pred. No. 2.2c+02; Matches 13; Conservative 9; Mismatches 17;

C; Superfamily: apolipoprotein N-acyltransferase

A,Gene: cutE; CP0094

C, Genetics:

A;Molecule type: DNA A;Residues: 1-541 <REA>

A; Residues:

A;Accession: B81615

Length 541,

A,Molecule, type: DNA' A;Residues: 1-541 <ST0> A;Cross terences: 0:BA000008; NID:48975025, FIDR:BAA08855.; SSPUR-THÖG142 A;Experimental source: strain J138

A;Status: preliminary

A;Accession: B86572

Gaps

0.6%; Score 60; DB 2; Length 541;

Pred. No. 2.2e+02;

33.38;

Best Local Similarity 33.39 Matches 13; Conservative

Query Match

C, Genetics:

9; Mismatches

ż

Ġ.Species: Streptomyces coelicolor G.Date. 05 Nov-1999 #sequence\_revision 05-Nov-1999 #Lext\_change 17-Mar 2000

probable ABC transporter - Streptomyces coelicolor

RESULT 169

C;Accession: T35245

A)Status: preliminary, translated from GR/EMRL/DDR.1

A; Experimental source: strain A3(2)

A:Residues: 1-544 <OLI>

A; Molecule type: DNA A; Accession: T35245

A; Gene: SCOEDB: SC5F2A.03c

C;Genetics:

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A;Title: Alpha- and beta-forms of the 65-kEa subunit of protein phosphatase 2A have a A;Reterence number: A34541; MUID 90241887
A;Accession: D34541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphoprotein phosphatase (EC 3.1.3-16) 2A-bata 65K regulatory chain - Piq (fragment c.species, Sus scrofa domestica (domestic piq)
C.species, Sus scrofa domestica (domestic piq)
C.bate: 29-Jun-1990 Macquence_tevision 29-Jun 1990 Mickel_change 24:84P:1999
P:Posenthal, P J.; Nolson, R.G.
Mol. Biochem. Parasitol. 51, 143-152, 1992
Affile: Tsolation and characterization of a cysteine proteinase gene of Plasmodium f
A;Reference Lumber. A45624; MUID:922228005
A;Accession: A45624
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Biochemistry 29, 3166-3173, 1990
                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M81341; GB.M86590, NID.4160247; FIDN:AAA29578.1; PID-4160248
A;Note: sequence extracted from NCBI backbone (NCBIN:98870, NCBIP:98874)
C;Superfamily: trophozoite cysteine proteinase
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Circlesion: F81072

Rifettelin, H.; Saunders, N.J.; Heidelberg, H.; Jeffries, A.C.; Nelson, K.F.; Fiseb, Hickey, E.K.; Heft, D.B.H.; Salzberg, S.L.; White, O.; Pleischmann, K.D.; Dougherty, H. in, M. H.; Olm, H.; Vamathevan, J.; Cill, J.; Scarlato, V.; Masiquani, V.; Property, H. Science 287, 1809-1815, 2000

A; Aittle: Complete qenome sequence of Neisseria meningitidis serogroup H strain M°CS. A, Accession, F81072

A, Accession, F81072

A, Accession, F81072

A, Residues: I 642 < TFF>
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A;Authors; Kaine, B.P.; Borodovsky, M.; Klenk, B.P.; Fraser, C.M.; Smith, B.O.; Woese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: GB:AE002503; CB:AE002099; NID:47226775; FIDM:AAF4189-11; FID:4722
A:Experimental source: serogroup B, strain MC58
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C.Superfamily, transcription initiation factor sigma 70, transcription initiation fac
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A;Reference number: A64300; MUID:95337999
A;Accession: G64412
                                                                                                                       Reisserla meningitidis (strain
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AsWolcoule type: DNA
AsRosidues: 1-643 <BUL>
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Cispecies: Methanococcus jannaschii
Lidde: Lis beprings asejucheciteriste: Insequente Linder Cistersion: G64412
                                                                                                          RNA polymerase siama tactor kpub bMB1510 (imported) — Neisseria meninditidis
CySpecies: Neisseria meninditidis
CyDate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19 Jan 2001
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CiDate: 20 Aug 1999 #sequence_refision 20 Aug 1999 #fext_charac 20-Aug-1999
CiAccession: B/5055
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45.8%; Ted. No. 2.6e+02;
ive 7: Mismatches 6; Indels
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34.3%; Pred. No. 2.60+02;
Live 9; Mismatches 14; Indels
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M.; Ohtuku, Y.; Funahashi, T.; Lanaka, T.; Kodoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
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A)Experimental source: strain of3
A:Note: this accession replaces at Interim accession for a sequence replaced by Genbank
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A:Status: preliminary; nucleic acid sequence not shown; translation not shown
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976 FUNDARA BAKANA MAMAKA BERATAN KANTAN MANTAN MAKANA MAKANA MAKANA MAKANA MARANA MARANA MAKANA MARANA MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.29 SALSTOKESTERATERATERYGENTERNELSTILLESTER FERTENYASE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Courty Match. 0.6%; Score 60; 18-2; Langth 642; Bost Local Similarity 44.4%; Pred. No. 2.5e+02; Marches 12; Ausservative 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; Score 50; UR 2; Length 641;
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Mitches 13, Conservitive by Mismatches 29, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protoble helicuse protein PRO 97 - Pyrocecus horikashii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTROPECTAS: AFP: morb-ofilds b nding: P-Loop
F187 44/Neilon, no leaf-of-binding mofil A (P-Loup)
F121 - 219/Region: nucleofide binding mofil B
F121 - 219/Region: BFAH mofil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            984 LORBERTANNESSTEIN LECTYNSTESYTARD. TOTS
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                                                                                                    with Britanier Winte with
                                                                                                                                                                                      # SV: Mel STITER (2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C. Accession: B71116
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Best tedal Sirilarity 37 90 Matches 11: Conservative

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A:Experimental source: strain Orsay

A;Gene: PAB1429

C) Geneties

1-643 -KAW >

A; Reference number: A75001

A;Status: preliminary

A; Molecule type: DNA A;Accession: B75055

A; Residues

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A;Cross-reletunces: GB:Apgnuon, NtD.g3236130, FIDN.BAA23709.1, PIP dIPGFS2; PIPGT3 A;Note: this accession replaces an interim accession for a sequence replaced by GenBa C;Generathis PIPGE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R.Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se M., Ohfuku, Y.; Ponahashi, T.; Tanaku, Y.; Yamadaki, J.; Nushida, H.; Oqu DNA Res. 5, 55-76, 1988
A.Title: Complete sequence and gene organization of the genome of a hyper-thermophili A.Reference number: A71000; MUID:98344137
A.Accession: C71106
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A:Reference number: Z21617
A;Accession: 136877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Gross references: EMBL:ALJU9848; PIUN-CAR52838.1; GSPUB.GN00070, SCOEDE:SC151.14c
A;Experimental source: strain A3(2)
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Status: preliminary, nucleic acid sequence not shown; translation not shown
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C;Species: Streptomyces coelicolor
C;Date: 03-bec-1999 #sequence_revision 03-bec-1999 #text_change 03-bec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cispecies: Pyrococcus horikoshii
Cibate: 14-Aug 1998 #sequence_revision 14-Aug-1998 #text_change 05-New-ladg
CiAcression: C71106
                                                                                                                                                                                                                                                                                                                                                                                                                                         194 SLVEKSVKVFABYPGSSAQLKVELAFYASTIVSALVAAELVSDRITAKEETYTTÄKOLKS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
             C;Superfamily, Saccharomycos corcvisiae probable membrane protein YNL279w C;Keywords: transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 2; Length 664; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                               Length 661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                30: Indels
                                                                                                                                                                                    Pj422-438/Fonmain: fransmembrane #status prodicted CTMS:
Pjo34-obú/Domain: transmembrane #status predicted CTMS:
                                                                                        F;24-46/bomain: transmembrane #status predicted <TMl>
                                                                                                                                                                                                                                                                                              udccn (0.6%; Score 60; DB 2; 1
Local Similarity 32.2%; Pred. No. 2.7e+02;
hes 19; Conservative (0.5. vi...)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PH9620 - Pyrococcus herikoshii
                                                                                                                       F,110-12o/Domain: transmembiane #status predicted F,297-313/Domain: transmembiane #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 728 RVFSLLQKKIKKLESVITAVEIPSEWHIE 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 RVHSLIQAKVPETERALRRADIPFDLEIE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%;
Local Similarity 37.9%;
nes 11; Conservative
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Best Local Similarity
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A; Pesidues: 1-664 <KAW>
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A; Map position: 14L
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A:Experimental scarce: strain S2889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H. funct
A; Poference number: Assoni: Mulu:98637514
A; Accession: G69177
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A;Experimental source: strain Delta H
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A; bescription: Pyrococous abyes! genome sequence: insights into archaeal chromosome stru
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                                                                                                                                                                                              A;Cross-references: GB:AJ248287; GB:ALG96830; NID:45458657, FIDN:CAB56335.1, FID.e15162
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R:Messenquy, F.: Dubois, E.: Vierendeels, F.: Scherens, B.; Pierard, A.: Giausdorff,
submitted to the Protein Sequence Database, April 1996
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N.Alternate names: hypothetical protein N0505
C)Species: Saccharomyces cerevisiae
C;bate: 27 Apr 1796 #Sequence revision 03:May-1996 #text_change 20-Inn-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nighternate names: methionyl-tRNA synthetase
Cispecies. Mithanobacterium thermaniotrophicum
Cibate: 05 Dec.1997 #sequence_revision 05-bec-1997 #text_change 16 out-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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C;Reywords: aminoacyl tRNA synthetase; ligase; protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.6%; Score b0; DB Z; Length 651; 35.5%; Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                    0.6%; Score 60; DB 2; Length 643;
37 9*: Prod No 2 60+02
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9; Mismatches

Obery Match Best Local Similarity 35.5% Matches 11, Conservative

.651 <MTH>

A; Residues: ]

A;Gene: MTH587 A;Start codon: TTG

C; Genetics:

C;Accession: G69177

RESULT 177

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647 VINSTREGELIGVANGEMEELAADNINGOP 677 

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RESULT 178

863253

A;Reference number: \$63245

A; Residues: 1-661 < MES>

A;Gene: MIPS:YNL279w

CyGeneties:

A; Molecule type: DNA

A; Acression: S63253

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4.3.3. EVPT. AMMBLER TWELTELE VEHICLE BAY ZALCH CHALLEVI CALCATU TOS PVEHLARELLITALLERTAPPGADEDILTEALRIALALARRALLITDAVADAE 155

myosia heavy chain - rainbow 'rest (tradment)

PESULI 181

Supertamily: myosin heazy chain: myosin motor domain homology

C:Regwords: AIF

Querry Muteh Best Local S

Marie Lies

A:Status: preliminary A. Modernier type: menn Match 0.68; Search 60; 100-2; Length 608; Local Similarity 0.198; Pred. No. 2.90-02; es  $\{2, -5, 0.9, 1.04\}, -9, -9, Missatches 16, indexs$ 

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Ridorzialia, M.; Green, K.; Nishikawa, K.; Taniquchi, K.; Jones, F.; Kapikian, A.Z.;
J. Virol, 62, 2978-2984, 1988
A.Tille: Sequence of the Fourth gere of human rotaviruses recovered from asymptomatic
A.Reference number: A28839; MUID:88275070
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A,010ss references. GB.AE002101. GB.AP222894, NID.46898957. FILM.AALY0119.1. SSH186.0N
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Albestifican The complete sequence of Breiplasma mealyficum: Alternate views of a Alkelerence number: A82870
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C;Species: human rotavirus A
C;Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #fext_change 0] Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2650 #sequence_tevision 20.Aug 2000 #1.at_ hunde 26 Aug 2000
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                                                                                                                                                                                                    C;Superfamily: unassiqued WD repeat proteins: WD repeat homology
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22.6%; Pred. No. 4.16-22;
ive 19, Mismatches 29; Indels
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85.0%; Pred. No. 40:02;
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Hest Local Similarity 35.0%; Pred. No. 40-32
Matches 14; Conservative 10; Mismatches
Appener SubstUPL, ABRD, SPLD
Appross-references: SGD:S0000680; MIPS:YCK084c
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P.409-422/Reqion: threonine-rich
P.522-26-flowmain: WD repeat bonology WNB>
P.572-26-flowmain: WD repeat bonology WNB>
P.572-605/Pognain: WD repeat bonology WNB>
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C.Fate, 18 Aug-25550 #sequebbe_revi
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A:Residues: 1-775 <60R>
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A;Genetic code: SGC3
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Reseavity, Lulu: Bancolmeru, B.B.
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Albestiptione Clonist of i Last Skeigtal myoslicheavy chain expressed both in embryo an
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A First properties a profession of the content of a proteins is involved in Affectioner conduct. Just 44.
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Ajectoreme number: SIIIco MUINCO042641
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Avketerence number: A46-642: MUD:918-61759
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R:Williams, F.E.: Frombly, R.J.
Mol. Cell, Rich, 10, 6500-6511, 1990
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M.Alternate names. AEMS protein tupl - yeast (Saccharamyces certwisiae)
M.Alternate names. SEMS protein. Iloud to the outprosent protein SILL, protein YGE084.)
Separates Saccharamyces certainstance of the color) #text_change 21 Jul 2000
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Artiass references: EMBC-244764 - MIC-4246770; PHYR-7AA84734 1; PHYR-4765771
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Apriless references: EMMLM-615.

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A: American Sleed

1981 (EK VE 1881-1981)

A; Molecule 17pe: DNA A; Residues: 1-714 + DBS+

A: Arcession: Sladas

Askerstdues: 45 714 - FULL

Cisupertamily: rotavirus outer layer protein VP3

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8; Mismatches 21; Indels

0.6%; score 60; 08 1, 1 35.6%; Pred. No. 3.3e+02;

Best Local Similarity 35.69
Matches 16; Conservative

Query Match

Length 775,

yeast (Saccharomyces cerevisiae)

probable membrane protein YPEC29c yeast (Sacchard N;Alternate names: hypothetical protein YP9367.09c C;Species: Saccharomyces Cerevisiae

RESULT 185 854503

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R;Badcock, K.; Churcher, C.M. submitted to the RMRL Data Library, May 1995 A;Reterence number: 854059 A;Accession: 854603

C;Accession: \$54503

A:Molecule type: DNA

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F;781-805/Domain: transmembrane #status predicted <TMM> F;533,544/Binding site: chondicitin sulfate (Ser) (coralent) #status predicted
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NyAlternate names: cell adhesion kinase beta
C.Species. Rattus norvegious (Norway rat)
C.Date. 08-beb 1996 Requence_terision 08-beb-1996 #lext_change 04-beb 2000
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I Similarity 26.1%; Pred. No. 4.5e:02;
12; Conservative 17; Mismatches 17; Indels
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A:Cross-references: EMBL:L15188; NID:9289640; PID:9289645
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A;Description: Sequence of the C. elegans cosmid C14H9.
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C,Date, 14 Sep-1994 #sequence_resi
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A,Residues: 1 1018 <FAV>
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Biochem. Biophys. Res. Commun. 189, 156-362, 1992
ArTitle: Molecular cloning and characterization of the human and porcine transforming 9T
A.Keterence number: JC1359, MJID:93080582
A.Accession: JC1351
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Superfamily: Transforming growth latter beta receptor type III; 2P demain homology C; Repwords: chondroith suffate proteoglycan; qfycoprotein; receptor, transforming the proteoglycan; qfycoprotein; receptor, transmissione proteogram is 20-78 main: siqual sequence #status predicted <SIG>P: 20-78 MB/Product: transforming qrowth factor beta 3 receptor #status predicted <MAT>
                                                                                      Cykeywords: dapsid protein, cout protein; glycoprotein; hemagglutinin
F):-240/Product: outer capsid protein VPB #status predicted <VPB>
F):241-246/Product: outer capsid protein VPB #status predicted <VPS>
F):24775/Product: outer capsid protein VPS #status predicted <VPS>
F):56,132,156,195,324,583,589,592,592,592,694;cling <ire>
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C;Species: Sus scrofa domestica (domestic piq)
C;Date: 10-3cp 1999 #sequence_rerision 10-3cp-1999 #text_rhange 03-per-1999
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608 VINNDELESAEMKIAFYLSKSGFGSEHFLLEGWERALENVIKSTREGKFIGVANOKMIEL 667

Ouery Match 0.68; Score 60; DB 2; Length 832; Best Local Similarity 25.48; Fred. No. 3.6e:62; Matches 17; Consorvative 18; Mismatches 32; Indels

F;195-211/Domain. transmembrane #status predicted <TMM>

C; Keywords: transmembrane protein

A; Map position: 16R A; Gene: SGD: APL4

A; Cross references: SGD:S0006233; MIPS:YPR029c

A;Residaes. 1 832 -BAD> A;Cossiteletenves. EMBL.245274, NFO.4809585, ilo:gboy594, Mils:YiEG256 A;Experimental source: strain AB972

DOS LADNINE 0/4 166 TEKDVSL 172

90 Š

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transforming growth factor beta receptor type III precursor - pig

RESULT 186

5

0: Saps

PESULI 189

Ajkesidues: 1-848 <MOR> Ajūloss references, GB.167595, MID.q164696, PiDM:AAA31126..., FiL.gic4691

A; Molecule type: mRNA

C; Accession: Jr1351

F;454-723/Domain. 2F domain homology <2FH>

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R.Sasaki, H.; Nagora, K.; Ishino, M.; Tobioka, H., Kotani, K.; Sasaki, T.
J. Biol. Chom. 270, 21206-21219, 1995
A,Title, Cloning and characterization of ocil adhesing kinger beta. a nevel proteinst
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A,Cross.teferences. GB.D45854, NID:q1000679; PIDM:BAA08290.1: PID:d1008885; PID:q1000
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AjArression: 742216
Ajstatus: preliminary: translated .rem GB/EMHL/NUBJ
Ajstatus: preliminary: translated .rem GB/EMHL/NUBJ
Ajstatus: 1 752 - 8HTR5
Ajcresidens: 1 752 - 8HTR5
Ajcressiteferences: EMBL/ABG10466, NID. 93242457, FIDN.BAA28954.1, FID. 97242458
Ajstyerimental source: strain Sprague bawley: liver
G;Superfamily: buman multidrug res stance protein cMcAl2; AFP-binding cassette homolo
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EMBO J. 7, 1129-1137, 1988
Aritie: The 11-1 gene of Plasmodium talciparum codes for distinct tast evolving reper
A;Reference number: S00485; MUID:88296416
A;Accession: S00485
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C;Species: Plasmodium faleiparum
Silate. [7 Sun 1909 #seperace_nestion [7 Jun 190] #fost_change 39 Jun 2009
                                                                                                                                                                                                                                                                     Sugarki, H. 1160, F. Chagawa, R. C. Kambel, R. C. Shimbon, T. C. Shana,
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AjResidnes: 1-1684 kBEM>
Ajčioss references: EMBLAjO04991. NID.43342751. FIDN:AN'2767511: PID:qrs42762
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CiSpecies: Homo sapiens (man)
CiDate: 05-Mar-1944 ssequenco_revision 05-Mar-1444 stext_change 05-Nev-1449
C.Species: Raffus norvegicus (Norway rat)
C.Date: 03:bec:1999 #sequence_revision 03 bec 1999 #fext_change 21:Jul-20e0
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19.8%; Fred. No. B.Le-02;
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Aj¢ross-references: EMBL:X07453
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Genetics 148, 1117-1125, 1998
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LORZ ENDPEROYULGETUNTERFERDIGHFISHERAYALMMP 2022 FOR EXPANDIBIBILITIES POSISSENYMENTS UNIVERSE NO

Score 17: 18-2; Pred, No. 4,5e+02;

14. 1 . 43

local Similarity (6.7) has 15; Conservative

Guery Mitch Best Local C

Matches

<u>:</u>

Asserbates plasmid Asmobile element: passmid bdp<sup>6</sup>

Appendient Legi-

 $\{4.22\}$  multiding resistance associated protein homolog MLP-I - ratematicaling

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214 SSLKET 7.11 735 SSPKES 740

41

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17; Indels

12; Mismatches

0.63 Best Local Similarity 31.09 Matches 13; Conservative

V; Introns: 71/3

A; Gene: 11-1 C; Genetics:

hemagglutinin A · Porphyromonas gingivalis

RESULT 194

qq 3

0.6%, Score 60, 55.2, Leuglh 1948, 31.0%; Pred. No. 9.6e+02;

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Cypecies: Homo sapiens (man)
Cybecies: Homo sapiens (man)
Cybett. 19 Oct 1995 #sequence_revision 26-Jan-1996 #text_change 10-Doc-1999
CyAccession: A56539; S37536
Eysering, H. P., Schramer, P., Schramer, H.; Wiemann, C.; Griffiths, G.; Renz, M.
Mol. Coll. 14, 2564-2576, 1997; M. A. Miller, M. A. Miller, M. A. Miller, M. A. Miller, Molecular genetic stalyses of a 376-kilodalton Goldi, complex membrane protein
A, Peference number: A56539; Miller, 94187728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyaccession: 152300
R; Sohda, M.; Misumi, Y.; Fuj'wara, T.; Nishioka, M.; Tkehara, Y
Biochem, Riochiys, Res. Commun. 205, 1399-1408, 1994
A,Tille: Molecular cloning and sequence analysis of a human 372-kDA profein localized
A,Reference number: 152300; MIID-95100974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1117 ALSDEKVQQKELLEMLEPLI VNOKNSHOAQTVSSVPPOTSVNAEQVRTELEPDERAKPLGT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1117 AISDEKVQQKLLRMLFDLLVNCKNSHCAQTVSSVFKGISVNAFQVRIELEPPDKAKPLGT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Species: Homo sapiens (man)
C.Jate: 01:Nor 1995 #sespachor_traising Ol Nor 1996 #*ext_charge 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1508 ALLQEERDKI,ITEMDRSLLENQSLSSSCESLKLALEGLTEDKEKLVKEIFSLKSSKIAES 1567
                                                                          TISÜ VERSISVNARÇVPTELPPPFAAFFIGTVÕCKPFÇPAGOKKSODI PSVORVORSVAGATI. 1209
                                                                                                                     1452 HETR STADVPSQVSVQNQPPDALLGPLAFLDSPDPRI TVPMPKSTERNDSFOGSCPSFKL 1511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.A.ressien A56539
A.Medecule type: mRNA
A.Residucs. 19259 - SRE:
A.g.ressier Figerandes: FMRL:X75304; NID-9405714; PIDN:CAA53052.1; PID:9405715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Rusidues: 1 3225 FPBS>
A,Thessipeforeness GB,DC542, NTD,3662389; PTDN-PAA95625 1: PID:9808869
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19.4%; Pred. No. 1.7e+03;
Live 30; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match -0.63,-85 {\rm core}~60,-58.2,-16 {\rm ngth},3225; Best Local Similarity 19.48, Picd. No. 1.7e+03, Matches 20; Conservative 20; Mismatches 53: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.Roywolds, culted coil, Golji apparatus, Fransmembrine protoin
P.9238-3254,75 amain Trinsmembrine #stitus prodicted TMMs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1568 TEWQEKHKELQKRYETLLQSYENVSNEAFRIQHVVRAVRQEKQ 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Status, prejiminary, frans,ated from CB,PMR1,/DDBJ
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A; Map position: 3q13.31-3q13.31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20; Conscrvative
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                                                                                                                                                                                                                              PIST MAMMEDIBLE 1219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N:Alternate names: gcp372
                                                                                                                                                                                                                                                                                                        1572 VVESVRQEKQ 1581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                qiantin - human
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A,Cross-references. RDBJ:C25543, RLD:g516825; PL94FPAAUS025.1; PLD:g516826
C,Comment. This profein plays a role in the formation and maintenance of the characteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Toki, C.; Fujiwara, I., Sohda, M., Hong, H.S., Misumi, Y., Ikchara, Y.
Cell Struct. Funct. 22, 565-577, 1997
A;Title: Identification and characterization of rut 364-kua Golgi-associated probein ted
A;Reference number: JC5837; MUID:98093490
           comment. This protein is associated with the membrane of red blood cells of the schind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CiSuperfamily: giantin
P;49-549,624-1176,1238-1707,1763-3134/Demain. Coiled Coil leucine cipper #status predict
P;3165-3187/Lomain. Membrane anchor #status predicted. MAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyaccession: T28651
KrHan, N.F. Whithock, J.: Proquisko-Pox, A.
Infect. Lamun. 64, 4000-4607, 1996
Arithe: The hemagqlutinin. 9cac A (LagA) of Posphytomonus ginginalis 221 cactains fant
Arketerace namber. Z20194, MUID.06406248
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A;Cross-references. EMBL.U41867, NID.91552410, PID.91469916, P;DN.AAB17128.1
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C;Accession: JC5837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species. Porphyromonas gindivalis
C;Date: 15-Oct-1999 #sequence_rowision 15-oct-1999 #text_change 15-oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                            C.Keywords: tandem repeat
P)1-71/Domain: signal sequence #status predicted <SiG>
F,72 1948/Freduct. game list probein (fragments) #status predicted >MAT>
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0

Ouery Match 0.6%; Score 60, UB 2, Dength 3187, Best Local Similarity 20.0%; Pred. No. 1.7e+03; Matches 26; Conservative 31; Mismatches 73, Indels

Length 2628;

Query Match 0.6%, Score 60, DB 2; Length 2629 Best Local Similarity 40.0%, Pred. No. 1.4e+03, Matches 14; Conservative 6, Mismatches 15, Indels

á Q: 364K Golgi complex-associated protein - rat

RESULT 195

C; Species: Rattus norvegicus (Norway rat)

A;Status: nucleic acid sequence not shown A;Molecule type: mRNA

A; Accession: JC5837

A;Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Gene: hagA

C;Genetics:

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Search completed. Movember: 6, 200., 12.21.54
Job time: 411 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rikawarabayasi, Yir Sawada, Mir Horikawa, Hir Harikawa, Yir Hino, Yir Yamamoto, Sir Sekir
Mir ohtuku, Yir Funahashi, Tir Fanaba, Eir Kadob, Yir Yamazaki, Jir Kushida, Nir Oquchi
DNA Resi 5, 55 76, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asfitjes čledina and sequencija of raf pjectin indicates a 460 kD polypeptide chain with
Asfecterare number: A896x8; MTD591268156
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                                                                                                                                                                                                                                                                                                                                                                                                                       Inher, K.; Weitzer, G.; Castanor, M.J.; Hauptmann, K.; Stratow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aproxidaes: 1 144 - KAW -
Aptroxo-references: GB:APPO00004; MHSq4226140; PIDN:BAA29946.1; PID:d1030979; PID:q3257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Altossinoterenees: EMBLIXT96 D. NID:41292885; PIDN:CAA42350.D. BID:41551642
Cisipertumily: plotfin: alpha actinia actin binding domain homology, ribosomal protein of Newpords: cytoskejetor: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Affiller Complete sequence and gene organization of the genome of a hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Askererence compers A71 acc; MUTH-FOR 644137
Askerssions (PST) 64
ASSTATUS: prediminary tourheir acid sequence not shown; translation not shown
Askoserale type: DNA
                                                                                                                                                                                                                                                                                    plectin - rat
C.Species: Ratius norvegicus (Norway rat)
C.Date: 10:Sep 1799 #sequence_revision 10:Sep-1999 #Lext_change 16 Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cospecies: Pyrococcus korikoshii
Cobute: 14:Ang 1996 Eseguence revision 14:Ang-1998 Ereal, Land 75 Bo. 1999
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Cibate: 05-bec 1997 #sequence_recision 95-bec 1997 #fext_change 21-Jul-2000
1542 AGGOFFRONTITEMORSGLAINOSISSSCESIAGALIGIGERARALVEGESLASKIABS 1901
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Estat 1997/ammora: alpha actinia actin binding Jomain homology (ASL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.6%; Score 60; OR 1. Length, 1687
11.4%; Pred. No. 2.60*03;
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1.2%; Pred, No. 57;
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                                                          1177 VQGKRPQBMQQBBSQDLBSVQBV~ISYWGRVILII.BII.QHBKK 1219
                                                                                                                        1602 IEMĢEKRIKELOKEVETILOS VENVSNEABRIJHVVEAVĒGKO 1614
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PHO842 - Pyrococcus horikoshii
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   114, 84-94, 1991
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R:Wiche, 3.: Becker, R.: Enk
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E;13-17/Region: ATP binding #status predicted
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AJEXPerimental source, strain 148
                                                    Rikunst, F.; Ogasawara, N.; Moszer, I.; Aibertini, A.M.; Alloni, G.; Azeredo, V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status; preliminary; nucleic acid sequence not shown; translation not shown
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                                                            SCIENCE 287:2185-2156(2000).
-1- FUNCTION: BEAUTHED FOR NULLEAR PROTEIN IMPORT AND MEDIATES DOORTING
-1- DIMPORT SUBSTRATE TO DISTINCT NUCLEOPORTINS.
-1- SUBDINT: FORMS A COMPLEX WITH AN IMPORTIN ALPHA SUBDINIT.
-1- SUBCETLULAR LOCATION: CYTCPLASMIC.
Par S., Lhu X., Smith H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharomy es cervisias (Baker's yeast).
Eukaryota: Pundi: Ascomycota: Saccharomycotes:
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FAY TIP HINCIR' (BY PIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sucry Match
Best Local Similarity 85.6%; Fred. No. 1.4;
Matches 16, Conservative 11, Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duesterhoeff A., Floeth M., Heuss-Neitzel D., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brickhor J.H., Puller R.S.;
Sebaltrod ("N 1997) to the test, West, Dobal databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wedler H., Wodler E., Scharfe M., Wambuit K.; Odrich of Max 1995, 1995, Preije okses, J.E.S. databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAV-1996) to the FNFE Shelverd Did databases.
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98695 MW: DEGDACH9278414EC FRC64;
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                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE IMPORTIN BETA FAMILY
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Transport, Profein transport: Repeat.
Transport Profein 489 FEAT REPEATS DOMAIN 1.
                                         "The genome sequence of Prosophila melanogaster.";
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UP-07-2000 (Ref. 40, Last amoutation apdate)
VATDGLAE PROTEIN SOFTING-ASSOCIATED PROTEIN VESTA.
VPSI3 of Soft of YLL0400.
                     Rubin G.M., Venter J.M.,
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                                                                                                                                                                                                     SIMILARITY: CONTAINS 11 HFAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50077; HEAT_REPEAT; 1.
Cibbs R.A., Theng i M., Thisa W. Gibbs R.A., Myers R.W., Rubin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBqnijnini986; Fs(2)Ket.
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01 NeV 1997 (Ref. 45, Last segm
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: AJC02729; CAA05691.2; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF222745; AAF34680.1;
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Interpres IPR001494;
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Q07878; O00040;
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Unpublished observations (XXX-1997).
-i- FUNCTION: PECHCIES PHESENAL CYCLING OF TOH MEMBEANE FECTEINS RY MODULATING THE FUNCTION OF TWO CYCLOSOLIC TOH LOCALIZATION SIGNALS.
-i- SIMILARITY: SOME, TO S. POMHE SPECIEGE.020.
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Eukuryotu, Metarea, Cherdata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Gallitormes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-8233755, F.EMcJ 651557, Geisler N., Weber K. "Comparison of the proteins of two immunologically distinct intermediate sized Ellaments by amino acid sequence analysis: desarin and vimentin.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The amino acid sequence of chicken muscle desmin provides a common structural model for intermediate filament proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domains along the protofilamout unit of desmin 10 nm filaments ";
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"Proteinchemical characterization of three structurally distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1462 SLMNII.QYLLKLPEEKEETIPKAVSFNKSESQEEMLQVFNVETHTSKQL 1510
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36.7%; Pred. No. 5.9;
3vo. 9; Mismarches 23; Indels
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01-FEB-1996 (Ref. 33, Last annotation update)
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MEDLIME-84207925; PubMcd 6202512;
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MEDLINE-85063701; Pubmed-6594672;
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23-027-1985 (Rel. 02, Last sequ
                                                                                                                                                                                                                                                                                                        EMBL: AF001317; AAC68284 1; -
EMBL: Z73144; CAA97490.1; -
EMBL: Z73145; CAA97491.1; -.
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Best Local Similarity
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This SWIES FEOT entry is outpylight, it is produced through a collaboration between the Swies Institute of Bhointormatics and the FMBL outstation the European Bioinformatics Institute. On the arc no cratrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. These the for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce.com/ensended/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comment/comm
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FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN
MUSCIE CPILS IN ADMIT STRIADED MUSCIE THEY FORM A FIRROUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPOSITE; PSON226; TP; 1.
Intermediate filament; Coiled coil; Reptad repeat pattern; Muscle.
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Mammalia; Butheria, Cetartiodactyla, Ruminantia; Perora; Bovoldea;
                                                                               NETWORK CONNECTING MYOPIBELIS TO EACH OTHER ANY TO THE PLASMA MEMBRANE FROM THE PERIPHPRY OF THE 2-LINE STRUCTURES.
                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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COIL 1B.
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                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC.
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                                                                                                                                                                       SURUNTY: HOMOPOLYMER
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    This SWISS-PR-1 entry is copyright. It is pronuced through a collaboration between the SWISS HISTITUTE OF BROINCOMMENTER and the BMBL outstation. The European Biodinformatics Institute. There are no restrictions on its use by non-profit has itstinions as long as its content is in no way modified and this structured. Usage by and for commercial entities requires a license agreement (see http://www.lst.sib.chpancomercial or send an email to itemsed (SBD-SBD-Ch).
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01:A03 loss (Ref. 15, Created)
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                                                                                                                  Vieart P., Dupret J.M., Hazan J., Li Z., Gyapay G., Krishnamoorthy E., Weissenbach J., Fardeau M., Faulin D., "Human desmin qene: cDNA sequence, regional localization and exclusion of the Locus in a familial desmin related myspathy.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Navas-Palacios J.J., Ariza A., Fuchs F.; "A dystunctional desmin mutation in a patient with severe generalized
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DISEASE: DEFECTS IN DES ARE THE CAUSE OF DESMIN-KELATED MYOPATHY.
A FAMILIAL CARDIAC AND SKELETAL MYOPATHY (CSM): CMS IS
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Sjoeberg G., Saavedra-Matiz C.A., Rosen D.R., Wijsman E.M., Perg K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coldfarb L.C., Park F. Y., Octorinkers I., Sarokhana S., Ike H.-S.,
Vasconcelos G., Nagle J.W., Semino-Mora C., Sivakumar K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A missense mutation in the desmin rod domain is associated with autosomal dominant distal myobathy, and exerts a dominant negative effect on filament formation.";
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-i. FUNCTION: DESMIN ARE CLASS-111 INTERMEDIATE FILAMERES PROPE IN MUSCLE CHILS. CALLS. IN ADULT STATALED MUSCLE THEY FORM A FIBROUS NEEWER CONNECTION MYOFIB 11.3 TO EACH OTHER AND TO THE FLASMA MEMBRAARE FROM THE FERTHHERY OF THE A LINE STRUCTURES.
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Roca X., Vela E., Mate J.L., Coll J., Pernandez-Fiqueras M.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intermediate filament, Coiled coil, Heptad repeat pattern, Muscle,
                                                                                                                                                                                                                                                                                                                                                                        CHESTE THAN BALL AND VAPIANTS CSM PRO-336; PRO-359 AND TIE-192.
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                                       TISSUE:Muscle;
MEDLINE:96384956; PubMed:8792816;
                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98361171; PubMed 9697706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANI CSM 172-ARG--GLU-178 DEL.
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                                                                                                                                                                                                                                                                                         98:422 429(1996).
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Horowitz S.H., Sejersen T.;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             Bum, Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myopathy.
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FEAD.

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EF3_PNECA
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                                                                                                                                                                                          N\to\gamma/\Gamma (3N CSM+ HFTEPOZYGOUS WITH PRO-358 GIVES A SEVERE CMS CHILDHOOD-ONSET).
                                                                                                                                                             A -> P (IN CSM; HETPPOGNOOGS WITH ILE 391 GIVES A SEVERE CMS CHILDHOOD-ONSET).
                                                                                                                                                                                                                                                                                                                                                      "Comparison of the proteins of two immunologically distinct
intermediate-sized filaments by amino acid sequence analysis: desmin
                                                                                                                                                                                                                                                                                                                        0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 78:4120-4123(1981).

-i. FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN MUSCLE CELLS. IN ADULT STRIATED MUSCLE THEY FOORM A FIRROUS NETWORK CONNECTING MYOFIBELLS TO EACH OTHER AND TO THE PLASMA MEMBERARE FROM THE FELTRHEPY OF THE 2-LINE STRUCTURES.

-i. SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metaroa, Chordaia, Cramiara, Vortebraia, Euteleosfomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                   \Lambda \rightarrow P \ (I \overline{N} \ CSM; \ MILLD \ ADULT-ONSET). /FT1d-VAR 007900 .
                                                                                                                                                                                                                         CEP -> VFS (IN PEF 1 AND 2).

C -> P (IN PEF 1 AND 2)

FINIT SPITW (IN PEF 1 AND 2).

MISSING (IN REF 1, 2 AND 3).

6A38116855409188 CRC64;
                                                                                        COIL 2B.
MISSING (IN CSM: SEVERE FORM).
                                                                                                                                                                                                                                                                                                  0.7%; Score 73; DB 1; Length 469;
30.7%; pred No 1.5;
                                                                                                                                                                                                                                                                                                                       12; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chikuni K., Tanabo R., Muroya S.;
"Desmin structure as related to meat tenderness.";
Submitted (MAR-1998) to the FMBL/Genhank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P02540; 062656;
21-JUL-1986 (Rel. 01, Created)
15-JUL-1999 (Rel. 38, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                           /FTId NAR_009188
                                                                                                                                                     ZFT1d-VAR 009189.
                                                                                                                                                                                      /FTId=VAR_007901.
                                                                                                                                                                                                                     /FTIG-VAR_007902.
                                                                                                                                            -> P (IN HDM).
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                                                         INFPP 12
                                   LINKER 1.
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38 G
122 FA
134 MI
53404 MW;
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38
118
134
469 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
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CONFLICT
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                                 between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Sec nith://www.isb-sib.ch/aumounce/or send an email to license@isb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Asconycota, Pneumocystidomycetes; Pronmocystidaceae;
Pneumocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2065 DAY LLEKTEESSPRVEFAALITVLALAERIFENYIVLI PESIPFIAELMEDECEEVEHO 2124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEPTY IMPROFES THE MAIN ROLE OF EF-3 MAY BE TO TRANSDUCE NUCLEOSIDE TRIPHOSPHATE ENERGY INTO MECHANICAL ENERGY FOR TRANSLOCATION DURING TRANSLATION. EF-3 STIMULATES EF-1 ALPHA-DEPENDENT BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILAKIIY: BELONGS TO THE AIF BINDING TPANSPOPT PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                  Intermediate filament, Coiled Coil, Heptad Repeat Pattern; Muscle.
INT_MET 0 BY SIMILARITY.
DOMAIN 1 108 HEAD.
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-i - SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0 /*; Score 73; 08 l, Langth 470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A2A8F7A8DB65DD12 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last Sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1042 AA.
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COIL 2A.
LINKER 2.
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PATHWAY: PROTEIN BIOSYNTHESIS.
SUBUNIT: MONOWER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COIL 2B.
STUTTER.
POLY-SER.
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MEDLINE=93014112; Pubmed=1339410;
                                                                                                                                                                                                                                                                                                                                                                                                         POD.
                                                                                                                                                                                                                                       BAA25134.1; -.
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                                                                                                                                                                                                               ЕМЫГ, АВО11676, ВАА25136.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 30.7%;
                                                                                                                                                                                                                                                                           InterPro, IFR001664; -. Pfam; PFC0038; filament; 1. PRG81FE, PSG0226, IF; 1.
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295
412
354
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                                                                                                                                                                                                                                                           PIR; A02955; DMPG
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P29551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIANE 1928/16: PibMed 10850571; Nethorn M.E., Dodson R.J., Nethorn M.E., Dodson R.J., Nethorn M.E., Independent R.J., Nethorn M.E., Therefore M.E., The Least M. Mediand M.E., Unterther R.D., Street M.M., Stewart A.M., Totton M.E., Pratt M.S., Phillips C.A., Rechardson D., Stewart A.M., Forton M.E., Pratt M.S., Phillips C.A., Rechardson D., Stewart A.M., Suitherd J.S., Smith H.E., Verter J.G., Fraser C.M., Eisen J.A., White C., Edidence P.L., Smith H.E., Verter J.G., Fraser C.M., Praser C.M., Presence S.L., Smith H.E., Verter J.G., Praser C.M., Maile C., Rechardson P. M., Marteria Philosophysic M.E., Smith H.E., Werter J.G., Praser C.M., Presence S.L., Smith H.E., Werter J.G., Presence Archaea and Bacteria from genome sequence of Thermotoga maritima."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characterisation of the enzyme and the DNA sequence of the genes for
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so MAY-2000 (Rel. 4), Las. annotation update)
lona DIRECTED RNA POLYMERASE BETA CHAIN (E.C. 2.7.7.6) (TRANSCRIPTASE
BETA CHAIN) (RNA POLYMERASE BETA SUBJONIT).
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PNA biodics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.74; Score 74; 58 1; Length 1942;
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Zillia W.,
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Leto AA: 1175 e MW: e54Be4D5eF56212F CRef44.
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ATP (BY SIMILARITY).
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                                               SIMILARITY: CONTAINS TO HEAT REPEATS.
(ARTIBANSPORTERS), BET SUBLAMILY.
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PROJIT | FOLDI, AW_IEAASFETEE, ...
PROSITE: PS50077; HEAL_REPEAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thermotogales: Thermotoga.
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This SWISS PROF entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMH, Outstation the European Bioinformatics Institute. There are no restrictions of mose by non-profit institutions as one as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license apresent (SWIP NAME is the view of the send an email to licenseriable by the view of the send an email to licenseriable by the view of the send an email to licenseriable by the view of the send and                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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FUNCTION: DNA DEFINDENT RRA POLYMERASE CATALYZES THE TRANSCRIFTION
                                                                                                                                                            CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site.
                                                                                                                                                                                                                                                  SUBUNÍT. THE ENZYME CHRICIS OF THE STOMA CHAIN AND THE CORE DUZYME WHICH IS COMPOSED OF 2 ALPGA CHAIRS, I BETA CHAIN, AND I
                                                OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE IRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                   STMIGARITY, BLAD MAD TO THE KHA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kunst F., Odasawara N., Yoshikawa H., Danchin A.;
Pomittod (N.W.1942) to the EMNI Jordhautz/DHGJ databases.
-!-SUBCELLUIAR LOCATION, INTEGRAL MEMBRANE PECTEIN (POTENTIAL).
-!- SIMILARLIY: RELONGS TO THE UPPOITS (PERM) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
HYPOTHERICAL 40, PRDA PROTEIN IN 16820-ALD INTEWSFNIC RESION.
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Conservative 9: 0****
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Lam: FPU01854, ENA_POL_A2: 1.
Promp: PPU0823; ENA_POL_A3: 1.
Transferase; DNA-directed ENA_Polymerase; Itanscription.
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Best Local Similarity
These 14, Conserva
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                                                                                                                                                                                                                                                                                                                                                                   BETA' CHAIN.
                                                                                                           SUBSTRATES
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between the Swiss Institute of Bioinformatics and the EMBL outstallon-
the European Bioinformatics institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
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or send an email to license** sib.ch).
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intermediate filament cDNAs from BHK-21 ceils: demonstration of distinct genes for desmin and vimentn in all vertebrate classes."; Proc. Natl. Acad. Sci. U.S.A. 815970-5974(184).
-!- FORCTION: DESMIN ARE CLASS-111 INTERMEDIATE FILAMENTS FOUND IN MUSCLE CELLS. IN ADDLE STRIATED MUSCLE THEY FORM A FIBROUS NETWORK CONNECTING MYOFTBRILS TO EACH OTHER AND TO THE PLASMA MEDIBINANE FROM THE PLASMA MEDIBINANE FROM THE FIRST OF THE Z. LINE STRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mesocricetus auratus (Golden hamster).
Eukaryota: Metazoa; Chordata; Craniała; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroguathi, Muridae, Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quax W.J., van den Henvel R., Egberts W.V., Quax Jenken T.E.E.M.,
Bloemendal H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of the hamster desmin gene; expression and tormation of desmin filaments in nonmuscle cells after gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                               0.6%; Score 70; DB 1; Length 369;
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Bloemendal H.;
                                                                                                                                                                                                                     21; Indels
                                                                                                                                                                                                                                                       398 SULFLEYISYSSQUEMOSHKVSLANEQFUTLIRLLESKTPRIEDVVL 444
                                                                                                                                                                                                                                                                         27 SEVPGOPETVPISTLEFPMLIAGILYFIFNPVVRIJEKKIPRTLSILL 73
                                                                                                                             5F86C34CF258C4B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                  21-501-19%; (Rel. 01, Created)
01-NOV-1988 (Rel. 09, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   468 AA.
                                                                                                                                                                                                                   9; Mismatches
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                                                                                                                             40896 MW;
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                                                                                                                                                                                 0.6%
Best Local Similarity 36.2%
Matches 17; Conservative
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PIR; A24783; A24783.
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 34
73
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369 AA;
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                                                                                                                                                                                                                                                                                                                                  2065 INYQILLIKTEDSSPKVPFAALITVLALAEKLKENYIVLIFESIPITAELMEDECEEVEHO 2124
                                                                                                                                                                                                                                                                                                                                                  192 LQEFIQLREEARNNLAAFPADVDAATLAPIDLEERIFISLNFFIAFLKKVHFFFIRELQAQ 251
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN MUSCLE CELLS IN ADULT STRIATED MUSCLE THEY FORM A FIBROUS NETWORK CONNECTING MYOFIRELS TO EACH OTHER AND TO THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Rakaryotus Metazoa; Chordata; Craniata; Vertebrata; Eutoleostomi;
Mammalia: Eutheria; Rodontia; Sciurognathi; Muridae; Murinae; Mus.
PROSITE; PSO0226; IF; 1.
Intermediate filament, Coiled coil, Heptad repeat pattern; Muscle.
INIT_MET 0
                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Regulation of the mouse desmin gene, transactivated by MyoD, myoqenin, MRF4 and Myf5.";
Nucleic Acids Res. 21:335-343(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Inhibition of desmin expression blocks myoblast fusion and interferes with the myogenic regulators Myob and myogenin ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Li H., Choadhary S.K., Milner B.J., Music M.J., Polsk I P.,
                                                                                                                                                                                                                                                                       DB 1; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEMBRANE FROM THE PERIPHERY OF THE Z-LINE STRUCTURES.
                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                         3915443165908PB9 CRC64;
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15-DEC-1998 (Rel. 37, Last sequence update)
30-MAY-2000 (Pel 39, Last annotation update)
                                                                                                                                                                                                                                                                     Score 70; DB 1
Pred. No. 3.6;
                                                                                                                                                                                                                                                                                                    13; Mismatches
                                                                                                                                                LINKER 12.
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                                                                                                                                                                               LINKER 2.
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                                                                                                                                 1B.
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                                                                                                   COIL 1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BALH/C: TISSUE-Spieen;
MEDLINE-93181210; PubMcd-8382796;
Li H., Capetanaki Y.;
                                                                                   TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94165148; PubMcd-8120103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell Biol. 124:827-841(1994).
                                                                                                                                                                                                                           53307 MW;
                                                                                                                                                                                                                                                                    Local Similarity 29.3%; es 22; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-39 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                2125 COKTIQQLETVLCEP 2139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                            252 LQEQQVQVEMDMSKP 266
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468
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149
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                                                                                                                                                                                                                            468 AA;
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Mammalla; Eutheria; Redectia; Schurognathi; Muridae; Murinae; Rattus.
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Blocking Rophys, Acta 1212 flot 109(1994);

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PROSLIES PSOGZZG, IES 1.
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of FEB Proc (Ref. 43, Last Sequence update)
of FEB-1996 (Ref. 43, Last annotation update)
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or send an email to license istail. a
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Rest Lossi Similarity 20 Kg.
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MAD: MGI: 44885; Des.
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                                                      EMBL: L.22550; ... NOLJANNO
EMBL: 218632; CAA79430;1
FTR: SAL404; SAL404;
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양동동종服당도조조보보통동동동() 위송의공동동동()
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01-071-2000 (Rel. 40, Last am notation, update)
SERIAR/THEFORINF PROTEIN PROTEIN PROSHARING ZA, 65 KDA KENIKATORY SOHGNII A,
BETA ISOFORM (PPZA, SOHGNII A, PR65-RETA ISOFORM) (FPZA, SHRONII A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S 101 :0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baysal B.E., Farr J.E., Goss J.R., Devlin B., Richard C.W. 111:
"Genomic organization and precise physical location of protein
phosphatase 2A regulatory submit A beta isotorm gone on chromosome
band 19(23.").
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Merleggie W., Hofsterepert, Steres S.K.;
"Alpha- and beta-forms of the 65-Kha subunit of profein phosphafase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Alterations of the PET2RIB gene in human lung and volon cancer."; Science 282:284-287(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hemmings B.A., Adams-Pearson C., Maurer F., Mueller P., Goris J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniala; Vertebruta; Eufeleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE 98438696; PubMed 9765152;
Wang S.S., Esplin E.D., Li J. ., Huang L., Gazdar A., Minna J.,
Evans G.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 70; DB 1; Length 468;
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BBDC667A5AE7FA8B C167643
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                                                                                                                                                            BY SIMILARITY.
                     or send an email to licensedisb-sib.ch).
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LINKER 2.
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INIT_MET 0 0 BY SIMILA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZAAR_HUMAN STANDAKU; P
P30154; 075620;
01.APR-1993 (Rel. 25, Created)
15 JUL-1999 (Rel. 38, Last Serg
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                                                           EMBL; X73524; CAA51920.1; -.
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                                                                                                 Ptam; PF00038; filament; l. PROSITE; PS00226; IF; l.
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                                                                                InterPro; IPRO01664;
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                                                                                                                                                                                                                                                                                                                                                                                   468 AA;
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-1: FUNCTION: THE PRES SCHONIT OF PROTEIN PROSEMBLY OF THE CATALYTIC SUBGINIT AND A VARIABLE REGULATORY R STRUNKT OF THE CATALYTIC SUBGINIT AND A VARIABLE REGULATORY R STRUNKT THE CASE OF THE CATALYTIC SUBGINIT: PREA CONSISTS OF A COMMON HETEROSTHERIC CORE ENZYME, COMMONT & A 36 KDA CATALYTIC SUBGINIT (SUBGINIT) AND A 05 KDA CATALYTIC SUBGINIT (SUBGINIT AND ASSOCIATES WITH A VARIETY OF REGULATORY SUBGINITS, PROTEINS THAT ASSOCIATES WITH THE CORE DIMER INCLUDE THREE FAMILIES OF REGULATORY SUBUNITS BY (THE RZZRYPRES/NES). RESPECTABLY OF REGULATORY SUBGINITS OF REGULATORY SUBGINITS RECOVER THREE PROTEINS THAT ASSOCIATE PAMILIES). THE 48 KDA VARIABLE REGULATORY SUBGINIT, VIPAL PROTEINS, FAMILIES), THE 48 KDA VARIABE AND CELL SIGNALING MOLECULES.

DOMAIN: EACH HEAT REPEAT APPEARS TO CONSIST OF TWO ADPHA HELICES JOINED BY A HYDROPHILIC RECION, THE INTRAREPEAT LOOP. THE REPEAT JUNITS MAY BE APPEARCED LATEFALLY TO FORM A POD-LIKE STRUCTUPE

DEFECTS IN PPP2RIB COULD BE THE CAUSE OF SOME LUNG AND DISEASE

SIMILARITY: BELONGS TO THE PHOSPHATASE 2A PEGILATORY SURINIT A COLON CANCERS

SIMILARITY: CONTAINS 15 HEAT REPEATS.

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AAC63525.1; JOINED. AAC63525.1; JOINED. EMBL; AF083439; AAC63525.1; -. EMBL; AF083425; AAC63525.1; JOINED. AF083426; AAC63525.1; JOINED. AF083427; AAC63525.1; JOINED. AAC63525.1; JOINED. JOINED. AAC63525.1; JOINED. AAC63525.1; JOINED. AF083438; AAC63525.1; JOINED. AAC63525.1; JOINED. AAC63525.1; AF08/438; AAC69624.1; AAC63525.1; AAC63525.1; AAC63525.1; AAC63525.1; M65254; AAA59983. AF083428; AF083429; AF083430; AF083431; AF083432; AF083433; AF083434; AF683435; AF083436; AF083437; MIM; 603113; EMBL; EMBL; EMBL; EMBL; EMB1.; EMBL; EMBL; EMBL;

> D (IN LUNG CANCER). > EPPP (IN PRF 2)  $E \rightarrow V \text{ (IN REF. 2)}.$ T -> I (IN REF. 3). /FTId=vAR\_006384. VLID -> BFRP (IN ) Repeat; Disease mutation. HEAT 6. HEAT 4. HEAT 1. PROSITE; PS50077; HEAT\_REPEAT; 12. HEAT 528 567 601 212 251 250 489 Multigene family; CONFLICT CONFLICT VARIANT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT KEPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT

0; Gaps

27; Indels

1737 MPSILITTMKNTSELVSSEVYLLSALAALQKVVETLPHFISPYLEGIILSQVIHLEKI 1792

0.6%; Score 68; DB 1; Length 59;

Pred. No. 0.54;

Ouery Match 0.6%; Best Local Similarity 32.1%;

18; Conservative

Matches

11; Mismatches

59 AA; 6708 MW; 4B5B3C9D25BD985A CRC64;

Ribosomal protein.

SEQUENCE

Archaea;  $Eur_{\gamma}$ archaeota, Methanococcales; Methanococcaee;

Methanococcus jannaschii.

MJECL37

SEQUENCE FROM N.A.

NCBI\_TaxID=2190;

Methanococcus.

01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) HYPOTHELICAL PROTEIN MJECL37.

237 AA

PRT;

STANDARD;

YZ37\_METJA

060292

DB 1; Length 601; 0.68; Score 69; Query Matich

4A5B10EEF7432F74 CRC64;

66201 MW;

601 AA;

SEQUENCE

CONFLICT

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                                                     2067 YGILLEKTRUSSEKVEFAALITVIALAEKIKENYIVILEESTERLAELMEGETERVEHQOO 1126
                                                                                       299 PONTLKHCEAEVPAAAAHKVKELGENLPLEPPETTIMNOTLPPIKELVSDTNOHVKSALA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE L30P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zucrner B.L., Hartskerl P A , van de Kemp H., Bal A.E.;
"Characterization of the Leptospira interrogans S10-spc-alpha
                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria: Spirochaetales; Leptospiraceae; Leptospira.
                                                                                                                                                                                                                                                                                                         30 MAY-2000 (Rel. 39, Created)
30 MAY-2009 (Rel. 39, Tast sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
; Pred. No. 6.7;
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       operon.";
PEMS Migrobiol Lett. 182:303-308(2000).
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SEROVAR LA1;
MEDLINE=20088835; PubMed=10620683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro, IPR000517; -. Pfam; PP00327; Ribosomal_E30; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF115283; AAD40601.1; -.
  22.28;
  Bost Local Similarity 22.2%
Matches 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                     50S RIBOSOMAL PROTEIN 130
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Leptospira interrogans
                                                                                                                                  2127 KTIQQLETVLGE 2138
                                                                                                                                                                       359 SVIMGLSTILGK 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPONENCE FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=173;
                                                                                                                                                                                                                                                                       RL30_LEPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zuerner E.L.
                                                                                                                                                                                                                                                                                           Q9XD18;
                                                                                                                                                                                                                                                    RL30_LEPIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1916 ILPOPROGET SKRIMTIERVVERSCHELLEGIGDRILFTVLOYFRAVA, SREERAFFTVY 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAPSIS COTONSERT
                                Bull C.J., While O., Olson E. I., Then F. Fleischmann F.D., Striebert B.A., Garagne F.B., Schrauser A.R., Bougherty B.A., Tomb J.-F., Adams M.D., Reich C.I., overtheeb F. Ritherss E.F., Meinster F. F., Fuhrmann J.D., Reich C.I., Scott J.L., Geodhaert N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D. Diterback F. R., Kelley J.M., Peterson J.D., Sadow P.M., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodorsky M., Kleik B. P., Flaser C.M., Smith H.O., Woese C.R., Venter J.C.; Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE 0212/USS) PubMed 17/073/0
Chem J.D., Chan C.S., Pirrotta V.;
"Conserved PWA Fading and acti association dumins. (The or sequita-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Ptergota: Neopotera: Endopterydota: Diptera: Brachycera: Muscomorpha:
Ephydroidea: Drosophilida: Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENE EXPRESSION), WHERE THE SYNAT... PATRING OF THOMOSOMES OAREYING THE MITH WHICH EXERTE AN EACHTS INTIDIANCES THE EXPRESSION OF THESE CONIS. ZESTE BINDS TO THA AND STIMULATES FRANCE TION FROM A NEARBY PROMOTER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zeste protein. 7
Mol. Cell. Biol. 12:598-638(1992).
-! FUNTION: INVALVET: N TEANSVETT: N PHENYMENA ( STRAPELS DEF
-! FUNTION: INVALVET: N TEANSVETT: N PAIRING OF THOMOSOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: SELF-ASSOCIATE FORMING COMPLEXS OF SEVERAL HUNDRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.68; Seere 68; DB 1; Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stobal :89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27184 MW; BODF621202CDDA11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBJECTIONAR CONTION: NOTLEAR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jul. 1998 (Rel. 36, Greated)
Jul. 1998 (Rel. 36, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prod. No. 2.
STRAIN JAL 1 / LAN 2461 / ATC: 43067;
                      MEDITINE 96337999; PubMed 8688087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prosophila virilis (Fruit fly).
                                                                                                                                                                                                                                                                                       Seience 274:1058-1074(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: 1.77118; AACH7106.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MONOMERS (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SECUENCE 247 AA: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 SIKINISKLYN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Georg March
Host Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .5-JUL-1998 (Red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JUL 1398 (Red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11/3R; M.DEC1.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZEST_DR-VI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marches
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial efficies requires a library of removal [\text{See BILE}]/\text{WWW} ishelf-dimensioned or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                       CLN/ALA-FICH (OPA-REPEAT INVOLVED IN
TRANSCRIPTIONAL ACTIVATION OF REPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidosis thallata (Mouserest cress).
Eukaryota: Viridiplantac: Embryophyta: Trachcophyta: Spermatophyta:
Magnoliophyta: cudicotyledoms; core endicots, Rosidac; eurosids II:
Mrassicales; Brassicacea; Arabidopsis.
                                                                                                                                                                                                                                                                                       AT DIFFERENT TARGET LOCI) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- DEVELOPMENTAL STAGE: EXPRESSED FARLY DURING FLOWER DEVELOPMENT.
-i- SIMILARITY: BELONGS TO THE MADS DOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. SIMILARITY: CONTAINS A PROBABLE DIMERIZATION DOMAIN FOUND IN
SRE-TYPE TRANSCRIPTION FACTORS (K-BOX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91160981; PubMed-1672119;
Ma H., Yanofsky M.F., Mcycrowitz E.M.;
"AGI1-AGI6, am Arabidopsis gere family with similarity to floral
                                                                                                                                                                                                                                                                                                                                                                                      0.6%; score 68; DB 1; Length 518; 37.1%; Fred. No. 9.4;
                                                                                                                                                                                                                   WITH ZESTE LOGUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS, PRO0404; MADSDOMAIN.
PROSITE PRO0350; MADS_BOX_1: 1.
PROSITE; PSSO;066; MADS_BOX_2: 1.
Transcription regulation; DNA-binding; Nuclear protein.
                                                                                                                                                                                             DNA-binding, Transcription reculation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                            Fred. No. 9.4;
8, Mismatches 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC 1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last Sevuence update)
01-DECT-2000 (Rel. 40, Last anrotation update)
ATAM-US-LIKE MADS POX PEOTETA ADL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1173 PLGTVOOKPPOKMOOKKSODLESVOEVGGSYWORV 1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            517 PTCAQQQLQLQQQQQQQQQQQQQQQQABSYEERI 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homeotic and transcription factor genes.";
                                                                                                                                                                                                                 SPECIFIC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                618 AA; 68102 MW;
                                                                                                                                                             FlyBase, FRgn0013149; Dvirl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMBL, MSSSS1; AAA32732.1; -.
                                                                                                                                              EMBL; M76700; AAA29052.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5:484-495(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                     13, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01486; K-box; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P11746; IMNM.
InterPro, IPR002100; -.
InterPro; IPR002487; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRF-TF:
                                                                                                                                                                                                                                          46.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B39534; B39534.
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam: PF00319:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGL2_ARATH
P29382;
                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                   DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Natches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGL2_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOUCCOUCCOCCERMENTAN OCCOCR NEEDED A
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458 AA; 52802 MW; E96167E1D8FDEB74 CRC64;

SEQUENCE

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the butopean Bioinformativs Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch.or.sch.ac.).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright, It is produced through a collaboration between the SWISS Institute of Bioinformatics and the FMRL outstation -
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                                                                                                                                                                            1929 KIYKÇIEKNWKNHMGFPMSILQEHIGXMKKEELTSHQSQLTAFFLEALDFFAQHSENDLE 1887
                                                                                                                                                                                                                 93. REVENTALAGRAM NOMORGOMIN GREGOSEN NSKREFRYZER ENGLEGST KYVKSTKT OYMINYZES. 152
                                                                                                                                     Sign Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus Jaevis, II. Identification and molecular characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-90832494; FubMed-2886128;
Herrmann H., Fouquet B., Franke W.W.;
"Expression of intermediate filament proteins during development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: DESMIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfan, FF00038; filament, 1.
PROSITE; FS50225; IF; 1.
Intermediate filament; Coiled coil; Heptad repeat pattern; Muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MUSCLE CELLS, IN ADDIA SIRIATED MUSCLE THEY FORM A FIRMOUS AS AWORE CHIRECTING MENTHELLS TO FACH CITRE AND TO THE TLASMA MEMBRANE FROM THE PERIPHERY OF THE 2-LINE SIRUCTURES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aruopus iaevis (Alrican clawed frog).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                            DB 1, Length 248,
                                                                                                                                     42; Indels
                                    248 AA, 28454 MW, 8B70DD4512AC906B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1991 (Rel. 20, Created)
01-RAV-1991 (Rel. 20, East sequence update)
01-FFR-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           PRT; 458 AA.
                                                                                                                Pred. No. 4.2;
                                                                                                                                   25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLL 1A.
LINKER 1.
                                                                                            Offery Match 0.6%; Score 67, Best Local Similarity 18.1%; Pred. No. Matches 15; Conservative 25, Mismatc
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STUTTER.
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SUBCELLULAR LOCATION: CYTOPIASMIC.
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                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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This SWISS-PPOT outry is engright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Burnpean Bioinformatics Institute There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial outifies requires a license agreement (See Milp.) www.istasib.chgunco.no.
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                                                                                  2065 TAYQITLETPDSSPRVPPAALITVLALABRITEPNYIVII PESTPPLARI MEDPCFFVPPQ 2124
                                                                                                    182 (285) QESTQUERBARNNIAAPPOUVDAATIAPTOURPPIEST QEFTAFIEKTHEFETFFTOAQ 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryoti, Metilool, Nematedi, Chromodise, Ehob Mila, Ehabditoidea;
Khabditidee, Pelodeiinae; Caenothabditis.
NGRI_TaxID~6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hyperthetical protein, Zinc Finger, Norther protein, DNA-binding.
ZN FING 28 51 C4-TYPE.
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0.6%; Score 67; DB 1; Length 458;
29.3%; Pred. No. 8.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                     ÕI-OCT-1996 (Pel. 34, Created)
1-OCT-1996 (Pel. 34, Last sequence update)
01-OCT-1996 (Pel. 34, Last annotation update)
HYFOTHEFICAE (Pel. 34, Last annotation update)
HYFOTHEFICAE 127.4 KDA PHOTEIN POTPE, 4 IN CHROMOSOME III.
                                           41; Indels
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1159 AA; 127429 MW; R0A7E5AABE815G63 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1995) to the EMBL/Asenbank/DDR1 databases -:- SUBMILLULAR LOCATION: NUCLEAR (PROBABLE). -:- SIMILARITY: RELONGS TO THE GCS1/SL03/SPS18 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1009 SCPSYIAKDLMKVLQGVNGFMVLSQLLPMAEQLLEKIQKEPT 1050
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                                                                                                                                                                                                                                                                                                                PRT; 1159 AA.
  Query Match 0.6%; Score 67; DB Best Local Similarity 29.3%; Pred. No. 8.8; Matches 22; Conservative 12; Mismatches
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PPINTS, PP00405, PEVINTRACTNG.
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                                                                                                                                                                                                                                                                                                                    STANDARD;
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A.H.4 ARAIR

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                                                                                                                                                                                                                                                                                                                                                                      Eukaryo'a; Viridiplantae: Embryophyta; Tracheophyta: Spermatophyta;
Marmed Eaphyta, caditotyledems, core eadicots, Kosidae, eurosids II,
Brassicales: Brassicaceae; Arabidopsis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEVELS PMENIAL STADES EXPRESSED BARLY DURING PLOMBER DEVELOPMENT, SIMILARITY: BELONGS TO THE MADS FOMAIN FAMILY OF TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDINE Floored: Purphed 107119;
Ma B., Yarotsky M.F., Meyerwattz B.M.;
Ma P., Yarotsky M.F., Meyerwattz B.M.;
Maril Alfric in Araticles's referencedly with similarity to floral humber let and transcription tartor genes.
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6-MAIN (4)
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ATA OF FIRE MADS Box PROTEIN ADIA.
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EMBL: AA00755; AAP3125.11 -
PIP: D7534; D79544.
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Piamo PPO0419; SRP IP: 1
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MOIL CELL BIOL 1114363-4370(1991).

-1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FET FECEPTOR TO THE ACTIVATION OF THE RESPICATORY HOUST. MAY ALSO CONTRIBUTE TO THE ACTIVATION OF THE RESPICATION TO THE ACTIVATION OF THE RESPICATION TO THE ACTIVATION OF THE PEGGRAULATION PROCESS OF WEITHOUBLIES.

-- VALATILET ACTIVITY ALL A FECTEIN TYROSINE - ADD -- PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                         Holtyman D.A., Gook W.B., Punn A.P.,
"isolation and sequence of a JAMA corresponding to a sic related gene-
expressed in murine hemopoletic cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: PS9-HOK AND PS6-HOK ARE ASSOCIATED WITH MEMBRANES. P59-HOK IS ALSO CYTOPLASMIC.
-1- ALTERNATIVE PRODUCIS: THE P59-HOK AND P56-HOK ARE PRODUCED BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Fuun A.R.; "Two isoloths of mutine htt, renetated by utilization of alternative translational initiation codous, exhibit different patterns of subcellular localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE SRC SUBFAMILY.
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Murihae; Mus.
                                                               01-NOV-1995 (Rel. 32, Last sephence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TYROSINE-EROTEIN KINASE BCK (E) 2.7.1.112) (P56-BCK AND P60-BTK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -t- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE MYELOID AND B-LYMPHOID LINEAGES.
                                                                                                                 (HEMOPOLETIC CELL KINASE) (B- SELL/MYELULD KINASE) (BMK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-22 FROM H.A., AND ALTERNATIVE INITIALION.
MEDLINE-91342636; Pubmed 1875,227;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
                                                                                                                                                                                                                                                     STRAIN ICR: ILSSUE-Marrophage:
MIGLINE &SSOC7EL, Pubbled (6845.7)
MIGRIS ALL MARROPHER S.P. Mak. B.A.;
"Nucleotide sequence of the mouse hek gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USE OF ALTERNATIVE INITIALION SITES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! SIMILARITY. CONTAINS 1 SH2 (SOMAIN. -!- SIMILARITY: CONTAINS 1 SH3 (SOMAIN.
                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 15.9600 9630(1987).
                  F.K.I.;
                                                                                                                                                                                                                                                                                                                                                                             MEDIJINE-88068587; PubMed-3317404;
                                                01-AUG-1988 (Rel. 08, Created)
                                                                                                                                                                                                                                       SEDUENCE OF 22-524 PROM N.A.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 22-524 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plam; PF00059; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Y00487; CAA58544.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMEL; J03023; AAA37305.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro: IPR000719; -.
InterPro: IPR000980; -.
InterPro: IPR001245; -.
InterPro: IPR001452; -.
Ptam: PF00017; SH2; 1.
                  STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00018; SH3; 1.
                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A27282; TVMSHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A 49 97 4; A 3 9 9 7 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P08631; 2HCK.
                                                                                                                                                                                                      NCB1_TaxID-10090;
                  HC.K_MOUSE
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HCK_MOUSE
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Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY). 
DP72FDMMH 48/49705 (PM154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WHITE LEGIGER, TISSUE-EMBLYG,
MEDLINE 92112031; FubMed-1730407;
Trumpp A., Blundell P.A., de la Pompa J.L., Zeller R.;
Trumpp A., Blundell P.A., de la Pompa J.L., Zeller R.;
Trumpp A., Bundell P.A., de la Pompa J.L., Zeller R.;
Gence fice cell types during morphogenesis.";
Gence Dev. 6:14 28(1992).

!- FURCITCH. 13 IMFORTANT FOR MORPHOGENESIS OF LIME AND KIDNEY AND MAY BE INVOLVED IN DETERMINER DERSOUBHTRAL NEURAL TUBE POLARITY AND MOTOR REHERON INDICTION IT MAY ALSO HAVE A FUNCITON IN DIPFERENTIATED CELLS OR BE INVOLVED IN MAINTAINING SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               - SUBCELLULAR LOCATION: NUCLEAR.
- SUBCELLULAR LOCATION: NUCLEAR.
- ALTERNATIVE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE PRODUCTS: MANY DIFFERENT FORMS OF THIS PROTEIN ARE PRODUCTS: MANY DIFFERENT TISSUE. A VARIATION IS SEEN ARMONG DIFFERENT TISSUES AND DIFFERENT SIZE TRANSCRIPTS EXIST WITHIN ANY ONE TISSUE.
- TISSUE SPECIFICITY. PRESENT IN THE ADDIT THE PMRHY?
- BRAIN, HEART AND INTESTINE AND THEOGRAPHY THE PROTEIN IS EXPRESSED IN THE ADICAL ENCORPORTED THE MESENCHYMAL COMPARIMENT, FEEDOMINALLY IN THE FOSTERIOR EDGION. DUPING KIDNEY MORPHOGENESTS. EXPRESSION IS INITIALLY RESTRICTED TO THE EPITHELIAL COMPARTMENT OF THE PRONEPHROS.
                                                                                                                                          Tyrosine protein kinase, Phosphorylation, ATP-binding, Pty downein: SH3 downein: Alternative initiation.

1 524 FYROSINE PROTEIN KINASE PS9 HCK.

22 524 TYROSINE PROTEIN KINASE PS6-HCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score ob; DB i; Length 524;
23.9%; Pred No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1210 TEBLIQHEPELFSPQILVPTLENELSBYLFFFFPQGGAMMFVFKQLT 1255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              464 VIRALEHGYRMPRPDNGPFELYNIMIRCWKNRPEERPTFFYTOSVL 509
                                                                                                                                                                                                                                        MYRISTATE (BY SIMILARITY).
MYRISTATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1213 AA
                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
               PRINTS, PRO0401; SHEDCMAIN.
PRONTS; PRO0452; SHEDCMAIN.
PROSTIE: PSO0107; PROTEIN_KINASE_ATP: 1.
PROSTIE: PSO0109; PROTEIN_KINASE_TYR: 1.
PROSTIE: PS50011; PROTEIN_KINASE_DOM: 1.
PROSTIE: PS50011; SH2: 1.
PROSTIE: PS5001; SH3: 1.
                                                                                                                                                                                                                      FOR P56-HCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FORMIN (LIMB DEFORMITY PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                          59129 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.68;
Best Local Similarity 23.9%;
PRINTS, PRO0109; TYRKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
                                                                                                                                                                                                                                                136
236
239
273
378
                                                                                                                                                                  SH2 domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCB1_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                        409
                                                                                                                                                    Transterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                  Myristato:
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
MOD_RES
                                                                                                                                                                                                                      INIT_MET
LIPID
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DOMAIN
DOMAIN
NF_BIND
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                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                             LIFIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gorden S.V., Righmeier R., Gas S., Barry C.E. III, Tekala F., Badcook K., Basham D., Brown D., Chillingworth T., Counor R., Hornors R., Devlin K., Felluell T., Geulles S., Hamlin M., Holroyd S., Hornsby T., Tagels K., Krogh A. McLean J., Moule S., Murphy L., Felluer S., Selerno J., Moule S., Murphy L., Chirat S., Selerno J., S., Squares S., Sqares R., Sulston J.E., Taylor K., Whitchoad S., Barrell R.; Sqares R., Sulston J.E., Taylor K., Whitchoad S., Barrell R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1674 IKLLCKNFGAENPDPFVPVLXTAVKLIAPERKEEKNVLGSALLCIAEVTSTLEALAIPQL 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1078 MKLVCRESSEEHLOPFKEKLEHFEQKAKEEKKKEESSLENAGKCFEBTVGYFGIKPKPGE 1137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomycetales; Corynebacterineae, Mysabacterias ai, Mysobacterium.
NCBL_TaxiD=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPT: 1316 AA
P47769: 006771;
01-FEH-1995 (PAL) 37, Created)
15-DEC-1999 (Rel) 37, Last sequence update)
15-JIL.1999 (Rel) 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE BETA (CHAIN (FC 2.7.7.5) (TRANSCRIPTASE BETA CHAIN) (RNA POLYMERASE RETA SUBUNIT).
                                             SIMILARITY: BELONGS TO THE FORMIN HOMOLOGY FAMILY. CAPPUCCINO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 66; DR 1; Length 1213;
05.4%; Pred No 39;
SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 1 (FH1) DOMAIN. SIMILARITY: CONTAINS 1 FORMIN HOMOLOGY 2 (FH2) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135240 MW; ADERREDBREPROPRES CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mynobarterium fuberculosis.
Bacteria, Firmicutes, Actinobacteria, Actinobacteridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             Pfam: PF02181; PH2; 1.
PPINTS; PRO0828; FORMIN.
Nuclear protein: Developmental protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COLLED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FH1 (PRO-RICH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prod No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98295987; PubMcd-9634230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPOC 47 FVONDA OF MT 11 47 070
                                                                                                                                                                                                                                                                                               EMBL: X62681: CAA44555 1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-148 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                         IPRON1265; -.
                                                                                                                                                                                                                                                                                                                                                 TPR003104; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            450
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1213 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          652
                                                                          SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.
                                                                                                                                                                                                                                                                                                                           InterPro
                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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DOMAIN
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**초**≲도로워이지? 등원용원위인원원원원인원원원품품품품품품출**조**명

us-09-603-665-5.rsp

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                   Miller L.F., Crawlord J. . Shinnick L.M.;
"The Ipon gene of Mycobactorium tubercujosis.";
Antimirota. Agents Themother, delugenti(1994).
I PUNCTION: INA DEFENDINT NAZ PETRHESASE CALATZES THE IBANSERIPTEN
OF DNA INLERNA USIN; THE PORK RIPONOSEEOSIGE TRIPHESSHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caps
                                                                                                                                                                                     N PYROPHOSPHATE
                                                                                                                                                                                                                                    SUBGINIT: THE ENZYME CONSISTS OF THI SIGMA CHAIN AND THE CORE ENZYME WHICH IS TOMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tstanchus caryophylius (Carmation) (Clove pink).
Enkaryota, Viridiplantaez Embryophyta, itachecphyta, Spenmatophyta,
Moducliophyta, endicotyledoms, vore endicots, Satyophyllidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRUM CV. SCANIA; ISSUE-Petal;
Bundinette S.C., Savin K.W.;
Submitted (MAR 1995) to the EMBL/Amengor/Figg. databases
simulited (MAR 1995) to the EMBL/Amengor/Figg. databases
: SUBFELLUIAR DO'ALTON: NUCLEAR (BY SIMILARITY).
: SUBFELLUIAR DO'ALTON: LETHER MADS COMAIN FAMILY OF TEANSCRIPTION
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                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%; Score 66; DB 1; Length 1816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF01854; RNA_pol_A.: 1.
Pfam: PF01854; BNA_pol_A.: 1.
Industriase: UNA_directe, RNA_polymorase: Transcription.
SEJGENTE: 1515 AA: 146559 MW: 4548248398855888 GEG54;
                                                                                                                                                                                  ACALVII ACLIVITY: N NOVLEOSIDE TRIPHOSPHAIE
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15-00L Fork (Boi. 95, Last Sequence update)
19-01 200E (Boi. 40, Last annestation ypdate)
MALSER X PROTEIN PMRE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caryophyllales: Caryophyllaceae; Dianthus.
NCMI TaxID: 657c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  444 RVINKNNELKELISELJAPELIVBNEKEMIN, 275
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MEDITINE SECOND OF PURMOR BESTER SEC
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EMMIL 127999 AAA21417.1:
Tober Hist, Reserve
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Best Local Similarity
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Interpretation (1986) 28793
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                                                                                                                                                                                                                                                                                 0.6%; Score 65; DB 1; Lynath 2×4;
25.0%; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                   14. Links
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-!- SIMILARITY: BELONGS TO THE 14-3-5 FAMILY.
                                                                                                                                                                             Transcription regulation; DNA-binding; Nuclear protein.
DOMAIN 58 9ADS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPOSITE: PS90796; 1433_1; 1.
PROSITE: PS00797; 1433_2; FALSE_NEG.
SEQUINCE: 251 AA; 28169 MW; 749042151HZ684HB CRC54;
                                                                                                                                                                                                                                CP8765618466191A CRC64;
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01 NoV 1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last amoutation update)
                                                                                                                                                                                                                                                                                         25.0%) Pred. wo.
or send an email to license ist sit. (h.).
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                                                                                                                                               PROSITE: PS00350; MADS_BOX_1: 1. PROSITE: PS50066; MADS_BOX_2: 1.
                                                                                                                                                                                                                                SEQUENCE 234 AA; 26888 MW;
                               EMBL: L40404; AAA62761.1; -.
                                                                                                                                  PRINES; PRU0404; MADSDOMAIN.
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Pfam; PF00244; 14-3-3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                             Piam; PF01486; K-box; 1.
Piam; PF00319; SRF-TF; 1
                                                                                                                                                                                                         158
                                                               InterPro: IPR002100; 1.
                                                                                 InterPro; IPR002487; -.
                                                                                                                                                                                                                                                                                       Local Similarity
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039757;
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1433_FUCVE
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                                                                                                                                                                                                                                                0; Gaps
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YERNB OR HELT OR YNLOIDW OR N2846.
Saccharomyces cercislac (Baker's yeast).
Eukarysta: Punqi: Ascomycola: Saccharomycetes:
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H LINKED (GLCNAC. .) (FOTENTIAL).
N-LINKED (GLCNAC. .) (FOTENTIAL).
H LINKED (GLCNAC. .) (FOTENTIAL).
W; 4725FP78c048A2814 *Pe784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 65; DB 1; Length 941;
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                                                                                                                                                                                      Viruses, dsBMA viruses, no RMA stuge, Bergosviridae.
Betaherpesvirinae; Cytomeqalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34, Last sequence update)
37, Last annotation update)
                                                                                                           01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last Sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to licensection sib.ch).
                                                                                                                                                                           Human cytomegalovirus (strain A0159).
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                                                                                       PRT;
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01-007-1996 (Rel. 34, Last sequ
15-DEC-1998 (Rel. 37, Last anno
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Best Local Elmilarity 22 F9
Matches 18; Conservative
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                                                                                       STANDARD;
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661
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  1054 KDEAMVLHLTL 1064
                        95 ADILKLIEAEL 105
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861 8
441 AA;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FINATION, THE MAIN WOLL OF RE 3 MAY BE TO TRANSDUCE MUCLEOSIDE IRLIPHOSPHATE ENERGY INTO MECHANICAL FURENT FOR TRANSPICATION POPULARS THANSLATTON EETS STIMULANGES ET 1 ALFHA DEPENDENT BIRDING OF AN INOACYL-TRNA TO THE SITMOSOME YETRACHERS SPEMS TO BE EXPRESSED ONLY IN SPECIAL CONIDITIONS; IT IS NOT REQUIRED FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PATHWAY: PROTEIN BIOSYNTHESIS.
-i- SIMILARITY. REFACKS TO THE AITH HINDING TRANSFORT PROFEIN FAMILY
(ARC TPANSPOPTERS). EF-3 SUBFAMILY.
-i- SIMILARITY: CONTAINS 10 HEAT REPEATS.
                                                                                                                                                           Sarthy A.V., McGonical T., Capoblanco J.O., Schmidt M., Green S.R., Moehle C.M., Goldman R.C., "Identification and Kinetic analysis of a functional homolog of
                                                                                                                                                                                                                                                                                                                                                      MEDIENE-S8451818, Pababad-9778796;
Montied T.C., Magguel C.P., Pamagathan C.S., Payn R.M., Wart G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              "A highly conserved intraspectes bounded of the Saccharomyces cerevisiae elempation factor 3 encoded by the HEF3 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein biosynthesis, Elöngation factor, Repeat; ATP-binding;
RNa-binding, Acetylation; Phosphorylation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 65; DB 1; Length 1043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION (BY SIMILARITY). HEAT REPEATS DOMAIN.
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IW; 3E990EEE579D88A8 CRC64;
                                                                                                                                                                                                                                       elongation factor 3, YEF3 in Saccharomyces cerevisiae."; Yeast 14-239-253(1998).
                                                 Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (POTENTIAL)
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30-MAY-2000 (Bel. 39, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00005; ABC_tran; 2, PROSITE, PS00211; ABC_TRANSPOPTER; 2.
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                                                                                                                                         MEDLINE-98205886; PubMed=9544245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yeast 14-1105-1113(1998).
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707
1030
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Matches 17, Conserv
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                       CHARACTERIZATION.
                                                                                                               CHARACTERIZATION
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Eastinate of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FONCTION: TAN DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
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A MAY gone (Ref. 3) List angeld for quality.
GNA OFFER BNA FELYMERASE BETA' CHAIN (EC 2.7.7.6) (TRANSCRIPTASE
BRIA' CHAIN) (ENA FELYMERASE BETA' SUBBNIT).
HOWE OR RETALL
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Andersser Schiel bemarkdippar Al. Andersson John.
Scherntz Berten Li. Alsmark E.C.M., Pedowski B.M., Naesburd A.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF DAMAINTO RANA USING THE POUR RIBOARDLEDISTOR TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBBINITE THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BED NOS TO THE RNA POLYMIRASE BETAT CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The general despendence of Klokertsin presentable and the entitle familiaries.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Racheria: Firminates, Ballios/Chastridina eroqo, Mollicates,
Mycoplasmataceae: Mycoplasma.
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Fransterise: ENA directed RNA polymerise: Transcription.
SE,UENTE: 1/72 AA: 15/061 MW: 72410E46596E465: CRC64:
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Priceri
Priceri
ULN WY 1997 (Roll, 4%, Prestrod)
GI NeW 1997 (Roll, 4%, Last sequence update)
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MEDLINE FILESAMS, Pubmed B9486345.
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Hest Local Similarity 40.0%;
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Interferor IPR/02879)
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the European Bioinformaties Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or first ordains a long a terminal transfer or sibility [[**** ]**** ]*** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **** | **
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                                                                                                                                                               This SWISS-PROT entry is copy-ight. It is produced through a collaboration between the SWISS Institute of Recipromatics and the BMH outstation the European Holontormatics Institute. There are no restrictions on its mass by non-profit institutions as load as its content is in no way.
                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Basee by and for commercial entities requires a license agreement (see hitp //www.isk sib chyana analy) or send an email to license dish sib.ch).
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"Complete sequence analysis \alpha, the denome of the backetism My opiasma pheumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
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01-0CT-1996 (Rel. 44, Last annotation update)
01-0CT-1996 (Rel. 44, Last annotation update)
01-0CT-1996 (Rel. 47, Last annotation update)
01-0CT-1996 (Rel. 44, Last annotation update)
((1->4)-BETA-GLUCAN ENDOHYDROLASE) ((1->4)-BETA-GLUCANASE) (BETA-T, 4
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levels in the extracellurar compariment of leaves in resignse to

    -1- CAIALYTIC AUTIVITY: HYDROLYSIS OF 1, 3-BETA-D-GLOCOSIDIC LINKAGES
IN 1,3-BETA-D GLOCANS.

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Plant Physiol. 96:390-397(1991).
-: FUNCTION, IMPLICATED IN THE BEHTHMSE OF FLANTE ASAINSE PATHWENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Embryophyta; Tracheophyta: Spermatophyta;
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Ward E.R., Payno G.B., Moyor H.B., Williams S.C., Dinchet S.S., Sharkey E.C., Berk J.J., Taylor H.I., Abl-Goy P., Moins F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- PTM: THE N-TERMINUS IS HOCKED.
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97A17C22F9D25425 CRC64;
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Solanales; Solanaceae; Nicotiana,
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STOURHOT 229 AA; 27920 MW;
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Bukaryota, Viridiplandae, Endaryehyta, Tracheoghyta, Spermatephyta,
Magnoliophyta, eudiactyledaen zore eudiauts; Asteridae, esasterids T,
Solamales, Solamaceae, Nicotiana.
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SIMILARITY: BELONGS TO FAMILY 17 OF GLYCOSYL HYDROLASES.
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Plant Physical of 200 307(199)
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01-NvV-1991 (Rel. 20, Last sequence update)
01-NvV-1991 (Rel. 30, Last sequence update)
01-NvV-1998 (Rel. 37, Last annotation update)
02.0.CAN ENDO-1,3-BETA-GLUCOSIDASE, ACIDIC ISOFORM GI9 PRECURSOR
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PR2.
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Ward P.P., Payne G.R., Royer M.B., Williams S.C., Dincher S.S.
Sharkey F.C., Beek I.L., Teylor H.T., Abl-Cog P., Meins P.,
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Cornelissen B.J.C., Bol J.F.;
"Analysis of gene families encoding acidic and basic
beta-1,3-queanases of tobacco.",
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Van den Byleke M., Bauw G., Castresana G., Yan Montagu M.,
                                                                                                                                                                    96 NUCLEGERIAL (BY SIMILARITY).
25. PROJEK DONCE (BY SIMILARITY).
30386 MW. EPDDBG13A5GC8FB5 CRC64;
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8; Mismatches 21; Indels
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                                                                     Pfam, PF00332, GLyco_hydre_17, 1,
PROSITE, PS00587, GLYCOSYL_HYDROL_F17, 1.
                                                                                                                   Hydrolase; Glycosidase; Multigene family.
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MEDLINE 91062359, Fubmed 2247115;
EMBL; M60462; AAA34105.1; -.
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Matches 13; Conservative
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                                                InterPro; 1PR000490; -
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                    HSSP; P15737;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation \cdot
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                                                                                      entities requires a license agreement (Sor litty //www.iskrsib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milson R., Ainscough R., Adderson K., Haynes C., Berks M., Wilson R., Ainscough R., Anderson R., Copper J., Cooper J., Coulson A., Frakello R., Fraser A., Evilton L., Gardner A., Dutbin R., Favello A., Fraser A., Tohnston L., Jones M., Kershaw H., Kirslen J., Laisster N., Lightning J., Lloyd C., Mortimore B., O'Calladhan M., Parsonille F., Lightning J., Lloyd C., Mortimore B., O'Calladhan M., Sims M., Smaldon N., Smith A., Smith M., Sounhammer E., Stadon K., Sulson J., Phomas K., Vaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                         GLUCAN ENDO-1, 3-BETA-GLUCOSIDASE, ACIDIC
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Phabditidae: Peloderinae: Caenorhabditis.
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PYRROLIDONE CARBOXYLIC ACID (PROBABLE).
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PROTON DOMNY (BY SIMILARITY).
N > D (IN REF. 2).
Y -> N (IN REF. 2).
K -> N (IN REF. 2).
MISSING (IN AS SEQUENCE).
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01 FEB-1994 (Rel. 28, Last sequence update)
01-JUN-1994 (Pel. 29, Last amortation update)
HYPOTHERICAL 45.5 KDA PROTEIN F4449.7 IN CHROMOSOME III.
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Sulston J., Thierry-Micg J., Thomas K., Vaudin M., Vaugi
Waterson P., Watson A., Weinstock L., Wilkinson-Sproat.
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Hydrolasc; Glycosidase, Signal; Multigene family.
SIGNAL 1. 29 PROBABLE.
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MEDITINE-44150718; PHPMed=7906398;
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EMPL; A17120; CAA01264-1; -.
FMPL; M60460; AAA34103-1; -.
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The But peat Bioinformatics institute. There are no restrictions on
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Wormberg: E4489.7; PE00174. Hypotharical protein. SEQUENCE: 450 AA: 45523 MW; JERHESRYBB4CZD7D PR054; EMBG: 1,24648; AAA28029,1; -. . [일본등등등등음음음음울중

111 F. BUVRTRIBBERGRANDERSTVLUPPOPMINEPPOINT EFVIEWEFFWEFFWEFFWERFT (FELLIGHE 1217) and interpolation where the property is the proposition of the property of th 0.6%; Score 54; D8 1; Length 400; 14: Mismatches (2) fadels Pred. No. Googl Similarity 25,48) es 15, Conservitye 1 Anery March Mary Hees Esst

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Eukaryota: Merazoa: Chordata; Graniata; Vertebrata; Enteleostomi; Mammalia: Eitheria: Medectia; Sciuroquathi; Muridae; Cricetinae; of FEM 1999 (FeE, 33, Prouted) of FEM 1996 (FeE, 33, Last Separace appliate) of FEM 1999 (FeE, 34, Last annotation update) Tricefulus ariseus (Thinese hamster). VIMENTIN (FRAGMENT).

Bloemenda) H., Odax W., gaax Souken V., Jerdement H., Pamaekers F. Omra I., Benedetti L., TINE B3297272; PubMed-5688458; SECHENIE ER M N.A. THE DESIGNATION OF SECTION Thermalis. 

"organization and expression of the vimentin gene."; Biol. Pep. 9:115 118(1985).

SECOENTE OF AN 448 FROM N.A.

ONE OF THE MOST PROMINENT PROSPHOPROTEINS IN VARIOUS CELLS OF TERES ALLS BENCHE MIRS STORED MAY 1997; \* 150 PMILS PRESIDENTIAL DATABASES. FUNTION: VIMENTIN ARE CLASS-THE INTERMEDIALE PHAMBHYS FORD IN VARTEUS NONEFLIBELIAL CELLS, ESPECIALLY MESENCHYMAL CELLS. STROUTL: HOMEPOLYMER.

MESENTHYMAL ORIGIN. PHOSPHORIATION IS ENHARDE EGRING CHELDIVISION, AL WELLEN THE UNE VEHILLE FILAMENTS ARE SIGNIFICANTER RE-ROAMEER (BT SIMILARITY). SIMILARITY: RELONGS 10 THE INTERMEDIATE FILAMENT FAMILY.

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Pram: PF00038; filament; l. PROSIES PS00226; IE; l. Intermediate filament; Goiled coil; Heptad tepeat pattern; EMBL: X87227; "AA6..679.1; -... BSSE: PO3069; ISWI. InterPres; IPROOLEGA; Phosphorylation. N.N. LER

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                                                                                                                                       Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Scinroquathi, Muridae, Cricelinae,
                                                                                            0.6%; score 64; DB 1; Length 448; 25.3%; Pred. No. 21;
                                                                                                             Mismatches 41; Indels
                                                                    51848 MW; 2518FDFE759B4B87 CRC64;
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448
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Best Local Similarity
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between the Swiss Institute of Rioinformatics and the EMHL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a License attendent (See http://www.isb.sib.ch/insergere) or send an email to licensedisb-sib.ch). This SWISS-PROF entry is copyright. It is produced through a collaboration PIME ONE OF THE MOST PROM NENT PHOSPHOPROFEINS IN VARIOUS CELLS OF DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY MESENCHYMAL ORIGIN, PHOSPHORYLATION IS ENHANCED DURING CELL. VARIOUS NONEPTHELLIAL CELLS, ESPECIALLY MESENCHYMAL CELLS SIMILABILY, REPORDS IN THE INTERMEDIATE FLUAMENT FAMILY. EMEL: K00927; AAA37104.1; -. EMEL: K00921; AAA37104.1; JOINED. - ! - SUBUNI1 : HOMOPOLYMER. REORGANIZED.

FUNCTION, VIMENTIN ARE CLASS 111 INTERMEDIATE FILAMENTS FORM, IN Conax-Jeuken Y.E.E.M., Quax W.J., Bloemendal H.; "Primary and secondary Structure of hamster vincentin predicted from the nucleotide sequence."; Proc. Natl. Acad. Sci. 0.5.A. 80:x548-3552(196x).

Quar W.J., Equeris W.V., Hendriks W., Opax-Touken Y.E.F.M., Bloemendal H.;

MEDLINE:84026520; PubMed=6194898;

SEQUENCE FROM N.A. NCB1\_TaxID-10036;

TISSUE Lens;

"The structure of the vimentin dene.";

CC11 35:215-224(1983).

SECUENCE FROM N.A.

MEDLINE=83221633; PubMed~6304716;

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2061 LWKPLAYQILLKTEGSSPKVBEYAALITVLALAPYIKENYIVLIPYSIPFLAELMEDPPEE 2120
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Mammalia, Eutheria, Primates, Catarthini, Hominidae, Homo.
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25.3%; Pred. Ro. 22;
ive 18; Miswatches 41, Indels
                                                                                                                                                                                                                                                                                                                       Intermediate filament, Coiled coil; Heptad repeat pattern;
Acetylation; Phosphorylation.
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Y -> D (IN REF. 2).
R -> I (IN REF. 2).
7AC417008CB04776 CRC64;
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01-0CT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
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COIL IA.
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EMBL, KO0922, AAA37104.1; JOINED.
EMBL, KO0924, AAA37104.1; JOINED.
EMBL; KO0924, AAA37104.1; JOINED.
EMBL; KU0925; AAA37104.1; JOINED.
EMBL; KO0925; AAA37104.1; JOINED.
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Best Local Similarity 25.3%,
Matches 20, Conservative 1
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PROSITE; PS00226; IF; 1.
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HSSP; P03069; ISWI.
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P08670;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as land as its seatent is in no way modified and this statement is not removed. Usage by and for commercial outilities requires a library agreement (See Mrtp //www.ish sib ch/anneages) or send an email to libemsedisb'sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- SUBUNIT: HOMOPOLYMER.
-i- FTM: ONE OF THE MOST PROMINENT PHOSPHOPFOTEINS IN VARIOUS CELLS OF PRESENCHYMAL ORIGIN. PHOSPHORYLATION IS ENHANCED DURING CELL. DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                                                                                                                                                                                                                                                                                                                                                                   Electrophoresis 18:588-598(1997).
--- FUNCTION: VIMENTIN ARE CLASS-III INTERMEDIATE FILAMENTS FOUND IN VARIOUS NONEPITHELIAL CELLS, ESPECIALLY MESENCHYMAL CELLS.
                                                                                                                                                                                                                                                   Simpson R J., Dorow D.S.; "Two-dimensional electrophoretic analysis of human breast carcinoma
                                                                                                                                                                                                                                                                                        proteins: mapping of proteins that bind to the SH3 domain of mixed lineage kinase MLK2.";
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                                                                                                                                                                     TISSUE-Breast carcinoma;
BEDLINE-97295304, PubMed-9150946;
PASTULSSEN P.K., J.H. Eddes I.S., Mority R.E., Reid G.E.,
SImpson R.J., Dorow D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intermediate filament; Coiled coil; Heptad Lepeat Pattern,
                                                                    Submitted (TAN-1909) to the EMM, Sembank OpPAL databases.
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858EC88732865FF1 CRC64;
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EMBL: Z19554; CAA79613.1; -.
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                                                                                                                                  SEQUENCE OF 16-24 AND 54-69.
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                                                    Zimbelmann R.;
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"Monse vimostin; structural relationship to tos. jan. CRER and tpr.";
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Ando S., David I., Sadiura H., Tanato K., Inaqaki M.;
Ando S., David I., Vananchi I., Sadiura H., Tanato K., Inaqaki M.;
"Evidence that Sor MZ is a unequephosphorylation site on vimentin
threfields of property protein kinase II.";
Biochem. Medphys. Post commun. 175055-922(1991).
! FURNIBALL VIMENTA ALE CLASS 111 INTERMEDIAL PROTECTION OF THE CALLS.
VARIOUS NONEPITHELIAL FELLS, ESPECIALLY MESERCHYMAL CELLS.
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"Itanscriptional regulation of the vimentin encoding gene in mouse
mpeloid leokemia Miselis.";
                                                                                                Enkaryota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:
Mammalia: Entheria: Rodertia: Sciuromaathi: Muridae; Muridae; Mus.
NPRI, Engli: (100-00)
                                                                                                                                                                         Wood L., Thertanit N., Vancii J.; "Vimentin chNA chores covering the camplete intermediate Hilament production are found in an EHS tennot chNA library."; Gene Zeill-1919/1749-1757(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 95009907; PubMed 7524108; Metrick B.A., Patterson E.M., Wickler L.L., He C., Selkirk T.Y., Metrick B.A., Patterson E.M., Wickler L.L., He C., Selkirk T.Y., Separation and an expression of lamiliar and novel murine proteins using preparative two adminisional gel electrophoresis. T. Electrophoresis 15:735–745 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIVISON, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (SEP 1995) to the EMBL, Generally Table Latabases.
                                                                                                                                                                                                                                                              Podolin P.L., Prystowsky M.B.;
Submitted (eff-1990) to the EMBL/Gongenk/DDRT databeses
         PRESENTATION AT SEP OF AND SEROBL.
 PHI
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                                                                                                                                                               MEDITINE 89 (06/54) PubMed 2744479;
                                                                                                                                                                                                                                                                                                                 MEDLINE 30220517; Pubmed 2325630;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDITINE 90265604; PubMed 2140537;
                                                                                                                                                                                                                                                                                                                                                      Mol. Gen. Senet. 221:33-4 (1998).
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE THOUSE SPICEON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECTENTE OF TOTAL FROM N.A. SIRAIN RALBZI
                                                                                                                                                                                                                                                                                                                                                                                                                                         mengene 5:645-655(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HI-MOPOLYMER.
 STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Willey 166:281-286(1995).
                                                                                      Mus musculus (Mouse).
                                                                                                                                                 SECUENCE FROM N.A.
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VIME MESSE
                                                          VIMENIIN.
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the Buropean Bioinformatics Listitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communcial entities requires a license attended. (See Little, [AAA] ob the hightherenes or send an email to license dish-sib.ch).
between the Swiss Institute of Bioinformatics and the EMBL outstation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Métazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia: Eutheria, Rodentiu, Seluroquathi, Muridae, Murinae, Ratus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (BY CAM-KINASE II). PHOSPHORYLATION (BY CAM-KINASE II).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE, PS00226, IF, 1.
Intermediate tilament, Coiled coil, Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C -> S (IN REF. 6).
UNDRFA -> ILLAEL (IN REF. 6).
EL -> DV (IN REF. 4).
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> V (IN REF. 4).
-> D (IN REF. 1).
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39, Last arrotation update)
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01-JUL-1993 (Rel. 26, Last sequage MAY 2000 (Pel. 39, last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 LOAQTQEQHVQTDVDVSKP 252
                                                                                                                                                                                                                                                                                                       PIR; JS0241; JS0241,
PIR; S12774; S12774;
HSSP; P019649; 18M1.
SWISS-2DPAGE; P20152; MOUSE.
                                                                                                                                                                  EMHL, X56397, CAA39807.1,
EMHL, M26251, AAA40556.1,
EMHL, X2256, CAA30251.1,
EMHL, X514.8; CAA35803.1,
EMHL, Y077.89, CAA69019.1,
EMHL, P0478.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECOENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2061 DWKPLATGILLKTRESSFKVRFAALITVLALAEKLKBAYIVLLFESIFFLAELMEDECEE 3120
                                                                                                                                                                                                 THE MOST PROMINENT PROSPHOPROTEINS IN VARIOUS CRILIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o; daps
                                                                                                                                Submitted (XXX-1992) to the EMEL, Greenearly Johnst databases.
                                                                                                                                                                                                                                 DIVISION, AL WHICH LIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
FROSPECRITATION (BY CAM-KINASE II)
                                                                                                                                                                                                               MESENCHYMAL ORIGIN, PHOSPHORYLATION IS ENHANCED DURING CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY CAM-KINASE II)
                                             "Differential expression of vimentin in rat prostatic tamors.",
Biochem. Biophys. Res. Commus. 182:1254-1259(1992).
                                                                                                                                                                   VARIOUS NONEPITHELIAL CELLS, ESPECIALLY MESENCHYMAL CELLS.
                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plam: PF00038; filament; 1.
PROSITE; PS06226; IF; 1.
Intermediate filament; Colled coil; Heptad repeat pattern;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.6%, Score 64; DB 1; Length 465;
25.3%; Fred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41; Indels
               Verhaegh G.W.C.T., man Rekhages A.,
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6587FE7652CB3682 CRC64;
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01-NOV 1997 (Rel. 35, Last annotation update)
DNAK PROTEIN (HEAT SHOCK PROTEIN 70) (HSP70).
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18; Mismatches
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COIL 1A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEAD.
MEDITINE 92171936; PubMed-1540169;
               Bussemakers M.J.G., Verhaegh G.W
Debruyne F.M.J., Schalken J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X62952; CAA44722.1; -. EMBL; M84481, AAA42339.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 LQAQIQEQHVQIDVDVSKP 262
                                                                                                  SEQUENCE OF 85 159 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                   SUBUNIT: HOMOPOLYMER. PTM: ONE OF THE MOST
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(2)
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FIR, JQ1389, JQ1389.
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Best Local Similarity
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95
131
153
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                                                                                                                     Paine M.L.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=ATCC 35210 / B31;
MEDLINE=98065943. PubMed-3403685;
MEDLINE=98065943. PubMed-3403685;
Praser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
Lathiata R., While O., Kreham K.A., Dodson R., Hickey E.K., Gwinn M.,
Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
Peterson J., Kerlavay- A.R., Quackenbush J., Salzberg S., Hanson M.,
var Vugt P., Paimer N., Adams M.D. Gorayne J.D., Weidman J.,
Otterback T., Watthey I., Montonald L., Artiach P., Howman C.,
Carland S., Pujii G., Cotton M.D., Horst K., Roberts K., Hatch B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                   "Nucleotide sequence of a Bacillus megaterium gene homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            548 FSSEVTISNLENLFQRAELSKNGEWYEVLKIAADILIKEEILSENDQLSNQV 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          514 FTTEKTERDEGKVEEAEVTRANEARDALKAAIERNDEEIKAKRDELQEIV 565
                                                                                                                                                                                                                                                                                                                  -:- SIMILARITY: BELONGS TO THE BEAT SHOPE PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.6%; Score 64; DB 1; Length 605; 32.7%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1CBCC2C4F34A9334 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
                                                                                                                                                                                                                         dnak gene of Escherichia coli.";
Nucleic Acids Res. 15:3923-3923(1987).
-!- FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).
                                      Bacteria, Firmicutes; Bacilius/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rorrelia burgdorferi (Lyme disease spirochete).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEC-1938 (Rel. 37, Created)
-DEC-1998 (Rel 37, Last sequence update)
-DEC-1998 (Rel 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Mismatches
                                                              Bacillus/Staphylonomus group: Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaperone, ATP-binding, Heat shock.
SEGHENCE 605 AA: 65250 MW; 1CBC
                                                                                                                                                     MEDLINE=87231083; PubMcd=3035506; Sussman M.D., Setlow P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                               INDUCTION: BY HEAT SHOCK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interpro: IPR001023; -. Pfam: PP0012; HSP70; 1 PPINTS: PR00301; HEATSHC
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                   Racillus medaterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECHENCE FROM N A.
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15-DEC-1998 (Rel
                                                                                      NCRI_Tax:D=1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N'HI_1AXID=139;
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                                                      the European Moontoformaties fastitute. There are no restrictions on its use by new profit institutions as lond as its content is in no way medited and this statement is not removed. Usage by and for commercial entities a parameter of (Per Hilly John Sci will Milion are consisted an email to Decise Misseshieth).
This SWISS PROTECTIFY is copyright. It is produced through a collaboration between the SWISS Estitute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       o: Gaps
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Schmitter (Abr. 1009) to the EME Aberrack (ERB) databases.
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SUBCEILLIAR INTALENCE TYPOPAGARITA AND NOTICEAR (BY SIMILARILY).
SIMILARITY: BELOADS TO THE IMPORTER BELA FAMILY.
SIMILARITY: CONTAINS 9 HEAT REPEAIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sarchatomyres rerevisiae (Baker's yeast).
Makaryota: Bundi; Ascamyrefa; Sarcharomyretina; Sarcharomyretes;
Sarchatomyretales, Sarchatomyretareae; Sarcharomyres.
NFBL: Laxio 4942.
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olean 1996 (Ref. 44, Last sequence update)
01 estrabor (Ref. 48, Last amodation update)
IMPORTIN BETA CSBGUNIT (RAPV-PHEPIN BETA 3 SUBUNIT) (PROTEIN

    2.6%: Score 64: 108 lt. Longth 971:
44:1%: Pred. Ro. 55.

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                                                                                                                                                                                                                                                                                                                                                 371 AA: 112959 MW: 088A688B73BC591A CROS4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             839 SEASYRDPNETKIYQAFEKSDELDANNANDDELYTYLIĞI. 879
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HEAT Z.
HEAT A.
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Host Local Similarity (4.18
Martches 14: Canservative
                                                                                                                                                                                                                                                                                                                Apportantion! protein.
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S0b; S0004925; PSEL.
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                                                                                                                                                                                                                                                                                                                                                                  341. EEVIYDHAKÇALDRVALKLOGFYLAAPI EÇYLÇÇMITSTEWRERFAAMMALSSAABGGAD 400
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Bukaryota: Metazoa: Chordata: Craniata: Vertebrata: Eutoleostomi:
Mammalia; Eutheria: Rodentia; Sciurounathi: Muridae: Marinae: Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RETINORIASTOMA PROTEIN (RB) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2006 (Fel. 39, Created; 30-MAY-2006 (Fel. 39, Last sequence update)
01-02F-2000 (Fel. 40, Last annotation update)
RETINDBLASTOMA-LIKE PROTEIN 2 (130 KDA RETINDBLASTOMA-ASSOCIATED PROTEIN) (PRB2) (P130) (RBR-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cioning and characterization of the rat p130, a member of the retinoblastoma gene family."; Blochim, Blochim, Acta 136, 22-27(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SPRAGUE-DAWLEY: TISSUE-Spleen;
MEDLINE-97884252; PubMed-9247086;
Sawada Y., Nomura H., Endo Y., Umeki K., Pujita T., Ohtaki S.,
Pujinaga K.,
                                                                                                                                                                                                                                 0.6%; Score 64; DB 1; Length 1089; 19.6%; Pred. No. 64;
                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                  1089 AA; 121030 MW; 905F7FH5B8824637 CR064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2F5, BINDS TO CYCLINS A AND E (BY SIMILARITY). SUBCELLULAR LOCATION: NUCLEAR.
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                                                                                                                            A -> S (IN REF. 1).
P -> A (IN REF. 1).
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                                                                              HEAT 8.
                                          HEAT
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Rest Local Similarity 19.6#
Matches 19, Conservative
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CONFLICT
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                                                                                                                                                                                                                                                                                                                            396 LASILLFEEYISYSSQEEMDSNKVSLLNEQFLPLIRLLESKYPPTLDVVLEEHLKETADLK 455
                                                                                                                                                                                                                                                                                                                                                         Caps
                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HISSUE-Bone marrow:
MICLINE 9628121, Fight of 8721849,
Micrise T., Seki N., Ishikawa M.-I., Tanaka A., Nemura N.;
Marrace T., Seki N., Ishikawa M.-I., Tanaka A., Nemura N.;
Mediction of the coding sequences of unidentified human genes. V.
The coding sequences of 40 new genes (MIGANOIGH-MIGANOIGH) acquired by
analysis of CDMA closes from human cell line KG-1.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Graniata, Vertebrata, Euteikostomi,
Mammaiia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
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39.4%; Pred. No. 88;
                                                                                                                                                                                                                        0.6%; Score 64; DH 1; Length 1135; 26 9%; Prod No 66;
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                                                                                                                                                 5C42A87E163E4298 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last Sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN KIAA0194 (FRAGMENI).
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                                                                                                                                                                                                                                                                          10; Mismatches
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                                                                                            POLY GLU.
POLY GLU.
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                       DOMAIN B.
                                                                         POLY - ALA
                                                    POLY-PRO
  SPACER.
                                                                                                                                                   127817 MW;
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                                                                                                                                                                                                                                                                             18; Conservative
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                                                                                                                                              1135 AA;
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Matches 13; Conserv
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Best Local Similarity
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Q12756:
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P49327;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-OCT-2000 (Rel. 40, Tast annotation update)
FATTY ACID SYNTHASE (EC 2.3.1.82) [INCLUDES, EC 2.3.1.38; EC 2.3.1.41, EC 1.1.100, EC 4.2.1 http://ec.acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GANYTE ACTIVITY: (3P)-3-HYDBOXYPALMITOYI (ACYL-CARRIER FROTEIN)
2-GEXADECENOYL-[ACYL-CAPPIER PROTEIN] + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MISCELLANEOUS: THE RELATIVELY LOW BETA KETOACYL, SYNTHASE ACTIVITY MAY BE ATTRIBUTABLE TO THE LOW 4'-PHOSPHOPANIETHEINE CONTENT OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + NADP(+) = 2,3-
PEHYDROACYL-(ACYL-CARRIER PROTEIN] + NADPH
CATALYTIC ACTIVITY: OLECYL (ACYL-CAPRIER PROTEIN] + H(2)O =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- CATALYTIC ACTIVITY: MALONYL-CCÁ + {ACYL-CAPPIER PROTEIN} - COA + AMACONYL-(ACYL-CAPRIER PROTEIN) - CATALYTIC ACTIVITY-CARPIER PROTEIN) + MALONYL-(ACYL-CAPPIER PROTEIN) + MALONYL-(ACYL-CAPPIER PROTEIN) + CO(2) + CAPPIEP FROTEIN) - CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBGNIT: HOMODIMEE, WHICH IS AFPANCED IN A HEAD TO TAIL FASHION.
TISSUE SPECIFICITY: PROMINENT PXPPESSION IN PPAIN, LUNG, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ANTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] + NALP(-) = 3-0XOA-YT-(3APTEP PROTEIN] + NADPH -!- CATALYTIC ACTIVITY- (3P)-3-HYDROXYPAIMITOYI (ACYL-CARRIER PROTEIL -) - CATALYTIC ACTIVITY- (3P)-3-HYDROXYPAIMITOYI (ACYL-CARRIER PROTEIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPON NATI. AND SCITUS A. 91-6379-6383(1994).
-!- FUNCTION: FATTY ACLD SYNTHETASE CATALYZES THE FORMATION OF LONG-CHAIN FATTY ACLDS FROM ACETYL-COA, MALONYL-COA AND NADPH.
THIS MULTIFUNCTIONAL PROTEIN HAS 7 CATALYTIC ACTIVITIES AND AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TORG CHAIN FATTY ACLD + (B+1) COA + N CO(2) + 2H MADP(+). CATALYTIC ACTIVITY: ACETYL-COA + [ACYL-CARRIER PROTEIN] = COA + ACETYL-[ACYL-CARRIER PROTEIN]
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Mctazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   Jayakumar A. Tai M.-H.. Huang W.-Y., Al-Peel W., Hsu M., Abu-Elheiga L., Chirala S.S., Wakil S.J.; "Byman faity acid synthases: properties and molecular cloning."; proc. Natl. Acad. Scri. H. S.A. 92.8648-8699(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACYL CARRIER PROTEIN.
-!- CATALYTIC ACTIVITY: ACETYL-COA + N MALONYL-COA + ZN NADPH -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood F D., Hennigar R A , Jacobs L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Fatty acid synthesis: a petential selective target for antineoplastic therapy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 753-758 AND 1285-1297. WRDLINE-9429438; PubMed 8022791; Kubhi P P , Jenner K Wood F D. Dick J.D., Pasternark G.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYL-CAPPIER PROTEIN + OLEATE.
                                                                                                                                                                                                                                                                                               MFDLINE=96004605; PubMed=7567999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00698; Acyl_transf; 1.
PF00975; Thioesterase; 1.
PF00107; adh_zinc; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [ACYL-CAPPIEP PPOTEIN].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpret TPP000255; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001227; -.
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                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                 TISSUE-Brain
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Pfam;
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Submitted (AFT Feeg to the EME, Seriate Printed diffiliations).
! CAIALYTH' ACTIVITY: REDOMIZES THE DOMINE SIRANDED SEQUENCE OCCORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           614 DIESAHMKIAIYUSESTITSUHRULMGWEEALENVIKSIKPGKUIGVANGKMIELLADNI 672
                                                                                                               Earty acid biosynthesis; Multitumetional enzyme; Phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                   RETA-KETOACYL SYNTRASE (BY SIMILAKITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heidmann S., Selfert W., Kessler C., Londey H., Telcinn et al. Telcinn and Periodogus expression of the Small restrict for modification system."

Nucleic Arids Res. [7:3784-974(1999).
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Ol JAN 1990 (Rel. 13, Last Sequence update)
Ol NV-1997 (Rel. 35, Last amon'ation update)
IYPE II RESIRECTION ENZYME SMAI (EU 5.1.21.4) (ENDONOTIEASE SMAI)
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PYRIDOMAL PROSPHATE (BY SIMILARITY).
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BETA-BYDROXYACYL, DEBYDRATASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%; Score 64; DB 1; Length 2504;
                                                                                                                                                                                                                                     ACYL AND MALDNYL FRANSFERASES.
ENDYL REDUCTASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THIOESTERASE (BY SIMILARITY). THIOESTERASE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                            REFA-KETOAGYE REDGITASE.
ACYE CARRIER (ACE).
                                                                                                                                                 exidereductase; Italisterase; Lyase; NADP;
                                                                                                                                                                                                            BELA-KED ACYL, SYNTHASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEACL REPRESENTED MAGNESTER AND PRINCESSION.
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                     Fram PF00550; pp binding (.)
PROSHE: PS00F0F; B_KED ANYL_SYNHASE: 1.
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Plann: PFOOLOG: Kedoaryl-synt; 1.
                                                                                      PROSTIE: PSSOUPS; ACP_DOMAIN:
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SMAIR.
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A*1 S17E
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modified and this statement is not removed. Usage by and for commercial
                      entities requires a license attenment (we brip //www.jef.sib (begin analog) or send an email to license isbesibleh).
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-!- FUNCTION: FIBRILLARIN IS A COMPONENT OF A NUCLEOLAR SMALL NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: NUCLEAR; FIBRILLAR REGION OF THE NUCLECTUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Khabditida, Khabditoidea.
Phabditidae, Peloderinae, Cacuchabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIBONOCLEOPROTEIN PARTICLE THEOGRIT TO PARTICIPATE IN THE FIRST STOP IN PROTESTING PRIPHEASMAL RWA IT IS ASSOCIATED WITH THE U3, U8 AND U13 SMALL NUCLEAR RWAS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear protein, Methylation, Ribonucheoprotein, rRNA processing
                                                                                                                                                                                                                                                                                    Hydrolase, Endonuclease, Nuclease, Restriction system: Magnesium, SEQUENCE 247 AA; 28782 MW; PRESCORGACENCORYA CROSA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PIM: BY HOMOLOGY TO OTHER FIREILLARINS, SOME OR ALL OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA BINDING (RRF2) (POTENTIAL).
52PDE6555DBCB717 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.6%; Score 64; DH 1; Length 247; Best Local Similarity 34.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22: Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 ALKTEAAKNISKSYIHVSKWMELCKGEWILELLLERFLEHLENYERI 153
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01-NoV-1997 (Rel. 35, Last Sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9, Mismatches
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PRINTS; PK00052; FIBRELLARIN.
PROSITE; PS00566; FIBRELLARIN
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352 AA; 36484 MW;
                                                                                                                                        EMBL; X16458; CAA34478.1; -. EMBL; M98769; AAA26569.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                        PIR; S06045; S06035.
REBASE; 1704; Smal.
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022053;
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DOMAIN
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Best Local Similarity

14:

Matches

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pfam; PF00493; MCM; 1.
PROSITE: PS00847; MCM_1; 1.
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                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                   P53091;
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                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See Mttp://www.isb sib.ch/announce/entities requires a license agreement (See Mttp://www.isb sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1551 LETVLOYISAVAQCMEPHANYLTVKPWPALLSKAYDLIDKVNALLPTETFIPVIRGLV 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beck F.J., Gonsales S., Ward C.I., Molineux I.J.;
"Sequence of bacteriophage T3 DNA from gene 2.5 through gene 9.";
J. Mol. Biol. 210:687-701(1989).
                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sarcharomyces cerevisiae (Baker's yeast).
Bukaryota: Pundi, Ascomycola, Saccharomycolina: Saccharomycetes;
Saccharomycetales, Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-07T-1996 (Rel. 34, Created)
01-07T-1996 (Rel. 34, Last sequence update)
01-07T-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 110,0 KGA FROTEIN IN MSUL-HASI INTERGENIC PEGION.
YMK288W OR YM8021.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.6%; Score 63; DB 1; Length 535;
25.9%; Pred. No. 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
---SIMILARITY: STRONG, TO S.LOMBE SPAC27F1 09C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structural protein.
SEQUENCE 535 AA; 58620 MW; 1791P955153557 CRC64;
                              705 HVILSVLVSCCSSLKETHPPFAIPVPSHARKFFSV 743
                                                                                                                                               01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17; Mismatches
                                                                                                          535 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensewish-sib.ch).
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                                                                                                                                                                                                                                                                                            MFDLINF=90133922 - PubMev1=2614843;
                                                                                                                                      01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                          HEAD-TO-TAIL JOINING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: X17255; CAA35152.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.9%
Matches 15; Conservative
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                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S07521; S07521.
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                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                            NCBI_TaxID=10759;
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                                                                                                                                                                                                        Ranteriophade
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                                                                                                             VHTJ_BPT3
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content. is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license attended (For http://www.isb-sib.ch/announce/or send an equal to licenscalab-sib.ch).
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"Characterisation of Succharomytes offerisiae ARPR and ARPR genes
encoding aromatic aminotiansferases I and II reveals a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycuta, Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 63; DB 1; Length 971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1813 LATTLAPRVELPAIKKTYKQIEKNWKNHMCHPMSIIQEHIGXMKKE 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bjöurson A.J., McPeynolds A D.K., Wright L.E.;
Submitted (MAX-1990) to the EMBL/denbaik/EDBJ Jalabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            788 VAKVCGPYNVEPVIMNEYTTPETNVQNGVLKAMSFMFFYIGNMSKD 833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27D26E4252A78RE2 CRC64;
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C+
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Mol. Gen. Genet. 257:238-248(1998).
-!: SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
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MAINCHEMONSOME MAINTENANCE PROFEIN 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 74;
                                                                                                                                                                                                                                                                       HEAT 1.
HEAT 2.
HEAT 3.
HEAT 4.
HEAT 5.
HEAT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110027 MW;
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                                                                                                                                                                                         EMBL; Z49704; CAA89786.1; -.
                                                                                                                                                                                                                                                     Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 34.8%;
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InterPro; IPR001208; -.
                                                                                                                                                                                                                       S0004901: YMK288W.
                                                                                                                                                                                                                                                                                                     310
387
550
633
                                                                                                                                                                                                                                               Hypothetical protein;
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the Buropean Bioinformatics fractions. There are no restrictions on its use by non-profit institutions as long as its content is in to way modified and this statement is not removed. (Sause by and for commercial orticles a license warmwith (see Diff.)*** ist all the answer or send an email to license@isb.sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1 - FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE POUR RIBONUCLEOSIDE TRIPHOSPHATES AS
        Aminoacyl-trna synthetase; Protein biosynthesis; Liqase; AlF bindina, SIFE 5.2 6.2 "Heal" ROSI'N.
SIFE 504 608 "MESE" PEGION.
BINDING 607 607 ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium leprae.
Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:
Actinomycetales: Corynchacter neae: Mycobacteridaeae. Mycobacterium.
NCBL_TaxID:1769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1994 (Rel. 26, Created, 01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 25, Last semotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Last annotation update)
18-DEC-1998 (Rel. 37, Leanschild)
18-DEC-1998 (Rel. 26, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE KNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-63188701; Fubbred 8445028;
Renere N.T., Fergh S., Charlere S., Loucet-Populaire F.,
Bengre K., Garnier T., Georges C., Lamois P., Limpaihoon T.,
Newton S., Niang K., del Portillo P., Ramesh G.R., Keddi P.,
Ridel P.R., Sittisombut N., Wi-Hunter S., Cole S.T.;
"Nucleotide sequence of the first cosmid from the Mycobacterium
                                                                                                                                                                                                                                                                                                                 em PERGLAKTIERSVQIKAVNEQLEENISEETHESPYETERAGEGLEWLIER 1∠0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leprae genome project: structure and function of the Rif-Str
                                                                                                                                                                                                           0.6%; Score 63; DB 1; Length 1266;
28.3%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                    295 PLEDYFERGRENGAFTVLVDNYVRIGEGTGVVHQAPYFGAEDYRVCMDFNTTR
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33.8; Fred. Ro. 1.1e 02;
ative 13; Mismatches 7; Indels
                                                                                                           3 M · J I (IN REF. 2).
144958 MW: 8869DD4D2ZABD541 CRC64;
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Prami PP01854, RWA_pol_A2; 1.
Prami PP01852; RNA_pol_A2; 1.
Transferaso; DNA-directed RNA polymerase; Transcription; SEQUENTE 1316 AA: 146980 MR; A:805144658:44046 CRC44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1316 AA
                                                                                                                                                                                                                                                              10 Mismatches
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Hest Local Similarity 19.3%
Witches 10, Conservative
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Matches 15; Conservative
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                                                                                                                                   1266 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Microbiol.
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P30761;
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                                                                                                                                                                                                                Onery Match
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MYCLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR ARG, ASP, GLU, GLN, 11E, LEO, LYS, MET AND PRO.
SUBCELLGIAR LOCATION: CYTOFIASMIC.
SIMILARITY: BELONGS FO CLASS-1 AMINOACYL-TRNA SYNTHEFASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Human isolencyl-tRNA synthetase: sequence of the cDNA, alternative mKNA splicing, and the characteristics of an unusually long determinal extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eskaryolas Metaznas Plactaatas Prinsilas Vertebratas Enteleostomis
Mammalias Entherias Primatess Catarrhinis Hominidaes Homo.
                                                                                                                                                                                                                                                                                                                 45.3 PVSLS1SE3RXQFLAFSESOL11MTS1NHS1APVF11AMM313F1MF13F2F1V1GFFF 51.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDICANE 94 x29525; Pak Med R. Szictt, Schimmel P., Neda T., Skiba E. Sverki N., Shipesett E., Schimmel P., Neda T., "Humman 177 epidasmic lawiew of tENA synthetase, seite tive divergent the anticedon binding domain and acquisition of a new structural
                                                                                                                                                                                                                                                                                                                                                                 61 FVNDSTQESSQHTQTOGSATNOMEGNESARSERSHALNHVKKVGOVLGEKVPEAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1412522

of PER 1905 (Ref. 4), cheated)

of PER 1905 (Ref. 4), Last sequence update)

15 JHL-1909 (Ref. 38, Last annotation update)

15 GESTYL TENA SYNTHETASE, CYTAGLACHET (PT 6 1.1.5) (ISBEBRINE
                                                                                                                                                                                                           0.6%; Score 64; DB I; Laugth 1017;
29:1%; Pred. No. 78;
                                                                                                                                                                                                                                                                 299 114 13
                                                                                                        22 ATP (POTENTIAL).
TILVEL MW: GDA85379ABDE774 CRC64:
PROSTED PSCOULD MYM 23 1.
Transville bas regulations (BWA English) Nuclear protein;
TWA replications cell cycle; Arrebieding.
TOWARD S25 S25 AZ MCM.
NP BING 575 502 AIP (PSENITAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nichols R.C., Rabes N., Beerkoel C.F., Plotz P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 91:74 (5 7439(1994).
                                                                                                                                                                                                                                                              the Conservative to Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT: 1256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEUTERNE FROM M.A., AND PARITAL SECURNE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL: Und'454; AAA80154.1; ALF_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE 95247628; PubMed 7721108;
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                                                                                                                                                                                                                                      29.1%;
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                                                                                                                                   19.17 AA:
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Rest Local Similarity
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unit.

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PRESIDENCESCONCERMENTS

Sides

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Length 1316;

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**А**егоругип.

STRAIN-K1;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed usage by and for commercial entities requires a license apprehenced (See Ettp://www.lsb-stb.ch/announce/or seed as exail to license@isb-stb.ch/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alm P.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C., Smith D.P., Noonan R., Guild R.C., delonge B.L., Carmel G., Trompino P.J., Carusio A., Ulia-Nickišen M., Mills D.M., Ives C., Gibson P.J., Martherg D., Mills S.D., Jiang Q., Taylor D.P., Vovis G.P.
                                                                                                                                                                                      MEDINE-95266321; PubMed-7747482; Gompels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J., Martin M.E., Estathiou S., Craxton M., Macaulay H.A.; Martin M.E., "The DNA sequence of human herpesvirus-6: structure, coding content, and genome evolution.";
                                                                                                                                                                                                                                                                                                  "Nucleotide sequence analysis of a 21-kbp region of the genome of human herpesvirus-6 containing homologues of human cytomegalovirus major immediate-early and replication genes."; Virology 204:738-750(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobaster pylori 399 (Campylobaster Fylori 499).
Basteria; Proteobasteria; epsilon subdivision; Helicobaster group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $0.MAY_2000 (Moi 39, Created)
OMAY_2000 (Mei 39, Last sequence update)
01-05T-2000 (Mei 39, Last annotation update)
ENOYL-[ACYI.-CAPPIFP-PPOTEIN] REDUCTASE [NADH] (EC 1.3.1.9) (NADH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,6%; Shore 62; DR 1; Length 250;
25 6%; Pred No. 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 22 mm; recommended in the conservative 11, Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      224080F4FD8031AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1135 LVNCKNSHCAQTVSSVFKGTSVNARQVRIELEPPDKAKPLGTV 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 VINCTKSEVPLLLEPIYQPPAYNEDVMSILLQPPTKKKPFSRI 81
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N-LINKED (GLONAC
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SEQUENCE FROM N.A.
MEDITNE-95027704: PubMcd-7941342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro: TPP002689; -. Pfam; PF01801; Cytomegalo_gL; 1.
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EMBL; X83413; CAA58331.1; ~.
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250
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166
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166
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                                               Nicholas J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haikawa Y.,
                                                                                                                                                                                                                                                                                                                                                 Archaea; Cremarchaeota; Desulturococcales, Desulfurococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pawarabeyusi Y. Hiso Y. Holiswa H. Yamazuki S. Buikawa Jin-no K., Takahashi M., Sekine M. Hata S. T. Aukai A. K. Bosoyama A., Fekul S., Naqai Y., Mishijina K., Nakarawa H., Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oquehi A., Anki K.-i., Kubota K., Nakamura Y., Nomura N., Sako Y., Kikuchi H.; Cenarchaeon, Aeropyrum pernix Kl."; DNA Res. 6:83-101(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62; DB 1; Length 245;
Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human herposvirus (type b / strain Oganda-1102) (HnV6).
Viruses, dsDNA viruses, no RNA stage; Herposviridae;
Betaherposvirinae; Roseolovirus.
NCBI_TaxiD-10370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27041 MW; 97713AP07646AF45 CPC64;
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40, Last annotation update)
                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30s KIBOSOWAL PROTEIN S6E.
                               1523 QLESSWIPLKKVVESGEREICHERFELLE 1552
                                                      :::: || || || :::: | | :|::|: | 346 | RVINRNNRIKRLIDLGAPDIIVNNEKRMLQ 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00578; RIBOSOMAL, S6E; 1.
                                                                                                                                                                                    FKT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99310339; PubMed=10382966;
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01-0CT-1996 (Rel. 34, Last sequ
01-4CT 2000 (Rel. 40, Last anno
                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
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Pfam; PF01092, Ribosomal_S6c,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCB1_TaxID=56636;
                                                                                                                                                                                                                                                                                                             RPS6E OR APE2371.
                                                                                                                                                                                                                                                                                                                                    Aeropyrum pernix.
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Gaps

6

(POTENTIAL) (POTENTIAL). Vovis G.F.,

"Genomic sequence comparison of two unrelated isolates of the human

gastric pathogen Helicobarter pylori.";

Trust T J.;

VGLL\_HSV6U P52508;

AC DT DT DT

SECUENCE

X X X X X X X

Matches

ΟY q Nature 347-176-180(1999).

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                                                                                                                                   this swiss PP-7 entry is expyriable. It is produced through a collaboration between the Swiss Laxitude of Bioinformatics and the BMB, obstation the European Bioinformatics firstlate. There are no restrictions on its way by compress! Institutions as long as its content is in no way modified in this not removed. Usage by and for commercial outfiles requires a license after and Jecober 185.
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Tribum P.E., energoes P., Shestel M.A., Keifer M., Aujay M., Huber R.,
Ferfman P.A., Sherf J.M., Association, Swanson R.V.;
"The complete elecane of the hyperthermopalitic bacterium Aquitex
accolouss,":
*AIALYTE* ATTIVITY: ASYL-(AYL-YARRIER PROTEIN] * NAD(*)
IRANS 2.4 CENTREMAYL [AYL-YARRIER PROTEIN] * NATH.
*FATHWAY: SET AN ERGO IVVE SIFE IN FATIV AYLO BLASVITHESIS.
*SUR-YELHIAR DOWATOW, INNER MEMBRANE ASSACTATED (BY SIMILARITY).
*SIMILARITY: SOME SIMILARITY TO THE SHORT CHAIN
*DEHYDROGENASES/FERM/TASES (SOR) FAMILY.
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                     exidereductase: NAC; Fatty acid blosynthesis: Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.6%; Score 62; DB 1; Length 275;
0.6% N; Pred: No. 22;
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: E44EA1A4#ZA0341B CRC64;
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SECTENCE: 370 AA: 4.494 MW: HAZEBEH5494945E CRESA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Software Associates purposed 95.82 v.2003
Backbott G. V. Morrico, F. V. Chapsterfaird J.C. (Veniel M.G.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.21 INEQETIPLIBLIBSEYPRILLIVVILREHIRETADILLEGEL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 LEKRUMIALADELINSPARELINSPEREFERINIELT B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILABILY BECOMIS TO THE REPORT PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 1687-1998 (Ref. 47, Cheared)
15-1681-1998 (Ref. 47, fast Sequence applate)
15-1687-1998 (Ref. 47, Last Seminotation applate)
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                                                                                                                                                                                                                                                                                                                                   interPro: IPRODZ194; ...
InterPro: IPRODZ 47; ...
Fram: PFOCTOK: adh.Short: 1.
Pram: PFOCTOK: adh.Short.(2); 1.
PKINIS: PKODO41; adh.Short.(2); 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 : U.Z.b. MW.;
                                                                                                                                                                                                                                                                                               EMBLS ARG 1456; AALDS765,13 -
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HYPOTHETIVAL PROFEIN AQ 454.
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This SWISS FROI entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by mon-profit institutions as long as its content is in no way modified and this statement is removed. Usage by and for commercial entities requires a increase accessed, it is the Mark of the Carlo or send an email to license sib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.
-!- DEVELOPMENTAL STAGE: LAIE EMBRYONIC, LAIE PUPAL AND SECOND INSTAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pterygota, Neoptera, Endoptervaota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila,
NCBL_TaxID-7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSTIE, PSO0236, NDUROTR_ION_CHANNEL; 1.
Boroptor: Postsynaptic mombraro: Lowic channel: dlycoprotein: Signai:
Transmembrane: Multiqene Tamily: Polymorphism.
                                                                                  sdpp (b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -! SIMILARITY: BELONGS TO THE LIGAND-GATED LONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
LIKE CHAIN 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bossy B., Ballivet M., Spierer P.; "Conservation of neural nicot nic acetylcholine receptors from Drosophila to vertebrate central nervous systems.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Arthropoda, Tracheata, Bexapoda, Inserta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-1989 (Rel. 10, Last sequence update)
15-JUL-1999 (Rel. 48, Last annotation update)
ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-LIKE CHAIN 1 PRECURSOR.
                      0.6%; Score 62; DB I; Length 470;
                                                                                  6.; indeas

    -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

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                                                                                                                                                                                                                                                                                                                                                               54.7 AA.
                                                    red, No. 41;
8: Mismatches
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                                                                                                                                             1453 BESVOHOTOSLMNILOYLLKIPEEKE 1478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Frui: 11y).
                                                                                                                                                                                                                                                                                                                                                                  PRT:
                                                                                                                                                                                                           17 EWOTONRIKITIKETKKYLKLIPEETE 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88283626; PubMed:2840281;
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PKINTS, PK00252; NKTONCHANNEL.
PKINTS, PK00254; NICOTINICK.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1989 (Rel. 10, Created)
                                                    46.28;
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ouery Match
Best Local Similarity 46.2%
Teaches [2] Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306
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N-LINKED (GLCNAC, . . .) (POTENTIAL).

CARBOHYD

Matches

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SEQUENCE FROM N.A.
MEDLINE-94127579: Pubmod-8590279;
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910 AA, 102737 MW,
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543
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Pteryjota, Neoptera, Endepteryota: Diptora; Brachycera; Musecmerpha;
Ephydroidea: Drosophilidae; Drosophila.
NCBI_Taxib-7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDMCd-3428600; MEDMCHIE BL., GOUR SECONDENCE BLOOM TRAILE BL., GOUR S., Browner G., Jasckle B., Browner G., Jasckle B., Browner G., Jasckle B., Browner G., Jasckle B., Borsal and neural expression of a tyrosine kinase-related Drosuphila gene during embryonic development.";
                                                                                                                                                                        Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- CAUTION: WAS ORIGINALLY THOUGHT TO BE A KINASE ON THE BASIS OF WEAK AND NON-SIGNIFICATIVE SIMILARITIES.
PIR; A27041; A27041.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VALYI-TRHA SYMTHETASE (Et 5.1.1.9) (VALINE--TPMA LIGASE) (VALPS)
       N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                       0.6%; Score 62, DB 1, Leagth 567,
11.2%; Pred, Ho. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: POSSIBLE REGULATORY ROLE DURING DEVELOPMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Indels
                                                                                                                                                                        8, Mismatches 12, Indels
                            н > т.з5084н67н90704АБ СКС64;
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Ruchella, Cyamobacteria, Chrobococaies, Eynechoeystis
NCBL_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F9853272A7DDBESE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      910 AA.
                                                                                                                                                                                                                          1541 FURIVPOLIATVQPKERGEFFQATINKQTALITE 1674
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POLY - ALA.
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712 PC
81021 MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
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                                                   567 AA; 64UIB MW;
                                                                                                                                                    47.2%;
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                                                                                                                                                                              14, Conservative
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          233
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21-JUL-1986 (Rel. 01, Last sequence update)
30-MAY-2000 (Pel. 94, Last annotation update)
40-MAY-2000 (Pel. 94, Last annotation update)
42-MAY-2000 (Pel. 94, Last annotation update)
42-MAY-2000 (Pel. 94, Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Company-Com
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Viruses, ssRNA positive strand viruses, no DNA stage: Piecrnaviridae:
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ppinnis; pPnong6; TRNASAYNTHVAL.
ppinnis; pPnong78; TRNASAYNTHVAL.
Aminoacyt tRNA synthetasc; Protein_biosynthesis; Ligase; ATP-binding.
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-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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Proc. Natl Acad Sci. H S A 81:1539-1543(1984).
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Kaneko T., Turaka A., Sato S., Kotani H., Saruka T., Miyajima N., Suqiura M., Tabata S.;
Suqiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium sypochemics analysis of the genome of Superior Superior Special Portagion from map postitions 64% to 92% of the genome.";
Final Post 2:153-166(1995).
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PG33GP, G84783; G84784; G84786; G84787; G84788; G84789;
Q84790; Q98592; Q98593; Q98594;
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Schild G.C., Almond J.W.;
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Best Local Similarity 13.2%, Pred. No. 93,
Best Local Similarity 13.2%, Pred. No. 93,
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the Burgeau Biointormatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Mountred R.Y., Mandr P.G., Schild S.C., Almond J.W.;
"The norbed de sempence of policeirus type 3 lean 12 alb. companison
                                                                                                                                                                                                                                                                                                                                                                                    PIM: SPECIFIC ENZYMALIC CLEAVAGES IN VIVO YIELD MAIGRE PROTEINS.
MISCELLANFAIS: THE SELAFENTE OF STRAIN SAKIN VACUINE DAY, FOW, 37 IS
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-!- FUNCTION: PEC POSTPEETIDE IS A PHOTEASE THAT CLEAVES AT CHETAIN CLEAVES. A CONTRIBUTION PEC POSTPEETIN TO A TESTED THIS PECTPEASE.

-!- SUBMINITE THE VIEWS CAPABILIES OF MARCHES OF G.J. COSABELMA, UNITS, PACH OF WHICH IS CAMBOSED OF G.J. COSABELMA, UNITS, EACH OF WHICH IS CAMBOSED OF ONE ADDRESS OF E.J. COSABELMA, UNITS, EACH OF WHICH IS CABBOSED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polyprotein; Coat protein; Core protein; Fransferase;
RNA-directed ENA polymerase; Hydrolase; Thiol protease; Myristate;
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                                                                                                              X BANT PRODUCTORANDE (2007 ANTOERSMO) EE 1 878.
MELLINE 9512-4609 PoloMod 782-548.
Rant Books, Hiromath 05No, Filman Dodo, Syed Roo Andries Ko,
Bodde Jones
                                                                                                                                                                                           "Structures of policitus complexes with anti-viral droas, employethers for viral stability and droa design.":
Fort. B. d. 4284-297(1994)
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COAT PROTEIN VP2.
COAT PROTEIN VP1.
COAE PROTEIN VP1.
COAE PROTEIN P2A.
COAE PROTEIN P2A.
COAE PROTEIN P2A.
COAE PROTEIN PAA.
                                                                                             11:56.9 564 (1984).
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Pfam: PF00547; Pf00; EA; 1.
Pfam: PF01552; Pf00; P2B; 1.
Pfam: PF-0560: ENA_beg_ENA_pol; 1.
                 MEDLINE BAZGUZRO, PubMed 6410508;
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EMBLO Xee925: FAA25444.1; ...
                                                                            with portovirus type 1.";
Nacheje Acida Bee, 11:56.
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InterPros IPROBOL99; -.
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STRAIN PROTEEN 12A[1]BS
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[PR0016765 -
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15 SEP 35.
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GAMMA TUBULIN IS FOUND AT MICKETUBULE SEGMIZING CENTERS (MICK)
SUCH AS THE SPINDLE POLES OF THE FUNDERORE; SUBMERSTING THAT IT
IS INVOLVED IN THE MINUS-END NUCLEATION OF MICKOTUBULE ASSEMBLY.
-i- SIMILARITY: BELONGS TO THE TUBULIN FAMILY.
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Pleosporales, Pleosporaceae; Cochliobolus.
NCBL_TaxID=5016;
                                                                                            ANA DIRECTED ANA PATRICHASE PRO-
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Parkinson C., Luo H., Kniqht A., Ahlquist J., Perlin M.H.;
Submitted (AUG-1993) to the FMRL/GenRank/HDBJ databases.
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Best Local Similarity 17.8%; Pred. No. 2.7c+62; Pests
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23 PROTRACE (POTENTIAL).
31 5 -- F (AN FOYAGEAN DALIJA).
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15-JUL-1999 (Rel. 38, Last amoutation appare)
178-118-184 AMMA 14A.R. (AMMA 1941.R.) (15A.RER)
Cochliobolus heterostrophus (Drechslera maydis)
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                                                TCORNAIN 3C.
                                                                                                                                       MYRISTATE.
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InterPro; IPR000217; -.
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0.6%; Score 61; DB 1; Length 265;

Query Match

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This SWISS-PROT ontry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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-- SOBUNIT: HOMOTRIBER OR HOMOTRIBE.
-- SIMILARITY: IN THE R. PERMINAL SECTION: BELONGS TO THE FRINA FAMILY.
-- SIMILARITY: IN THE C-LEMINAL SECTION: BELONGS TO THE HPPK FAMILY.
                                               Gaps
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-!- CATALYTIC ACTIVITY: 2-AMINO-4-HYDROXY-6-(D-ERYTHRO-1,2,3-FRHYDROXYMETHIC-1,2) ABLINDRESTERFINE 2 AMING-4 RYDROXY 6-HYDROXYMETHIL 7,8-DHYDROXFRENIER 3 GIVGLALEBHYDE.
-!- CALALYTIC ACTIVITY: AIF 2-AMINO-7,8-DHYDROX-6-HYDROXYMETHIL 7,8-DHYDROYTERIDINE.
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Lacks S.A., Steenberd B., Lopez P.;
Lacks State four genes encoding enzymes for five steps in the
A cluster of tour genes encoding enzymes for five steps in the
folate biosynthetic pathway of Streptococous promocise ",
J. Bacteriol, 177:66-74(1995).
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"DN sequence of Foltate biosynthesis gene sulD, encoding
hydroxymethyldihydropteria pytophosplokimase in Streptococcus
procumoniae, and characterization of the enzyme.";
                                                                                                                                                          1307 LLGTVAGIPPDKVLHNIMSTFTFMGANVMMITGTTYSFQVINKTVKMVIP 1355
                                                                                                                                                                                                                                                                            187 LYGIVASEIPTPRCHPLMTSYTPSGENVEQAKTVRKTTVLDVMRRELLQP 235
                                                     24; Indeis
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                                               11; Mismatches
Pred. No. 28:
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28.68;
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                                                           14; Conservative
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Best Loral Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Duplication; Transmembrane; Sugar transport, Transport, Slycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIJNE=91342646; Pubmed-1875932;
White M.K., Rall T.R., Weber M.J.;
"Differential regulation of glucose transporter isoforms by the sre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oncogene in chicken embryo fibroblasts.";
Mol. Cell. Biol. 11:4448-4454(1991).
-!- FUNCTION: FACHLITATIVE GLUCOSE TRANSPORTER. PROBABLY A NEHRONAL.
PROSITE: PS00794; HPPK; 1.
Translerase, Lyase, Felate biasynthesis, Maltifucctional enzyme.
DOMAIN 1 19 DHNA.
BOURAIN 120 270 HPPK
SEQUENCE 270 AA; 31097 MW; B3CD8/34584495584 CMC54;
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                                                                                                                    0.6%; Score 61; DB 1; Length 270; 35.3%; Pred. No. 29;
                                                                                                                                                       16; Indels
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-i- SIMILARITY: HELONGS TO THE SUGAR TRANSPORTER FAMILY.
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                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last Sequence update)
01-NOV-1997 (Pol 35, Last annotation update)
GLUCOSE TRANSPORTER TYPE 3 (CEF-GT3).
                                                                                                                                                                                        1747 TSELVSSEVYLLSALAALQKVVFTLPHFTSPYLF 1780
                                                                                                                                                        6, Mismatches
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PRINTS; PR00171; SUGRTRNSPORT.
PRINTS; PF00172; GLUCTENSPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1192; GLUCTRSPORT3
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                                                                                                         Query Match
Best Local Similarity 35.55
Best Local Similarity 35.55
For 12; Conservative
                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus qallus (Chicken).
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                                                                                                                                                                                                                                                                               RESULT 62
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TRANSMEM

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Vijaya Gorfi B.S., Rema V., Kamarkar S., Swarop G.;
"Nucleotide seprement of a cDNA coding for raf lek tyrosine kinase and charactericitis on of this erre product."

J. Brosci. 19:117 12:04[959]

FUNCTI N. MAY SERVE AS FARL OF A SIBMALING PATHWAY COUPLING THE PC REPETOR TO THE ATTIVATION OF THE RESPIRATORY BURST. MAY ALSO DOUBLING TO THE ATTIVATION OF THE RESPIRATORY BURST. MAY ALSO DOUBLING TO THE METHOR AND MAY REQUIATE THE GENERAL METHOR AND MAY REQUIATE THE GENERAL METHOR CHILS.

ANALYTIC ACTIVITY ATE AT PROJECT TYROSINE - ADP +
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Of NeW-1997 (Ref. 5) Last annotation update)
ThosinE-PeofFin FinAsh 105 (PC 2.7.1.112) (PSA-H2K) (HEMOPOLETE) SELL
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MEDITAR V. SAMINGE V. FUKROKA M., MATSIL A., Najatu K.L., Nezawa Y.; Helentification of part of NA encoding box tyrosine kinase from meaakirpocytes.
                                                                                                                                                                                                                        937. ANTO TROBESTVASPEYTE DIELESKABELTESPAANVERLAGTEFT UVERKERSHOME. 996
                                                                                                                                                                                                                                                        1.36. AV MACVALLECTERSCERFILMENEREPP AND VIGETING CONSCIENCE MERCEAN MINIOUS COR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Edwargetu, Metaseai Phereata; Praniata; Vertebrata; Edgeleostomi;
Mammalia; Edtheria; Roderfia; Sciaroquathi; Muridae; Murinae; Battus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCHLULAR LOCATION: ASSOCIATED WITH MEMBRANES.
SIMILARLIY: "NAINS 1 SHZ FOMAIN.
SIMILARLIY: "OUTAINS 1 SHY FOMAIN.
SIMILARLIY: "OUTAINS 1 SHY FOMAIN.
SIMILARLIY: "OUTHE SKOTSTERN TINGSHEEF HAD BYS IN THE "VALATIT"
DOMAIN. BELOAGS TO THE SKOTSURFAMILY.
                                                                                         N-LINKED (GIGNAC) . .) (PHENTIAL). 7584COF61A7A92A5 CRO64;
                                                                                                                                             construction of the Secretary (B. 1) Length 496; token Shallarity 24, 8) Pred, No. 40; e.g. etc. Discontinuo (B. Mismertelaes (Co. 17)
                                                                             "YTOPLASMIO" (POFIDMITAL).
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SEQUENCE OF 22-526 FROM N.A. MINIMES PASS 525 MINIMES PASS 525 FROM N.A. WINIMES PASS 525 FROM N.A. GALLAR B. M. Bishop J.M., Pettenati M.J., Lebo M.N., Diaz M.N., Minimes H., Bishop J.M., Pettenati M.J., Lebo M.N., Diaz M.N., Minimes M.N., Diaz M.N., Minimes M.N., Diaz M.N., Minimes M.N., Diaz M.N., Minimes and is expressed in behaviorable cells. T. Cell. High. 7:2267-2275 (1987).
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"Mosel protein 'frosine Financ and ('-E) proteinfially expressed in cells of hematopoletic origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase: Tyrosine-protein kinase: Phosphorylation: ATP-binding:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota, Metazoa, Chordata, Craniala, Vertebrata, Enteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBL_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TYESSINE PECTEIN KINASE HCK (EC 2.7.1.112) (P59 HCK AND PEO-HCK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.6%; score 61; DB 1; Length 503; Best Local Similarity 21.7%; Pred. No. 61; Maxches 10; Conservative 15: Mismatches 21; Indels
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Lipip WRISTATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                               PRINTS: PRO0452; SH3DOMAIN.
PPOSITE: PSO0107; PROTEIN_KINASE_ATP;
PROSITE: PSO0109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50011; PROTEIN_KINASE_DOM:
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                                                                                                                                                                                                                            Ptam; PF00069; pkinase; L. PRINTS; PR00109; TYRKINASE. PRINTS; PR00401; SH2DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HEMOPOIETIC CELL KINASE).
EMBL; X62345; CAA44218.1;
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                                                    lnterPro; IPR000719; ..
InterPro; IPR000980; -.
InterPro; IPR001245; -.
                                                                                                                                                                                                    PF00018; SH3; 1.
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                        P08631; 2HCK.
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388
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PO86 41;
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MOD_RES
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RENEWS AND REPRESENTATION OF STREET AND REPRE
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SEQUENCE OF 1 22 FROM N.A., AND ALTERNATIVE INITIATION

EMBL: S'4141; AABROTS4.1; EMBL: MRYOF; AAA1/12.1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
RECEPTOR TO THE ACTIVATION OF THE BESPIRATORY BURST MAY ALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: PROFIEM AND PS9-HOK ARE ASSOCIATED WITH MEMBERARES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
ALTERNATIVE PRODUCTS: THE P60-HCK AND P59-HCK ARE PRODUCED BY THE
                                                                                                                                                                                                                                                                Gmeiner W.H., Byrd R.A.;
"Solution structure of the human Hck SH3 domain and identification of
                                                                                                                                                                                                                                                Horita D.A., Baldisseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97263487; PubMed-9104402;
Zhang W., Smithgall T.E., Gmeiner W.H.;
"Sequential assignment and secondary structure determination for the
Src homology 2 domain of hematopoietic cellular kinase.";
              Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.P.; "Two isoforms of murine hek, generated by utilization of alternative translational initiation codons, exhibit different patterns of subcellular localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USE OF ALTERNATURE INTITATION SITES.
TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE MYELOID AND B LYMPHOID LINEACES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "RT loop fletibility antainers the specificity of Src family SH3
domains for HIV-1 Net.";
Biochemistry 37:14683-14691(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98453315; PubMed-9778343;
Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
Ladbury J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTRIBUTE TO NEUTROPHIL MICRATION AND MAY REGULATE THE
                                                                                                                                             Sicheri F., Moarefi I., Kuriyan J.; "Crystal structure of the Src family tyrosine kinase Hck.", Hathre 285:602-609(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.6 ANGSIRUMS) OF 81-137.
                                                                                                                  X-RAY CRYSTALLCCRAPHY (2.6 ANGSTROMS) OP 78-526
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                                                                                   . cell. biol. 11:4363-4370(1991).
                                                                                                                                    MEDLINE-97177106; PubMed-9024658;
                                                                                                                                                                                                                                     MEDI.INE=98239731; PubMed-9571048;
     MEDLINE-91342636; PubMed-1875927;
                                                                                                                                                                                                                                                                                                                     Mol. Biol. 278:253-265(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 406-131-135(1997).
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EMBL; M16592; AAA52644.1; -.
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                                                                                                                                                                                                                                                                                                         its ligand binding site.
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PHOSPHORYLATION (AUTO:) (BY SIMILARITY).
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                                                                                                                                                                                                                               Transletase, Tyrosine Protein Rinase, Thespherylation, ATP-binding,
Myristate; SH2 domain, SH3 domain, Alternative initiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDITUE-91260705. PubMed-2046669; Wang Y., Xu H.F., Rigus M., Rodgers L., Wigler M.; Wang Y., Xu H.E., Rigus M., Rodgers L., Wigler M.; Schizosaccharomyces pombe gene encoding a protein kinase capable of partial suppression of the rasl mutant phenotype."; Mol. Cell. Biol. 11:3554-3563(1991).
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C
                                                                                                                                                                                                                                                                                            TYROSINE-PROTEIN KINASE P60-HCK.
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MYRISTATE (BY SIMILARITY).
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347E877A0A6412B3 CRC64;
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Eukaryota, Pengi; Ascrmycota: Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaees;
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01-DEC-1992 (Rcl. 24, Last sequence update)
01-DEC-1992 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                      FOR P59-HCK.
                                                                                              PRINTS: PR0401; SH2DOMAIN.
PRINTS: PR00452; SH3DOMAIN.
PROSITE: PS00107; PROTEIN_KINASE_ATP;
                                                                                                                                                       PROSITE; PSOULOS; PROTEIN_KINASE_ITK: PROSITE; PSSCULL; PROTEIN_KINASE_DOM: PROSITE; PSSCULL; SH2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mol. Gen. Genet. 235:122-130(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-93062799; PubMed-1435723,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59583 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE) (MAPKKK).
BYR2 OR STE8 OR SPBC1D7.05.
                                                             Pfam; PF00069; pkinase; 1.
PEINTS; PF00109, TYFKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                      PPOSITE: PS50002; SH3; 1
                                                                                                                                                                                                                                                                                                                                                         23
138
241
515
276
290
381
InterPro; IPR001452; -. pfam; PF00017; SH2; 1. Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
526 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCB1_Tax.ID-4896;
                                                                                                                                                                                                                                                                                 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BYRZ_SCHPO
P28829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                                          INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BINDING
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYR2_SCHPO
                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                  LIPID
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the Buropean Bioinformatics institute. There are no restrictions on its use by non-profit institutions as lond as its content is in no way modified and this statement is not trunced. There is, not it conserving entities requires a license agreement ($\frac{3}{2} \cdots \cdot
                                                                                                                                                                                                                                                               This SWISS Re-Learny is cappright. It is produced through a cuilaboration between the Swiss Institute of Ricinformatics and the EMBL outstation -
Wood V., Rajandroam M.A., Barrell B.G., Skelton J., Churcher C.M.,
Submitted (A75-195) to the PMSG/SecondRelet databases
-1- FUNTION: Shernb/THR CHIRE PROJETH KINASE INVOITING ON HUBBITED
MAY SPECIALION IT IS THEORIET IT PROJECTION THE BYRI
PROJETH KINASE WHOTH TRYILE PROSPERRY OF PROJECT KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: MAY PLAY A FUNDAMENTAL ROLL IN DACA GENERAL OF CNS. MAY RESULATE GENE EARINESSON AND DEVELOPMENT OF PESIMITOLLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure and chromosomal localization of the human homeobox gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thorsata: Tambata; Vertebrata; Entelegatomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1579 ALLSKAYDLLBKVNALLPTETETPVIROLVONPLPSVRRKALDLLNNKL 1627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSTIE: PSOULO: PROTEIN KINASE_ST: L.
PROSTIE: PSSOUL: PROTEIN_EINASE_OM; I.
TELESTOLESC: Series/Ahrowhire-protein kinase: AIP bindina:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Enkaryolas Melasons Thorontas Tranjatas Vertebratas Estelee
Mammaltas Estberias Primatess Satarrhinis Hominidaes Homes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Seare 61; DR 1; Length 659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-1078F151FARBOD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polinson L.E., Porres R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5-JUL 1998 (Ref. 6. Terated)
15-JUL 1998 (Ref. 6. Last Sequence update)
15-JUL 1998 (Ref. 7. Last aunotation update)
HPMEGROX PROSPHED LIKE PEDITUN PROXI (PROX 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.35 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PSOOLO7; PROTEIN KINASE_AIP; I. PROSITE: PSOOLOG: PROTEIN KINASE_SI: I. PROTEIN KINASE_SI: I. PROTEIN KINASE_SI: I.
                                                                                                                                                                                                           -1- SIMILARITY: CONTAINS 1 SAM DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No.
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BERLINE FOOTHER FLAMEN MILLIAMS
Zincelovi P.D., Penesan M.K., Delins
Polymeropoulos M.H., Fondrey S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.46.42 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group Martch
Rost Locald Similarity (1998)
Martches Ph. Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (0061)775 (1946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: M74.293; AAA35289.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stations Sports at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIAMIMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X58851; CAA48731.1
298270; CAR10381.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prame Process S., SAM: 1.
Prame Proceeds planases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homos aprecis (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTP: A43724; A44724.
PTR: S40094; S40034.
HSSP: Q64450; IA04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterProj IPROBATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [PR003] 6.600;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECHENCE FROM N.A.
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US278F.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpress
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caps
                -+- SHRTELLTLAK LOGATION: NUCLEAR (PROBABLE).
--- TISSUE SPICTRITIT MAST ACTIVED EXPERSIBLED IN THE DEVELOPING
LENS. DETECTED ALSO IN EMERYONIC BRAIN, LIUNS, LIVER, AND KIGNEY.
IN ABOLT, IT IS MORE ABUNDANT IN HEART AND LIVER THAN IN BRAIN,
SKELETAL MUSCLE, KIDNEY, AND PANCHEAS.
--- SIMILARITY RELONGS TO THE PROSPERO FAMILY OF HOMBOBOX PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorzialia M., Hoshino Y., Buckler-White A., Biumentals I., Class F., Flores J., Kapikian A.Z., Channek K.M., "Donservation of amino acid sequence of VIB and clearage region of 84-KDa outer capsid protein among rotaviruses recovered from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Ref. 16, Last sequence update)
01-APR-1993 (Ref. 25, Last annotation update)
00TER CAPSID PERFORMACIUIININ) (OUTER LAYER PROTEIN VEG)
(CONTAINS: OUTER CAPSID FROIEINS VES AND VEB).
                                                                                                                                                                                                                                                                                                                                                            Homeobox; DNA-binding; Nuclear protein; Transcription regulation;
Developmental protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic intentions.";
3. Virol. 62:2978-2984(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: VP8 IS ONE OF TWO IRMPSIN CLEAVACE PROPORTS OF VP4; THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oprajajia M., Ojeven K., Mishidawa K., Tabinethi K., Joads K.,
Kapikian A.Z., Chanock R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY. PITS: C28839; VDXWE. PITS: R25904; VDXWE. InterPro; IPR000416; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.6%; Score 61; DB 1; Length 746;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 736 AA; 83162 MW; 8EC93BFB8A0E7A18 CRC54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1472 KLPEEREE LIPKAVSFNESPAGEEMLOVENVETHISPOTRH 1512
UNDIFFERENTIATED YOUNG NEURONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 HOLOGOGGERGER VEARVILLEN FREGORGER OF THE 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 83:7049-7044(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                         HOMEOBOX (ATYPICAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human rotavirus (serotype 3 / strain P).
Viruses, darma viruses, Reprieddae, Estavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSPERO-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 97;
                                                                                                                                                                                                                                                                                                                                                                                                      POLY - GLN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        asymptomatic neonatal intection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-86313706; PubMed-4018754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-88275070; PubMcd-2839714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1989 (Rel. 11, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Conservative
                                                                                                                                                                                                                                                                                                                      EMBL; U44060; AAC50656.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER PRODUCT IS VP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     634
736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10957;
                                                                                                                                                                                                                                                                                                                                                                                                    215
572
635
                                                                                                                                                                                                                                                                                                                                           MIM; 601546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VP4_ROTHP
                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P11195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP4_ROTHP
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Pfam; PFUU4zb; VP4; 1.

HEAT REPEATS DOMAIN 2.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
IMFORTIN HETA I SUBUNIT (NARYCHHERIN BETA : STECHIT) (:MPORTIN 95).
                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                         .) (POTENTIAL).
                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1045 IÇKEPTAVEKSEAMVEHETESKYREPSVSELNEDPKSEDJFFFRAVIFFFRA 1097
                                                                    (POTENTIAL)
                                                                                                                           (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
SURCELLHIAR LOCATION: CYTOPLASMIC AND NUCLEAR ENVELOPE (BY
                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 667 APPENDED HILLIGHT STREAM HITTININ PENNIN PENNIN PROPENDED A 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAN-CTP BINDING (BY SIMITARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR NUCLEAR LOCALIZATION SIGNALS. SUBUNIT: FORMS A COMPLEX WITH IMPORTIN ALPHA SUBUNIT (BY
                                                                                                                                                                                                                                                                                                                                                                                    0.6%, Score 61, DB 1, Length 775, 30.2%; Fred. No. le/02;
                                                                                                                                                                                                                                                                                                                                                                                                                            26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport; PS50077; HEAT REPEAT; 1.
Transport; Protein transport; Repeat; Nuclear protein.
DOMAIN 124 482 HEAT REPEATS DOMAIN 1.
                                                                                                                                                                                                                                                                                                                . > PS (IN REF. 2).
68431C8A5D3FDB38 CRC64;
               OUTER CAPSID PROTEIN VP4.
                                                    CUTER CAPSID PROTEIN VP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE IMPORTIN BETA FAMILY. SIMILARITY: CONTAINS 11 HEAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schiosaccharomyers pembo (Fission youst)
Bakaryota, Fundi, Ascomycota, Schizosaccharomycetales;
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                   -LINKED (GLCNAC. .
                                                                                    N-LINKED GLCNAG.
N-LINKED GLCNAG.
N-LINKED GLCNAG.
N-LINKED GLCNAG.
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in to way modified and this statement is not removed. Usage by and for commercial cutifies requires a livenuse agriculement (See http://www ish ship-shononing or send an email to licensee(sb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Esknipoli, Metazoa, Chordata, Chambato, Vertebrata, Faceteoscomio
Mammalia; Butheria, Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDINE-98424247, PubMed-9753325;
Lowe M., Pabhouille C., Nakamura N., Watson R., Jackman M., Jamsa E., Pahman D., Pappin D.J., Warren G.;
Pahman D., Pappin D.J., Warren G.;
Cdc2 Kinasc directly phosphorylates the cis-Golgi matrix protein CM130 and is required for Golgi fragmentation in mitosis.";
                                                                                                                            Gaps
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"The vesicle docking protein pl15 binds GM130, a cis-Golgi matrix
protein, in a mitotically regulated manner.";
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--- DOMAIN: EXTENDED ROD-LIKE PROTEIN WITH COILED-COIL DOMAINS.
--- SIMILARITY: HIGH, TO HUMAN GOLGIN 95
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Slusarowicz P , Kreis T E , Warren G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterization of a cis Solyi matrix protein, GM136.",
y. Cell Biol. 131:1715-1726(1995).
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                                                                                       0.6%; Score 61; DB 1;
26.5%; Prod No 1 20+02;
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30-MAY-2000 (kel. 39, Last annotation update)
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                 POLY - ALA.
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863 AA; 94747 KW,
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Submitted (SEE 1994) for re-SWISS-Ber data back
! PHOTOR: HE MAIN POLE OF EF-4 MAY BELIE TRANSDUCE NUCLEOSIDE
! PHOTOR: HENCE WINDER WINDER MAY BELIEVE TRANSDUCE NUCLEOSIDE
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Sandhaken M.S., Lopisella J.A., Didomenico B., Chakraburtty K.;
Frotein synthesis in yeast, Structural and tunctional analysis of
the gene encoding clouds in actor 3.7;
J. Riol. Chem. 265:158484-15844(1990).
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Eukaryota: Funsti Ascompreta, Saccharomyeetima: Saccharomyeetes;
Saccharomyeetales: Saccharomyeetaceae; Saccharomyees.
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Thur S., Xiv A., Bonato M.C.M., McLandhlin C.S.;
"Sequence indigsts of the translational elongation factor 3 from
Sarcharomyers ortevisian.";
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Kucada I., Hallsworth K., Hawkins J., Hillifer L., Jier M.,
Johnson D., Johnston L., Lansston Y., Latreille P., Le T.,
Martis E., Meneres S., Miller N., Nhan M., Ponley A., Pelnso L.,
Filker L., Plies L., Lajeh A., Treesskis F., Vonari D.,
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Wilcax L., Wohldman E., Vandin M., Wilson R., Waterston R.,
Submitted (MAR 1995) to the EMBL/Sestink/June (analasas).
0.(%) Score 61; DB 1; Length 986;
4.1%; Pred. No. 1.40:02;
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YEPSA OR YEPS OR LEFOS ROBOTO OR 19672.5.
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Udaston M., Andrews S., Brinkham P., Chapper J.,
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25-087-1998 (Ref. 37, Last annotation update)
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                                              Similarity 24.1%;
[4] Conservative ]
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Filker I., Piles L., I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EF (A_YEAS)
     Querry Match
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                                                                                                                                        Caps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-5EC-1998 (Rel. 37, Created)
15-5EC-1998 (Rel. 37, Last secuence update)
30-MAY-2000 (Rel. 39, Last annotation update)
bba-DIRECTED RNA POLYMERASE BETA* CHAIN (FC 2.7.7.6) (TMANSCHIPTASE
BETA* CHAIN) (RNA POLYMERASE EETA* SUBUNIT).
                                                    -!- SIMILARITY: BELONGS TO THE AD-HINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). EF-3 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :0
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50077; HPAT_KEPEAT 1.
Protein biosynthesis: Elongat on lactor; Repeat; AlP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.5%; Score 61; DB 1; Length 1043; 33.3%; Pred. No. 1.56+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115861 MW; REBD7FF0FC469CDB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002 PHAALITVLALAERTERNYLVLLPESTPPLARIMEREPTEVE 2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 KIAILAAFSAMVDAAKDQVALRMPELIPVLSETMWDTKKEVK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEAT REPEATS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F -> I (IN REF. 4).
L -> V (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1574 AA
                                                                                                                                                                                                                                                                                                                                                                                                          RNA binding; Acetylation; Phosphorylation.
                                                                                  CONTAINS 10 HUAT REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                PTAM: PF00005; ABC_tran; 2.
FRASITE, PS00211, ARC_TRANSFORTER, 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN I.
OF AMINOACYL-TRNA TO THE KIBOSOME.
                !- PATHWAY: PROTEIN BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                             EMBL, J05197; AAA35232.1; -. EMBL, J05583; AAA35233.1; -. EMBL, U20855; AAE67391.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 33.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                          -!- PIM: PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   322
607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             469
707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1030
                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001617;
                             MONOMER.
                                                                                                                                                                                                                                                                          PIR; A35027; DVBYE3.
                                                                                                                                                                                                                                                                                                                    SGD; S0004239; YEF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1043 AA;
                                                                                                                                                                                                                                                                                          HSSP; P000080; 1HRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             462
700
1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPOC OR AU_1945.
                                                                                    SIMILAFITY:
                                                                                                                                                                                                                                                                                                       YEPD; 6850;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN VF5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPOC_AUUAE
                                                                                                                                                                                                                                                                                                                                                                                                                     INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         067763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPOC_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                       This SWISS PROI entry is eapyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for confincted entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
               -i- FUNCTION, DNA DEPENDENT RNA POLYMORASE CATALYCES THE TEANSCRIFTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: MEROZÓTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KEA, 42 KEA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOTTES. THE MATURATION TAKE PLACE DUPING SCHIZONT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
                                                                                           SUBGNIT: THE ENZYME CONSISIS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, I BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Centa U., Rodmann D., Matile H., Reber Liske R.,
"A naturally occurring game encoding the major surface antigen
precursor pigo of Plasmodium falciparum lacks tripeptide repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P19598, 025921;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MEROGOITE SUBERTE FEATEIN 1 PPFCURSOF (MERCACITE SUBFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95354793; PubMed 7628565,
Tolle R., Bujard H., Cooper J.A.;
"Plasmodium falciparum, variations within the C-terminal region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                              OF DNA INTO RNA USING THE FOUR RIBONUCLEGSIDE TRIPHOSPHAIES AS
                                                                                                                                            SIMILARITY, BELONGS TO THE RNA POLYMERASE BUTA' CHAIM PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 61; DB 1; Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16, Indels
                                                                                                                                                                                                                                                                                                                                                                                   DNA-directed RNA polymerase; Transcription.
74 AA: 178500 MW: 4861AF291FEF7E78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmodium falciparum (isolate ro-33 / Ghana)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1682 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1520 FMSQLLSSHNFLKKVVESGGREILKGLBEFLLF 1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 PYERVINERNELKELIELMAPPITTENEKRMLQ 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88166657; PubMed=3327688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1032-1682 FROM N.A.
                                                                                                                                                                                                                                                                                                     EMBL; AE000764; AAC07724.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         merozoite surface antigen 1.",
Exp. Parasitol. 81:47-54(1995)
                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01854, KNA_pcl_A2, 1.
Pfam; PF00623; RNA_pcl_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECUENCE OF 1-1061 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                 O.69
Bost Local Similarity 33.39
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                        InterPro; IPR000722; -
                                                                                                                                                                                                                                                                                                                                                                                   Transferase; DNA-dire
SEOUENCE 1574 AA;
                                                                                                                                                                                                                                                                                                                                   TPP002879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=5834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                              BETA' CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (PMMSA) (P190).
                                                  SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSP1_PLAF3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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        entities fortures a license agreement (See hilp ) www ish and for commercial or send an email to Hensedtsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KDA AND 19 KDA ANTIGENS WHICH APE THE MAJOR STREACE ANTIGENS OF MEROCOLTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88142999; Pubmod-2449612;
Peterson M.G., Coppel P.L., McIntyre P., Langford C.J., Woodrow G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (96), 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURPACE PROTEIN 1 PRECURSOP (MEPOZOITE SUPPACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.I. P.O.H.A. PATASÍTOL 27-201-302(1988).
-!- SURCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPL-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- PTM: MEROZÓTTE SHRFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA,
                                                                                                                                                                                                                                                                                                                                                                                                                          MEMBIGANE ANTHER (POTENTIAL).

N.LINKER (GICNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         908 SPAATVIQDIATUPERIQERKIPSHQKIJSETIPNII SOVYSOPSYTAPDIMK 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1365 SSNEYITEDSFKLLNSEQKNTLLKSYKYIKESVENDIKFAQEGISYYEKVLAK 1417
                                                                                                                                                                                                                                                                                                                    Malaria, Morocolte, Polypretein, Repeat, Signal, Glycoprotein,
use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Alvēclātā, Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Langth 1682;
                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. MERCICITE SURFACE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C8_A1E159948CAD5 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum (isolate PC27 / Papua New Guinea).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 2.7e:02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0 69. Source 61. DR 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1701 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brown G.V., Anders R.F., Kemp D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1682 AA; 192462 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Pel 13, Created)
                                                                                                                                                  EMBL; M35727; AAA29715.1; -.
                                                                                                                                                                          235326, CAA84555.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ogery Match
Best Local Similarity 30.2%,
Matches 16, Conservative 1
                                                                                                                                                                                                                                                                                                                                                     Transmembrane; GPI-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                               Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                 InterPro; IPR000561;
                                                                                                                                                                                                                                      PIR; S06286; S06286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCRI_TaxID=5837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSP1_PLAFF
P13819;
                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PMMSA).
                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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*Alloyle dimorphism in a surface antigen gene of the malaria parasite thas month in the figure m. .

1. Mol. 1850. 1952.7 c.24*(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIM: MEROZOTTE SURPACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 42 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MER WOLTES. THE MATURATION TAKE FLACE OBERGE SCHIZCHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                        SUBJELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of AUS-1900 (Ref. 99, Last sequence update)

40-MAY-2006 (Ref. 99, Last annotation update)

40-MAY-2000 (Ref. 89, Last annotation update)

MEROFOLIE SURFACE PROTEIN 1 PRESURSOR (MEROZOLTE SURFACE ANTIGENS)
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MEDIUE 661 Acada Papamed 4074.972;
MARKAY M., Soman M., Bone N., Hyde J.E., Scaite J., Certa U.,
Stunnenberg H., Buland H.;
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Eukaryota: Alveolata; Apicomplexa: Haemosporida; Plasmodium
NGBL_FaxID-70153;
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                                                                                                                                                                                            MEROZOTTE SURFACE PROTEIN 1.
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and the EMBL outstation
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-:- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBERNE BY A GPI-ANTHOR
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PITE, MESSOCITE SUBFACE ANTIGEN CONTAIN THE SECUENCE OF 94 FIA. 42
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOK SUBFACE ANTIGENS OF
MERGEGITES. THE MATURATION TAKE FLACE BURING SCHIZONT.
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"Variation in the gene encoding a major merozoite surface autique of
the human malaria parasite Plasmodium falcipatum.";
Nucleic Acids Res. 14:3311-3323(1986).
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01-0CT-1996 (Rel. 34, Last aniotation update)
MIRGZOITE SURFACE FROIEIN 1 PRECURSOR (NERGELIE SURFACE ANTIGENS)
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Piam; PP00008; EGF; 1.
Malaria: Merozoite: Polyprotein; Repeat: Signal: Glycoprotein;
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Eukaryota, Alvecluta, Apicomplexa, Haemospyridu. Plasmodium.
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0 0; Gaps 968 SDAAYVIQDLATLFEBIQREKKIKSHQKLSETIKNLLSCVYSCPSYIAKDIMK 1020 i.enqth 1726; 10; Mismatches 27; Indels 0.6%; Score 61: DB 1, 30,2%; Pred. No. 2.7e(02) Ouery Match Best Local Similarity 30.2%; Matches 16; Conservative 1 ŝ

"Plasmodium falciparum: gene structure and hydropathy profile of the major merozoite surface antigen (gp195) of the Uganda-Palo Alto : SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR MEROZOTTE SURFACE PROTEIN I PRECUESOR (MEROZOTTE SURFACE ANTIGENS) Plasmodium falciparum (isolate Palo Alto / Uganda). Eukaryota: Alveolata: Apicomplexa: Haemospotida, Plasmodium. Chang S.P., Kramer K.J., Yamaga K M , Kato A , Case S E., 34, Last sequence update) 34, Last annotation update) PRT; 1726 AA. MEDLINE-89605525; PubMcd-3049134, 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequ 01-0CT-1996 (Rel. 34, Last anno Parasitol, 67:1-11(1988). STANDARD; SEQUENCE FROM N.A. Eukaryota; Alveoly NCBI\_TaxID-57270; (PMMSA) (GP195). Siddiqui W.A. MSP1 PLAFP P50495; 

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PTM: MERGZGITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KIDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SUBFACE ANTIGENS OF MERGZGITES. THE MATURATION TAKE PLACE DURING SCHIZONY

entities requires a license agreement (See Littp://www.isb.sib.ch/ancounercial or send an email to licenseelsb.ch). N-LINKED (GICNAC...) (FOTENTIAL).
N-LINKED (GICNAC...) (POTENTIAL).
Malaria, Merozoite, Polyproteis, Repeat, Signal; Clycoprotein; MEROZOITE SURFACE PROTEIN 1 SBSSCEPFAZESA026 CRC64: POTENTIAL. 1221 1221 N-1 1613 1613 N-1 1726 AA, 196174 MW; EMBL; M37213; AAA29611 1; -. Transmembrane; GPI-anchor. 944 990 1016 11114 1221 Pfam; PF00008; EGF; 1. IPR000561; 567 638 944 990 1114 CARBOHYD CAPROHYD CARBOHYD SEÇUENCE InterProj CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBURYD CARBOHYD CARBOHYD CARBOHYD SIGNAL CHAIN 

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Drosophila virilis (Fruit fly). Bukaryota, Metazoa, Arthropoda, Trachcata; Hexapoda; Insecta; Pteryota; Neoptera; Endpteryota, Diptera; Brachycera; Muscomorpha; Ephydrososa; brosophildae; Prosophila WITH GENES OF BITHORAX (BX-C) AND ANTENNAFEDIA (ANI-X) COMPLEXES IT CAN BEHAVE AS AN ACTIVATOR OF BX-C. .i. FUNCTION: FUNCTIONS IN SECMENT DETERMINATION THROUGH INTERACTION -:- SUBCELLUTAP LOCATION: NUCLEAR. MEDITINE-96100387; PubMed-8555104;
Tillib S., Sedkov Y., Mizrokhi L., Mazo A.;
"Conservation of structure and expression of the trithorax gene
servation of structure and expression of the trithorax gene
between brosophila yrrnlis and brosophila meianogaster.";
MACH DAV 53:113-122(1995). 01-0CT-2000 (Rel. 40, last sequence update) 01-0CT-2000 (Rel. 40, last annotation update) PRT; 3828 AA 01-0CT-2000 (Rel. 40, Created) STANDARD: TRITHORAX PROTEIN. SECUENCE FROM N A. NCB1\_Tax ID=7244; TPX\_DPOVE 024742;

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InterPro; IPROU0345; -.
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PDB: ICYI; 29-JAN-96.
PDB: ICYJ; 29-JAN-96.
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        "The Cu(II) repressible plastudic cytochrome c. Cloning and sequence of a complementary DNA for the precapaprotein.";
I. Biol. Show. 2020:0622:067([087]).
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Eukaryota: Viridiplantae: eklorophyta: Chlorophyeeae: Volvocales:
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of NeW 1997 (Ref. 35, Last annotation update)
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POLY - GLN .
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Interfero, IPRes L214; -.
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Tomb J.F., White O., Kerlavace A.E., Clayton E.A., Sutton G.G.,
Fielschmann E.D., Ketchma K.A., Klenk H.-P., Gill S., Doughetty B.A.,
Nelsen E., Qasekonbush J., Zhou L., Kirkness E.F., Peterson S.,
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ENGYL-[ACYL-CARRIER-PROTEIN] REDUCTASE [NADH] (FC 1.5.1.9) (NADH-
"The structure of chloroplast cytochrome c6 at 1.9-A resolution: evidence for functional objective in the structure of the second object of the second objec
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Electron transport; Heme; Chloroplast; Thylakoid membrane;
Photosynthesis; Transit peptide: 3D-structure.
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-!- SUBCELLULAR LOCATION: LUMEN OF THE THYLAROLD MEMBRANE.
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091567E642F457E8 CRC54;
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PRINTS; PRU0605; CYTCHROMECIC.
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FABL OR HP0195.
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                                                           FAB1_HELPY STANDARD;
024990;
30-MAY-2000 (Rel. 89, Created.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 118 [
167 107 ;
148 AA; 15426 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: M67448; AABOU729.1; -.
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Loftus B., Richardson D., Dedson P., Khalak H.G., Glodek A., McKenney E., Elicquiald L.M., Lee N., Adams M.D., Hickey E.K., Herg D.E., Godaywe J.D., Elicaback T.P., Pererson J.D., Kelley J.M., Cotton M.D., Weidman J.M., Pojji C., Bowman C., Watthey L., Wallin E., Hayes W.S., Perendovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBSELLULAR LOWATION: INNER MEMBRANE ASSOCIATED (BY SIMILARITY). SIMILARITY: SOME SIMILARITY TO THE SHORT-CHAIN
                                                                                                                                                                                                                                    "The complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                        1- CAPALYTIC ACTIVITY, ACTI-(ACTL-CARRIER FROTEIN) - MAD(+)
TRANS-2,3-DEHYDROACYL-(ACYL-CARRIER PROTEIN) + NADH
-1- PAIHWAY: SECOND KEDUCIIVE SIEP IN FATTY ACID BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 60; DB 1; Length 275; 35.9%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Daniel R.A., Williams A.M., Errington J.;
Supwitted (DRC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1894A5AA2105895A CRC64;
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30-MAY-2000 (Rel. 39, Last annotation update)
HYFOTHETICAL 35.3 KDA PROTEIN IN FTSL 57REGION (ORPR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 LNEGFLPLIPLEESKYPPFLPVVLEEHLKETADEKKOEL 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 LEKRVRPIAGELNSPYVYELDVSKREHFKSLYNSVKKDL 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEHYDROGENASES/KEDUCTASES (SDR) FAMILY.
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NCBL_Taxib∻1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00106; adh_short; 1.
Pfam; PF00678; adh_short_C2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 108-311 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
                                                                                                                                                                                                                                                                                                             Nature 388:539-547(1997).
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007876;
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                                                                                                         entitles requires a license agreement (See Litp //www.ist sib.ch.unhounce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217 LRVFEEALEQAIEVLKPGGRVSVITFHSLEDPICKTTFKEKSSIPELPPGLPVGLPEEFEP 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORTHOPHOSPHATE + O(5)-(1-CARBOXYVINYL)-3-PHOSPHOSHIKIMATE.
-!- PATHWAY: SIXTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITHIN THE RIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATHWAY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            637 LRGWEEALENVIKSTKPCKLICVANQKMIELLADNINLGDPSSMLKMVEDLISVGEHESF 696
                                                                                                                                                                                                                                                                                                                                                                                                                       O; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      salmonicida is attenuated in fish and is effective as a live vaccine against the salmonid disease furunculosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 34, Last annotation update)
3-PHOSPHOSHIZHMATE 1-CAPROXYUNIVIPRANSFERASE (EC 2.5.1.19) (5-ENOLPRIQYILSHIXIMATE-3-PHOSPHATE SYNTHASE) (EPSP SYNTHASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATOCT: Immun. 61:2172-2181(1993).
-!- CATALYTIC ACTIVITY: PHOSPHOENOLPYRUVATE + 3-PHOSPHOSHIKIMATE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93239331; PubMed-8478107;
Vaughan L.M., Smith P.R., Foster T.J.;
"An aromatic-dependent mutant of the fish pathogen Aeromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                               0 6%; Score 60; DR 1; Length 311;
                                                                                                                                                                                                                                                                                                                                                                                                                       34; Indels
                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 311 AA; 35305 MW; C50C609129DFD4AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR INCATION CYTOPLASMIC (PROBABLE). SIMILARITY RELONGS TO THE EPSP SYNTHASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                     9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      Pred No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00275; EPSP_syrtase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1993 (Rel. 27, Created)
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                                                                                                                                                                       EMBL; 268230; CAA92525.1; -. EMRL; L09703; AAC36835.1; -
                                                                                                                                                                                                                  CAR13387.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   Query Match 0 6%;
Best Local Similarity 31.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAA01426 1;
                                                                                                                                                                                                           EMEN. 294111; CAR13387.1;
Subtilist; PG10219; ylxA.
                                                                                                                                                                                                                                                                                                                                                                                                                         20; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                              Pfam; PF01795; DUF36; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aeromonas salmonicida.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEOUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; A18838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                697 NLK 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AROA_AERSA
Q03321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
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the European Bioinformaties Institute. There are no restrictions on its ase by and profit institutions as long as its entered is in accommercial mobilities and this statement is not removed. Usage by and for commercial entities requires a literare adventment (see http://www.isb.sib.eb/announcy/or send an email to literase*isb-sib.eb).
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                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merkeuch D.J., Daltymple M.A., Davison A.J., Bolan A., Frame M.C.,
McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA seperice of the long unique region in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Softlibe J., Marcy A.L., Coen D.M., Challberg M.D., The herpes simplex wines t_1 pr i Wide sene product: a subunit of BNA polymerase that limition to increase processivity. L. J. Virol, 64:5976-5947(1990).
                                                                                                                                                                                                                                                                                                                                   Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01 MAR 1949 (Rel. 10, Last sequence update)
of oCT 1996 (Rel. 44, Last annotation update)
DNA POLYMERASE PROFESSIV IN FACTOR (POLYMERASE ACCESSORY PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medicach bolo, Galigmple M.A., bolan A., McNab D., Perry L.J., Faylor E., Challford M.D.;
Martin took of chapters simple colors type I aprece required for replication of virus DNA.
                                                                                                                                                                                                                                                               0.0%; Score 60; DB 1; Length 427;
                                                                                                                                                                                                                                                                                                                                8; Indels
                                                              INNA binding: DNA replication.
SEQUENTE: 488 AA: 51159 MW: 432974563DF0A81B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpes simplex virus (type 1 / stain 17).
Viruses: dsbwa viruses, ne PWA state: Herpesviridae;
PP SITE: FS5VI 4; EPSP_SFNTHASE_I; 1,
PP SITE: PS00085; EPSP_STNTHASE_2; FALSE_NEG;
                                                                                                                                                                                                                                                                                                                             4: Mismatehes
                                                                                                                                                                                                                                                                                                 Pred No.
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J. Sen. Virol. EstiSilel'74(188).
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                                                                                                                                                                                                                                                                                                                                                                                              ZHZM ENKLESEEKFLEKVIKHLIMIN 2050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE 88274327; PubMed 2839594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PAP) (DAA-BINDING PROTE N UL42).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 EYMLOGEPRMEERPIGHLVDOLA 134
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                                                                                                                                                                                                                                                                                       47.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virol, 62:444-453(198E).
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                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                                                                                                                                                                                                                                                                                              Best Local Similarity
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                                                                                         SOMETIME.
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This SWISS-PROT entry is capyright. It is produced through a coilaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as lone as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a finefact affected in the removed. The content is not commercial entities requires a finefact affected in the result in the content is not removed.
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                                                                              Sabs
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MEDITINE 9F952821; PubMed 7644896;
Bernard H.O., Chan S.Y., Manos M.M., ona C.K., Villa L.L.,
Bernard H.O., Chan S.Y., Manos M.M., whoeler C.M.;
"Identification and assessment of known and novel human papilithomativuses by polymerase chain reaction amplification, restriction fragment length polymorphisms, nucleotide sequence, and phylogenetic algorithms."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.6%; Score 60; DB 1; Length 500;
   DB 1; Length 488;
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                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (ACT-1995) to the PMRE/Separakank/UDBJ databases.
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SEQUENCE - 500 AA; 55849 MW, 277A44H7CAA421F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      ILY44
VEX. 080919;
01-07T-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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                                                                          3; Mismatches
0.6%; Score 60;
                                       Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 44.
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                                                                                                                                                101 LSPYFILKPAUKCLEWLIH 119
                               57.98,
                                                                                                                                                                                                                      309 VSAVFLLKPOKICLDWLGH 327
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Matches 17; Conservative 1
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                                                                              Conservative
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                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
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O18400;
                                                                      11;
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                                                                                                               Pterygota; Neoptera; Endopterygota; Diptura; Brachycera, Muscomorpha,
Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                          1. Dev. 68:139-147(1997).
FUNCTION: MIGHT CONTROL PHYSIOLOGICAL CELL FUNCTIONS THAN FATTERN
FORMATION DURING EMBRYOGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE: FIRST DETECTED IN THE POSTERIOR REGION OF THE HASTODERM EMBRYO, IN LATER STAGES OF EMBRYONIC DEVELOPMENT, DETECTED IN THE POSTERIOR PORTION OF THE MIDGUT, IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPING MALPIGHIAN TUBBLES, IN A SUBSET OF VENTRAL SOMATIC
MUSCLES, IN THE DEVELOPING CNS AND IN BOLWIG'S ORGAN.
SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMFOROX PROTEINS
                                                                                                                                                                                                                                                                                             "Embryonic expression and characterization of a Ptx1 homolog in Drosophila.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homeobox; DNA-binding; Developmental protein; Naclear protein;
                                                                                                                                                                                                                                 MEDLINE-980703
MEDLINE-980708: PubMed-9431811;
Orbringqin G., Constien P., Zilian O., Wimmer E.A., Dowe G.,
Tanbert H., Noll M., Jaeckle H.;
                                                                                                Metagoa; Arthropoda Trachesta: Hexapoda; Insecta:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3E6B5C19ECEB2E45 CRC64;
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                        PITUITARY HOMEOBOX 1 HOMOLOG (D-PTX1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMEOBOX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 franscription regulation; Activator.
                                                                                 Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLIULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00024; HOMEOBOX.
PROSITE; PS00027; HOMEOROX_1; 1
PROSITE; PS50071; HOMEOBOX_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homeobox; 1.
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InterPic, iPF001356;
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327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       513 AA;
                                                                                                                                                                                                     SECUENCE FROM N.A.
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                                                                                                                                                          NCB1_TaxID-7227;
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                                                                                                                                                                                                                      TISSUE=Embryo;
                                                                                                      Bukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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GWIND M., Netson M., Deboy R., Kolonay J., McClarty G., Salzberg S.L., Fisen J., Fraser C.M.;

"Genome sequences of Chlamydia trachomatis Moen and Chlamydia

pneumoniae AR39."; Nucleic Arids Res 28:1397-1406(2000)

MEDLINE-20330349; PubMed-10871362;

SPOURINGE FROM N A

STRAIN-J138;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hirkey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouti H., Graven R., Powman C., Podson R.,

MFDLINE=20150255; PubMed-10684935;

SEQUENCE FROM N.A.

STRAIN=AR39;

Kalman S., Mitchell W., Marathe R., Lammel C., Pan J., Hyman R.W., Olinger L., Grimwood J., Davis K.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";

21.145-184(1999).

MEDLINE-99206606; PubMed-10192388,

SEQUENCE FROM N A.

STRAIN-CWL029;

Matches 30-MAY-2000 (Rel. 39, Last sequence update) 01-GCT-2000 (Rel. 40, Last annotation update) APOLIPOPROTEIN N-ACYLTRANSFERASE (EC 2.3.1.-) (ALP N-ACYLTRANSFERASE). Gups 0; 0.6%; Score 60; DB 1; Length 513; 30.6%; Pred No 85; lo; Indels 334 LHGISETYDVSPLERYMLPHLVVSIIHHVTGEETEG 369 9; Mismatches 541 AA. PRT; 092701; 0930G2; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequ Best Local Similarity 30-69 Matches 11; Conservative STANDARD; LNT\_CHLPN Ouery Match

Chlamydia pneumoniae (Chlamydophila pneumoniae). Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila.

NCBI\_TaxID-83558;

INT OR CUIE OR CPN0653 OR CP0094.

0;

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                                                                                                                                                                                                                                                                                                                                                   Nacleic Acids Res. 28.2311 2314(2000).
-i- FUNCTION: TRANSFERS THE FATTY ACYL GROUP ON MEMBRANE LIPOPROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                         --- PATHWAY: LIPOPROTEINS BIOSYNTHESIS.
--- STATHWAY: LIPOPROTEINS BIOSYNTHESIS.
--- SIMTLAPITY: BELONGS TO THE APOLIFOCKOTEIN N-ACYLIRANSFERASE
                                                                                                                                                                                                                                                                                            Shirai M., Hirakawa H., Kihoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; "Comparison of whole geneme sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.6%; Score 60; DB 1; Length 541; 33.3%; Pied. No. 91,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61260 MW;
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102
136
177
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N.-1.NKED (GLCNAC. ...) (POTENTIAL).

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SIMILARITY: BELONGS TO PEPTIDASE FAMILY CL; ALSO KNOWN AS THE
PAPAIN FAMILY OF THEOL PROTEASES.
                                                                                                                          MELLINE (22280-5) PiDMod 1565129;
Rosenthal P.T., Nejson R.G.;
"Isolation and character zation of a cysteine proteinase gene of
of MAY LOG (Rob. 22) Last sequence splate)
of NeV 1995 (Rob. 32) Last annotation update)
Theoriesotic TSTEINE PROTEINASE PREDUKSOF (EU. 5,4,22,1) (TCP).
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                                                                herd at as Ar homplessa, Baseespeatidas Plasmediams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Etum; PF00112; Poptidase_C1; 2.
PRINTS; PR00705; PAPAIN.
PR0811E; PS00549; PH101_PR0EASE_HTS; 1.
PR0811E; PS00404; PH101_PR0EASE_ASN; 1.
PR0811E; PS00404; PH101_PR0EASE_ASN; 1.
PR0811E; PS00404; PH101_PR0EASE_ASN; 1.
PR0811E; PS00404; PR0FEASE_ASN; 1.
PR0811E; PS00404; PR0FEASE_ASN; 1.
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                                                                                                                                                                                                          FUNCTION: PROBABLY DESIRADES ERYTHROCYTE HEMOSLOBIN.
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X
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PTR: A45624; A45624.
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                                                                                                                                                                           Plasmodium talciparum.";
Mol. Biochem, Parasitol.
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P545.1 4;
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115 ZAAB,
Ac 25451
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                                                                                                                                                                                                                   Thesis (1992), Fiedrich Misscher Institut / Hasel, Switzerland.
Thesis (1992), Fiedrich Misscher Institut / Hasel, Switzerland.
I EUWCYLON: THE FRES SUBONT OF PROTIENT PRESENTANCE ZA SERVES AS A SCAMEDINE MOLECULE TO CHOFOTHE THE ASSEMBLY OF THE CATALYTIC SUBUNIT AND A VARIABLE PRESIDENCY B SUBONIT.
-!- SUHUNIT: PPZA EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH COMPUSET OF A CATALYTY SUBONIT ASSOCIATED WITH A 65 KDA REGULATORY SUBUNIT (F65) (SUBUNIT A). THE CORE COMPLEX ASSOCIATES WITH A THIRD, VARIABLE SUBUNIT (SUBUNIT B), WHICH CONFERS DISTINCT PROPERTIES TO THE HOLOGRAPHE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 FÜNLLKEIGEAEVRAAAAHKVELCENLPIEGFETTIMNDILECIKELVSDFNGHVKSALA 359
01-0CT-1996 (kel. 34, Created)
01-0CT-1996 (kel. 34, Last sequence update)
01-0CT-2000 (kel. 40, Last annotation update)
8-EPINE/THEFONIND PROTEIN PHOSPHATASE 2A, 65 KDA REDULATORY SUBUNII A.
BETA 180POMM (PD2A, SUHGMIT A, PP65 BETA 180POMM) (PP2A, SUBUNII A,
RI-BETA 180POKM) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                  JOINTA BY A HYDROGHILLS KAGAON, THE INTRAMERAL TOWN THE REPEAT ONLYS MAY BE ARRANGED LAFARALLY TO FORM A ROD-LINE STRUCTURE.

-!- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBDINT A
                                                                                                                                                                                                                                                                                                                                                                   -1- DOMAIN: EACH HEAT REPEAT APPEARS TO CONSIST OF TWO ALPHA HELL/TES
                                                                                                                             Enkaryota, Metazoa, Cherdata, Craniata, Vertebrata, Euteleosfomi:
Mammalia, Entheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38: Indels
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22.2%; Pred. Mc. 10:02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HEAT 1.
HEAT 2.
HEAT 3.
HEAT 4.
HEAT 5.
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HEAT 7.
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Best Local Similarity
Matches 16, Cunserr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   602 AA;
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                  Sus scrota (Pid).
                                                                                                                                                                                                            Mayer-Jackel R.E.
                                                                                                                                                           NCBI_TaxID=9823;
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between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its mase by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (Swe http://www.isb.sib.ch/announce.or.send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration
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Sutton G.G., Blake J.A., Fitzgerald L.M., Flayron R.A., Godayne J.D.,
                                                                                                                                                                                                                                                                                                                   Subbarao S., Morse S.A.;
Submitted (MAY-1995) to the EMBL/DenBank/ToB3 databases.
-!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O, Gaps
                                                                                                                                                                                                  Bacteria; Profeobacteria; beta subdivision, Neisseriaceae, Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYMERASE CORE BINDING (POTENTIAL)
H-T-H MOTIF (BY SIMILARITY).
, 3AF25EBA18A12EEC CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                          THEN IS RELEASED, THIS IS THE PRIMARY SIGMA-FACTOR OF THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 0.6%; Score 60; DB 1; Length 642; Best Local Similarity 34.3%; Pred. No. 1.1e^{\circ}02; Matches 12; Conservative 9; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea: Eurgaichaeota; Methanococcales; Methanococcae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SIGMA-70 FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  984 LOREKKLKSHUKLSETLKNILISCVYSCPSYIAKDI 1018
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5-JUL-1998 (Rel. 36, Last annotation update)
                                                              01-071-1996 (Rel. 34, Created)
01-071-1996 (Rel. 34, Last sequence update)
NO -071-1996 (Rel. 34, Last annotation update)
NOA POLYMERASE SIGMA FACTOR REOD (SIGMA-70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 LIREDEILIAKKIENALKNMVQAISACPGSIAEIL 164
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MEDLINE-96337999; PubMed-8688087,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKT;
                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00715; SIGMA70_1, 1. PROSITE; PS00716; SIGMA70_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00046; SIGMA70FCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00140; sigma70; 1.
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                        STANDARD;
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                                                                                                                                                                                      Neisseria gonorrhoeae.
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                                                                                                                                                                                                                          NCBI_TaxID=485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIA.
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                        RPSD_NEIGO
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                          entitles regaines a license agreement (see http://www.isbraib.dk.ancourage) or send in email to license@lsb-sib_ch)
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Kerlayage A.P., Dougherty R.A., Tomb J.-F., Adams M.D., Keich C.I., Overbeek R., Kirkhew, E.F., Weinstock E.G., Merrier I.M., Gloder A., Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nquyen D., Itterback T.P., Fellow D., Sadow P.W., Hanna M.C., Cotton M.D., Poberts K.M., Henrat M.A., Kaine B.P., Borodovsky M., Klonk H.-P., Praser C.M., Smith H.O., Woose C.R., Venter J.C., "Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (kel. 36, Last sequence update)
30-MAY-2000 (Pel. 39, Tast annotation update)
METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE--TRNA LIGASE)
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SIQUENCE 613 AA, 72968 MW; BEEBOURZERHRRDD CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      651 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                Science 273-1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U67533; AAB98908.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11; Conservative
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                                                                                                                                                                                                                                                                                                                                                PRINIS: PEGLAT: INNASYNTHMET.
PROSITE: PSOC178: AA_IKNA_LIGASE_L: FALSE_NEG.
Aminoacyl IKNA synthetaso: Protein biosynthesis: Ligase: ATP-binding:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Bukaryota: Punai: Ascomponta: Sporbaromyostina; Sporbaromyostos.
Sacharomyostios: Sacobaromyostaroaci, Sacobaromyoss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ol ali zook (kel. 40, Last, andatation update)
HYPOTHERITAL 28,4 KDA PPOTEIN IN EPIZ4-MELZ INTPACENTS RESIGN.
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SIPONI, D. SYSTEINTE, IENA STRIBLIAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         611 VLVNLKPAKLEGVKSFORVLATGESLNILDP 641
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Hypothetical protein: Hensmembrane measurement 17 (2) Popeling Popeling
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Submitted (MAY ) ev.
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                                                                                                                                                                                                           24.96.00
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P5 (8 (5)
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-i- FUNCTION: MAY FUNCTION AS AN ALAPTER OR COFACTOR TO FACILITATE COMMUNICATION HERMS SEQ DENCE-SECLET UNA HINDING BROTEINS AND THE GENERAL TRANSCRIPTIONAL MACHINERY. SEEMS TO BE REQUIRED FOR NORMAL CELL SURFACE ASSEMBLY. INVOLVED IN REPRESSION OF HEME-REGILARTH AND CATAROL THE SEPTEMS SED GENERAL FEBRESSION.
-i- FUNCTION: MEDIATOR OF GLUCIASE REPRESSION.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRE ASP DOMAINS).
                                                                                                                                                                                                                                                                                                                      194 SLVIRSVRVEALYIOSSAQUPVI LAFEASI IVSALVAAFINGONO AFLEOTIGEOTIKS 252
                                                                                                                                                                                                                                                                                                                                                     TUPI_YEAST STANDARD; PKL; 713 AA.
P16649; P17995; P18323;
01-ANG-1990 (Rel. 15, Created)
01-ANV-1990 (Rel. 16, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GLUCUSE MEMERSION REGULATORY PROTEIN TUPI (FLOCULATION SUPPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91153643: PubMed-1960249:
Zhang M., Bosenblum-Vos L.S., Lowry C.V., Boskye K., Zifomet P.S.;
"A yeast protein with homology to the beta-subunit of 6 proteins is
involved in confrol of heme-regulated and catabolite repressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The SEL2 (TUP12) products of Sancharomynes organistae contains a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Fundi, Ascomyota, Saccharomyota ina, Saccharomyoetes;
Saccharomyotaires, Saccharomyotatarea, Saccharomyots.
NCHLTAXID 4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TUP! OR AERE OF SELE OF CYCS OR UMR? OF AAP! OF AMM! OF FLE! OF YOROBAC OF YORBAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams F.E., frumbly R.J.; "Characterization of TUP1, a mediator of almouse repression in
Surcharomyres coregisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Misumi Y., Robayashi H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fujita A., Matsumoto S., Eubara S., Misumi Y., Robayashi B.
"Cloning of the yeast SP12 gener its disruption results in
pleictropic phenotypes characteristic for tupl mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeating motif homologous to beta subunits of G proteins.
                                                                                                                                                                                                    0.6%; score 50; DB 1; Length 651;
                                                                                                                                                                                                                             ; Pred. No. 1.20-02;
10; Mismatches 30; indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Puesterboeft A., Erdmann D., Begemann J., Philippsen P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chairted (MAR 1992) to the FMHQ Sendade (SAB) databases
                                                                                                                    2038CACDCED4927D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Samplandard corportation (Baker's peact).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY TO BETA SUBUNIT OF G-PROTEINS
                                 PULENLIAL.
                                                          POTENTIAL POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell. Biol. 10:6500-6511(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90323611; PubMed-2197185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDI.INE=91192608; PubMed-1901558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91061758; PubMed 2247069;
                                                                                                                    73352 MW:
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                                                                                                                                                                                                    vacij Match
Best Local Similarity (2.2%;
Matches 19; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN) (REPRESSOR AER2)
                                                    445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 97:153-161(1991).
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                                                                                                                    661 AA;
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195
297
425
631
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CARBOHYD
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This SWISS-PROT entry is empyright it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as lond as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb.sib.ch).
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01-APR-1993 (Rel. 25, Last annotation update)
00TER CAPSID PROTEIN UP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
(CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.6%; Score 60; DB 1; Length 713;
15.0%; Fred. No. 1.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_1; 5.
PROSITE; PS50244; WD_REPEATS_REGION; 1.
Transcription requiation; Repressor: Repeat, WD_repeat.
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R -> O (IN REF. 1).
P -> S (IN REF. 1 AND 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 KHEKESI EQPPHQTASLTVQQQPQQQQQQQQHLQQQQQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsRNA viruses, Ferwiridae, Retayirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKT; 775 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human rotaminum (serotype 2 / strain DSI).
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                                                                                                                                                                                      EMBL; M31733; AAA35182.1: ..
EMBL; X16365; CAA34411.1; ALF_INIT.
EMBL; X59720; CAA42259.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WD 4.
WD 5.
WD 6.
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MC
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                                                                                                                                                                                                                                                                                                                                                                                        GPROTEINHRPT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78307 MW;
                                                                                                                                                                  EMBL; M35861; AAA34413.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.0%;
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Best Local Similarity 35.0%
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118
198
409
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658
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                                                                                                                                                                                                                                                                                                                                               InterPro; 1PR001680; - Pfam: PF00400; WD40; 7
                                                                                                                                                                                                                                                PIR, A36362, A36362.
PIR, JN0133, JN0133.
PIR, S11169, S11169.
PIR, S19499; S19499.
                                                                                                                                                                                                                                                                                                                              SGD; S0000680; TUP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             713 AA;
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                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
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399
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P11196;
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"Sequence of the fourth qene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
J. Virol. 62:2978-2984(1988).

SEQUENCE OF 1-280.

Gorciqlia M., Green K., Nishibawa K., Taniquchi K., Jones R., Kapikian A.Z., Chanock R.M.;

MEDLINE-88275070; Purmed:2839714;

SEQUENCE FROM N.A.

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- - SUNCELLUIAR LOCATION: EXISTS BOTH AS A MEMBRANG-BOUND FORM AND AS SOLUBLE FORM IN SERUM AND IN THE EXTRACELLULAR MATRIX.
- - PTM. HEAVILY MODIFIED BY GLYCOSAMINGLYCAN GROUPS (GAG).
- - SIMILARITY: SOME REGIONS OF SIMILARITY TO ENDOGLIN.
- - SIMILARITY: CONTAINS 1 ZP DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sabs
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                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
IG -> SW (IN PFF 2).
IA > SS (IN REF 2).
IA > SS (IN REF 2).
FF (IN PFF 2).
FF (IN PFF 2).
FF (IN PFF 2).
         Consiglia M., Heshimo V., Rucklor White A., Riumontals I. Glass P. Plores J., Kapikian A.Z., Channek R.M., "Conservation of amino acid sequence of VPR and cleavage region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Euthoria; Cetartioduct;ia; Suina; Suidae; Sus.
                                                                                                                                     -!- PTM; VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE
                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                            . .) (POTENTIAL)
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C
                                                                     84-kha outer capsid protein among rotaviruses recovered from
                                                                                                                                                                      -!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1994 (Rel. 28, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 60; DB 1; Length 775;
35.6%, Ered. No. 1.44.02;
ive 8, Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1045 IQKEPTAVLKDEAMVLHLTLGKYNEFSVSLLNEDPKSLDIFIKAV 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPASSESSENA451RE9 CRC64;
                                                                                                                                                                                                                                                                              OUTER CAPSID PROTEIN VP4.
                                                                                                                                                                                                                                                                                             OUTER CAPSID PROTEIN VP8.
                                                                                                                                                                                                                                                                                                               CAPSID PROTEIN VP5
                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
                                                                                    asymptomatic neonatal infection.";

Proc. Natl Arad Sci. U.S.A. 83:7039-7043(1986).

-1- SUBCELLOLAR LOCATION: OUTER CAPSID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITINE-94080582; FubMcd-1333192;
MEDLINE=86313706; PubMed=3018754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequ
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87592 MM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.68,
                                                                                                                                                                                                                                                                protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Comservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                         OTHER PRODUCT IS VP5
                                                                                                                                                                                                           PIR; CZ5904; VPXRDS.
InterPro; IPR000416; -
                                                                                                                                                                                                                                        Pfam; PF00426; VP4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                          EZBR44; VPXPW4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280
775 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      593
593
599
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324
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922974; OKCHS75; OCLUSS;
01-NV-1997 (ROL, 16, Strated)

61-NV-1997 (ROL, 14, Last Sequence update)

61-NV-1997 (ROL, 14
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Mammalia: Entherla: Primates; Catarrhini; Hominidae; Homo.
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Chili Boscowich94(1996).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstaid on the European Hobinformatics lastfulte. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Beage by and for connected not the connected or send an email to licenset shelloch.
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-:- FUNCTION: INVOLVED IN NUCLEAR IMPORT OF M9-P-NIAINING PROTEINS. IN VITRO, BINDS DIRECTLY TO THE M9 REGION OF THE HETEROGENEROUS NUCLEAR RIPORDGLED FOR (HNRIP), A1 AND AZ AND, TOGETHIR WITH ATP AND, POSSIBLY GIPORE RAN, MEDIALES THEIR IMPORT INTO THE NUCLEUS. APPEARS ALSO TO BE INVOLVED IN HNERR ALZAZ NUCLEAR
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01-OCT-2000 (Rel. 40, Last sequence update)
EJGAL AJHESLAN KINASE 2 (E2 2 7.1.112) (FASE 2) (TLL AJHESL N EIRASE
BERN) (CAR BERN) (GALTIUM-DEPENDENT TYROSINE KINASE).
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                                                                                                                                                                                                      "Transportin: nuclear transport receptor of a novel nuclear protein
                                                                                                                                            Nakielny S., Siomi M.C., Siomi H., Michael W.M., Pollard V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%; 3core 56; DB 1; Length 890;
20.7%; red. Nc. 1.7e+02;
ive 19. Mismatches 54; Indels
Fridell R.A., Thorne L.W., Berson R.E., Cullen E.F.;
Sabmitted (a.7-1946) to the PMRL/COCKERA, 1008.) databases
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BEAT 5.
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I -> T (IN REF. 2).
Q -> L (IN REF. 3).
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HEAT 3.
HEAT 4.
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                                                                                                                 MEDLINE 97141410; PubMed 8986607;
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15 JUL 1998 (Rel. 36, Created
15-JUL-1998 (Rel. 36, Last seq
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MIM; 602901; -.
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                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                              NCB1_Tax1D=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wohldman P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPOSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                          C14B9.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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    ADDE POT SERVICE SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Gaps
        Eukaryota, Metazoa, Phordata, Cramiata, Vertebrata, Euteleöstömi,
Mammalia, Eutheria, Rodentia, Seiurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyrosine-protein kinase, Transferase, ATP binding, Phosphorylation.
DOMAIN 425 683 PROTEIN KINASE.
NP_BIND 431 439 ATP (BY SIMILARITY).
                                                                                                                                                                                                       MEDLINE-97094711; PubMed-8939945; Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Dawson T., Wilm M., Anderege R., Graves L., Earp H.S.; "Anderege R., Graves L., Earp H.S.; "Activation of a novel calcium dependent protein-tyrosine kinase. Correlation with e-Jun N·terminal kinase but not mitogen activated protein kinase activation.": A Hind Chem 271:29494(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.6%; Score 60; DB 1; Fength 1009;
23.3%; Pred No 1 92:48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E -> A (IN REF. 2).
W; D435A475BCA49E9B CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1203 YWQRVTLILELLQHKKKLRSPQILVPTLFNIJSRCLEPLPQEQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        627 PWLENKDVISVLEKODPI PKPELJPPVLYTIMTENWFYFPSDR 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC (FOTENTIAL). PTM: PHOSPHORYLATED ON TYROSINES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRT; 1018 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to licensewish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00107; PROTEIN_KINASE_ATP; 1. PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50011; PROTEIN_KINASE_DOM: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115784 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U69109; AAC52895.1; -. EMBL; D45854; BAA08290.1; -.
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es 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549
579
205
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                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                             NCBI_TaxID=10116;
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RESULT 97 YKZ6\_CAEEL

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                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson R., Ainscough K., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Durz., Durbin R., Favello A., Fraser A.,
Johnston L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latrellie P., Lightening J., Lloyd C., Mottimore B., C'Callaghan M.,
Parsons I., Perry C., Fifker E., Bropra A., Saunders D., Shownkeen R.,
Sins M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Salston J., Thierry-Mieg J., Thomas K., Yaudin M., Vaughan K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Mérassa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Katlus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                            Eukarjota: Metarca; Nomaroda; Ohromadorea; Phabditida: Phabditoidea;
Rhabditidue; Peloderinac; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 Mb of contiguous nucleatide sequence from chromosome 111 of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-99279126; PubMed-9614210;
Hirchashi T., Suruki H., Ito K., Ogawa K., Fumo K., Shimizu T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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MULTIDROG RESISTANCE-ASSOCIATED PROTEIN 6 (MRP-LIKE PROTEIN-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%; Score 60; DB 1; Length 1018; 26.1%; Fied. Mc. 20:02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterson R , Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17; Indels
01-JUN-1994 (Ref. 29, Last annotation update)
HYPOTHETICAL 113,7 KDA PROTEIN C1489.6 IN CHROMOSOME III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1180 PPPOPMOOKKSONLESVOEVOGSVWORVTILLELLOHKKKIRSPQI 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113690 MW; 9F/5A31765216E9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    871 KODODODODODOSNEMODEGNTNPOFLALILODODODOVODAOV 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT: 1502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY 2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGHE-DAMLEY: TISSHE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00249; myb_DNA-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94150718; PubMed=7906398;
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InterPro; TPR001005; -.
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                                                                                                                           Caenorhabditis elegans.
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                                                                                                                    "Colluin localization and functional characterization of a novel rat
liber molfiding resistance associated protein (mrph).";
Submitted (FEB-1999) to the EMHL/Abedone/PHRT databases,
!- FUNCALABLA NEW ARKIETER DIRECTLY IN THE ACTIVE TRANSPORT OF
FROM: INTO SUBCELLUIAR PROAMELLES OR INFURENCE DRUG DISTRIBUTION
INDIRECTLY (BY SIMILARITY).
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Study une Y.:
"Helper to expression of munification resistance associated protein-like profession solutioned to essai hyperbilitubinemic rats.";
Mol. Pharmacol. Scilob-1075(1999).
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Prasile Periodi, Aktimis                                                                                                                                                                                                                                                                                                                                                                                    or sond an email to license (isb-sib.ch).
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                                                                                                         Madon J., Hagenburh B., Stieger B., Meier P.J.;
                                                                                                                                                                                                                                                                            (ABC TRANSPOPTERS), MRP SUBFAMILY.
                                                                                         STRAIN SPRAIME-DAWLEY: TISSUE-LIVER;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Han N., Whitlock J., Progulske-Fox A.;
"The hemaquithin gene A (hadA) of Porphyromenas singivalis 381
"The hemaquithin gene A (hadA) of Porphyromenas singivalis 381
rontains four large, continuous, direct repeats.";
Infect. Immus. 64:4000-4007(1996).
-1- FUNCTION: AGGLUTINATES ERVIHROCYTES.
                                                                                                                                                 Score 60; DB D; Length 1502;
Pred. No. 3.1e+02;
0; Mismatches 12; Indels
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                       ATP (POTENTIAL).
MW: 539901B674A74AZB CRC64;
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PEPTIDASE C25-LIKE 4.
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c. Mismatches 15;
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30-MAY-2000 (Rel. 39, Created)
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                                                                                                                                                                                                                    10; Mismatches
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Ffam, PF01364, Peptidase_C25; 5.
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1502 AA: 164995 MW:
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ses 10, Conservative
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  "Plectin transcript diversity: identification and tissue distribution of variants with distinct first coding exons and todless isoforms."; Genomics 42:115-125(1997).
  1. FUNCTION: PLECTIN IS PROPOSED TO PLAY A ROLE IN CROSS-LINKING INTERMEDIATE FILAMENTS, TO INTER-LINK INTERMEDIATE FILAMENTS WITH MICROTUBLIES AND MICKOF HAMBANIS, AND TO ANCHOR INTERMEDIATE FILAMENTS TO MEMBRANES, TO THE PRIVATE AS WELL AS TO THE NOCLEAR MEMBRANE AS WELL AS TO THE
  TISSUE-Glial tumor;
MEDIATE-9158156; Palabed-2050743;
Wiche G., Becker B., Luber K., Weitzer G., Custumes M.J.,
Wiche G., Becker B., Luber K., Stewart M.;
Hauptmann R., Stratowa C., Stewart M.;
"Cloning and sequencing of rat plectin indicates a 466 ND polypeptide
"Cloning and sthree-domain structure based on a central alpha-helical
colled coil.";
  FORM NETWORKS THAT STABILIZE THE CYTOPLASM.
SCHRUIT: A TETRAMPPIC STHOUGHTHE IS PRODUCED WHERE THE IWO CHAINS
IN OWE MOLEOULE ARE PARALLED, TO ONE MOLTHER AND THE TWO MOLEGULES
ARE ARRANGED ANTIPARALLED, AND OVERLAP TO A GREAT EXIENT.
   ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE
   PARTIAL SEQUENCE FROM N.A. (TSOFORMS 2; 3; 4), AND TISSUE SPECIFICITY
  Mammajia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Kuttus.
   .i- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN SKELETAL MUSCLE AND LOWEST IN THYMUS.
-i- SIMILARITY: TO DESMOPLAKIN AND TO RULLOUS PEMPHIGOID ANTIGEN.
-i- CAUTION: ISOFORM 4 IS A FRAGMENT AT THE N TERMINUS.
  Bukaryota, Metamoa, Chordata, Cramiata, Vertebrata, Euteleostomi,
  Liu C.-G., Maercker C., Castanon M.J., Hauptmann R., Wiche S., "Human plectin: organization of the gene, sequence analysis, and chromosome localization (8q24).";
   Elliott C.E., Becker B., Ochler S., Castanon M.J., Hauptmann R.,
   Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
  or send an email to license@isb-sib.ch).
   Pfam; PF00681; Plectin_repeat; 21.
PROSITE; PS00019; ACTININ_1; FALSE_NEG.
PROSITE; PS00020; ACTININ_2; FALSE_NEG.
  PRODUCED BY ALTERNATIVE SPLICING
  TISSUE=Glial tumor;
MEDLINE=97321050; Pubmed=9177781;
  TISSUE-Glial tumor;
MEDLINE-96210632; PubMed=8633055;
   SEQUENCE FROM N.A. (ISOFORM 1).
   cell Biol, 114:83-99(1991).
   EMBL; X59601; CAA42169.1; -. EMBL; U96274; AAC53209.1; -
   EMBL; U96275; AAC53210.1; -. EMBL; U96276; AAC53211.1; -.
  PROSITE; PS50021; CH; 2.
   IPR001715; -.
   InterPro; IPR001101; -.
  Rattus norvegicus (Rat).
  Pfam; PF00307; CH; 2.
  PIR; A39638; A39638.
PIR; S21876; S21876.
  HSSP; Q01082; 1AA2.
   NCBI_TaxID:10116;
   EMBL; 1966274;
  PLECTIN 1.
  InterPro;
  REVISIONS
  Wiche G.;
```

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CVTHLEVMMA -> IVVSN:SSGSPSPCTTI PWNI GKTOPSR PSGGSWTWNSVI IPSPRAVITEN (IN ISOFORM 4).

MISSING (IN ISOFORM 2).

MISSING (IN ISOFORM 4).
  MEPSGSLFPSLVVVGHVVSLAAVWHWRKGHPQAQDFQ (IN
  MVACMLMPLDQLPATYEVLFPFGVMVAKKDPPFSLHPHVP
  Gaps
  COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
INTERACTION WITH VIMENTIN AND LAMIN B.
   MVAGMLMFLDQLRAIYEVLFREGVMVAKKPPPPPSLH
   MVAGMEMPEDOERA LY EVEFPESVMVAKKPPPPRSEH
   MSQQRLRVPEPEGLGSKRTSSEDNLYLAVLRASEGKK
  4 X 4 AA TANDEM REPEATS OF G \cdot S \cdot P \cdot X. SER-RICH.
  ċ
   Ovine respiratory syncytial virus (strain WSU 83-1578) (ORSV).
  0 6%; Score 60; DB 1: Length 4687;
  6 X TANDEM REPEATS OF MOTIF A.
                 Actin-binding, Atternative splicing.

BOMAIN 1 400 ACTIN-BINDING (BY SIMILARITY).
  RI COLLED COLL.
P2 COLLED COLL.
P2 COLLED COLL.
R2-8 SUBDOMAIN (POTENTIAL).
P2-C SUBDOMAIN (POTENTIAL).
P2-C SUBDOMAIN (POTENTIAL).
R2-E SUBDOMAIN (POTENTIAL).
R2-E SUBDOMAIN (POTENTIAL).
R2-E SUBDOMAIN (POTENTIAL).
   CENTRAL FIBROUS ROD DOMAIN R.
   2e+03;
s 7. Indels
  Viruses; ssRNA negative-strand viruses; Mononegavirales;
  9966CAF71B929751 CRC64;
Coiled coil; Repeat; Structural protein; Cytoskeleton;
   COILED COIL (POTENTIAL). COILED COIL (POTENTIAL). COILED COIL (POTENTIAL).
   15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
NONSTRUCTURAL PROTEIN 1 (NONSTRUCTURAL PROTEIN IC).
  MOTIF A (APPROXIMATE).
MOTIF A (APPROXIMATE).
6 X 19 AA REPEATS.
  MOTIF A (APPROXIMATE).
  (APPROXIMATE).
  (APPROXIMATE).
  MOTIF A (APPROXIMATE).
   Parumyxovilidue; Pacamovirinae; Paesmovirus.
   136 AA.
  10; Mismatohos
  1170 KAKPLGTVQQKREQKMQQKKSQNLFSVQF 1198
  ZERE KAKULUEPIUPPOUQOMBŪEKOBIVASMER 2694
   ISOFORM 3)
  Pred, No
   GLOBULAR.
  MOTIF A
  MOTIF A
   PRT;
   [5-JUL-1998 (Pel. 36, Created)
  533527
  41.4%;
  Best Local Similarity 41.49
Matches 12, Conservative
  STANDARD;
  180
  4367
4520
4597
3015
3343
   1474
2648
1686
1927
2124
2648
4620
1140
   4008
4252
4597
4643
4687
   180
  1897
4620
3113
  3444
   37
   5
   434
   1760
  4024
  8674
  4687 AA,
   SECURNCE FROM N A
   NCB1_Tax1D-79699,
  4025
4368
  3839
   38
  1790
  2845
   3173
  3504
  4082
   1475
   1727
   2298
   787
  1727
2786
2786
  3114
   27.86
   241
  VNS1_ORSVW
065703;
   Query Match
   VARSFLIC
   VARSPLIC
  SEQUENCE
   VARSFLIC
  VARSPLIC
   VARSPLIC
   DOMAIN
DOMAIN
DOMAIN
DOMAIN
COMAIN
DOMAIN
DOMAIN
  DOMAIN
   NIAMOG
   DOMAIN
   DOMAIN
   DOMA!N
   NIVWOO
   DOMAIN
   DOMAIN
   DOMAIN
   DOMAIN
   REPEAT
  REPEAT
  REPEAT
  PPPPAT
  REPEAT
  REPEAT
  DOMAIN
  PEPEAT
  REPEAT
  REPEAT
  REPEAT
  REPEAT
  REPEAT
  VNS1_ORSVW
  RESULT 101
    NAME OF THE PROPERTY OF THE PR
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RESULT 104
   RESULT 103
  Matches
  YI6A_MYCMY
  P 40
    S
   q
  the Buopean Biointernatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license advendent (%+ h'rr []*** it sit b, incommercial or send an equal to license tisb-sib.ch).
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  entities requires a license agreement (see http://www.isb/sib.ch/announce/
or send an email to license (sb/sib.ch).
  between the Swiss Institute of Hebinformalies and the FMRH outstation the European Hebinformaties Institute. There are no restrictions on it use by non-profit. Institutions as ins content is in no warmodilied and this statement is not removed. Usage by and for commercial
   Between the Swiss Institute of Bioinformatics and the EMBL outstation
   aro(H.E.F.H), trp(A-F), hisH, and tyrA genes ";
Submitted (JAN-1992) to the FMH Janfani/TigH databases
-!- FUNTION: MAJOR ROLE IN THE SYNTHESIS OF NUCLEOSIDE LEIPHOSPHAIES
                           "Nucleation and predicted amino acid sequence analysis of the owine respiratory sproytical virus non-structural id and 1s genes and the small hydrophobole protein general."

J. Gen. Virol. 75:401 401(1994).
   gerC(1-3), ndk, cheR
   [16] FWILLPVEQSSIME ARCHIT CHESPIECE PROCESSIVENCE SYSPECE APPROXIZED/ULT, 217.
   of-Jun-1994 (Rot. 26, Proated)
of-JUL-1994 (Rot. 26, Last sequence update)
to-MAY-2000 (Rot. 39, Last annotation update)
wheleostop ofenoschafe K'NASE (PC 2-7-4-6) (NPF) (NPF FINASE).
   "ATALYTE" ACTIVITY: AIF + NOCLEGICE DIFFIGSEATE AGE
NUCLEOSIDE TRIPHOSPHATE,
SUBBRIT: HOMOTERMANER (BY SIMILARITY).
  0.5%; Score 59; DB L: Longth 136;
  stobal 1945
   136 AA; 15203 MW; B066B718°51B6629C (18094);
   Macteria: Firmicutes: Macillus/Cleatidius group.
Macillus/Staphyloneses group. Macillus
  "Sequence of Bacillus subtilis dbpA, mtr(A,B).
   14.3 AA
  : Fred, No. 24;
11; Mismatches
  SIMILARITY: BELONGS TO THE NOR FAMILY.
  SUBSTITUTAR LOCATION CYTOPLASMIC
  FET
MEDILINE #415249#; PribMed 8114762;
  PROSITE: PS00469; NDP KINASES: 1.
  fransferise: Kinase; Ark-binding.
                  Alabsari H.M., Potajeter L.N.D.;
  PRINTS: PRO1243; NUTBERINASE.
   EMBL: 1,15452: AAA42834,1: -.
  Best Local Sumilarity 29.8%;
Matches 17: Conservative
   EMBL: M80245; AAA20857,1: -
  EMBL: Z99115; CAB14189,1; -
HSSP: P22887: ZHEF.
   STANDARD
   Subtilist; Bolly282; mdk.
InterPro; IPR001564; *.
   NonStructural profess.
  PFOUAS4: NDK;
   THER THAN ALP
  SECUENCE PROM N.A.
  Bacillus subtilis
   NCBI_TaxID 1423;
  NDK_BACSU
P31103:
   Salat illist;
   SECUENCE
   guerry Marters
  NUK HACSU
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  Frey J., Cheng X., Kuhnert P., Nicolet J.; "Identification and characterization of 1812% in Mycopiasma mycoides subsp. mycoides SC and presence in related mycoplusmas."; Gene 160:95-100(1995).
   Caps
   Cheng X., Nicolet J., Miserez R., Kuhnert P., Krampe M., Pilloud I.,
   ..
O
  lipeprotein of Myceplasma myceides subsp. myceides small colony
   ÷
  01-NOV-1997 (Ref. 35, Last sequence update)
01-NOV-1997 (Ref. 35, Last annotation update)
INSEKTION ELEMENT IS1296 HYPOTHETICAL 21.4 KDA PROTEIN (ORFA).
   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
  Abdo E.-M., Griot C., Frey J., "Chiracterization of the gene for an immunodominant 72 kDa
   Score 59; DB 1; Length 180;
  0.5%; Score 59; DB 1; Laugth 149;
  21. indels
   16; Indels
  !- SIMILARITY: BELCNGS TO THE ISTSUZISTESS ORFA FAMILY.
  Transposable element, Hypothetical protein.
SFORENCE 180 AA, 21369 MW, A2HOMH7BAQ05H46F CMC64;
   501 HERRIMKTSKPDVPFSPIKPAVEARIGDDNEDVUSALSAFETFR 545
                                    0.09FCH9DBB9F84Dk7 (TRC64);
   5 NIEKKIKIVKEAKKUNIKKSTYLANKYDISVOTVESLVNRFEAFR 49
   607 VVINNPPTFSAFMKTALYLSKSGICSLHPLLRGW 640
   Missist thes
   114 TIHGSDSLESAEREINIFFKNEETVSYGUMAGW 147
  Mismatches
BY SIMILARITY
  or send an email to licensewisb-sib.ch).
  Pred. No.
   Pred. No.
  ..
..
  STRAIN SUBSP. MYCOIDES SG / 1.2;
MEDLINE-97158242; PubMyd 9004514;
  STRAIN-SUBSF, MYCOIDES SC / L2;
MEDLINE=95454965; PubMed-7628725;
  Microbiology 142:3515-3524(1996).
  Query Match
Best Local Similarity 33.3%; Pr
  7 ;
   01-NOV-1997 (Rel. 35, Created)
  01-AUG-1992 (Rel. 23, Created)
                                 149 AA; 16959 MW;
  EMBL; X84021; CAA58849.1; -. EMBL; U61140; AAC44572.1; -.
  32.4%;
   Conservative
   STANDARD;
   STANDARD;
      115
   Mycoplasma mycoides.
   Local Similarity
wes 11; Conserv
  Entomoplasmataceae.
   SEQUENCE FROM N.A.
   SECUENCE FROM N.A.
   N'BI_TaxID-2102;
   Y16A_MYCMY
  MIP CHLTR
   ACT SITE
SEQUENCE
   Onery Match
  0502492
   P26623;
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   Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
  "Chlamydia trachomatis contains a protein similar to the Legionella
  "Genome sequence of an obligate intracellular pathogen of humans:
01.JUL-1993 (Rel. 26, Last sequence update)
30-MAY-2000 (Rel. 39, Last aunofation update)
27 KOA MEREKANE PROTEEN PRECUESOR (PEPTIDYL-PROFYE CIS-TRANS
ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE A) (CHL-MIP).
  Lundemose A.G., Rouch D.A., Rickelund S., Christiansen G.,
   Lundemose A.G., Birkelund S., Fey S.J., Mose Larsen F.,
   SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
   QY -> HD (IN REF. 3).
. 2pargssranhpppe CRC64;
  27 KDA MEMBRANE PPOTEIN.
PPIASE, FKBP-TYPE.
  A \rightarrow S (IN REF. 2).
E \rightarrow K (IN REF 2)
  Bactelia, Chlamydiales, Chlamydiaceae, Chlamydia
NCBL_TaxiD-813;
   pROSITE; PSO0453; PKBP_PPTASE_1; 1.
PROSITE; PSO0454; PKBP_PPTASE_2; 1.
PROSITE: PSSO059; PKRP_PPTASE_3: 1.
OUTET MEMBRANE: ISOMETASE; Rolamase; Signal.
   "Chlamydia trachomatis Mip-like protein.";
Mol. Microbiol. 6:2539-2548(1992).
   POTENTIAL.
  STRAIN-SEROVAR L2;
MEDLINE=91194539; PubMed=2013997;
  MEDLINE=94023883; PubMed-1406289;
   STRAIN-D/UW-3/CX;
MEDLINE-99000809; PubMed-9784136;
  138
25548 MW·
   Xb612/; CAA46918.1; -.
   EMBL; X66126; CAA46917.1; -.
   EMBL; AE001324; AAC68143.1;
PIR; S25255; S25255.
  SEQUENCE OF 69-243 FROM N.A.
  EMBL; X66128; CAA46919.1;
  Pfam; PF00254; FKBP; 1.
Pfam; PF01346; FKBP_N: 1.
   Chlamydia trachomatis.";
Science 202·754-759(1998)
  23.43
53.5
56
   5
  HSSP; P20071; TFKK.
InterPro; JPR000774; -
  Chlamydia trachomatis.
  interPro; IPR001179;
   243 AA;
   SEQUENCE FROM N.A.
   STRAIN SEROVAR LZ;
  SEQUENCE FROM N.A.
   Christiansen G.;
  Davis R.W.;
  CONFLICT
CONFLICT
SPORFNCE
  CONFLICT
   DOMAIN
   VARIANT
  VARIANT
  SIGNAL.
   CHAIN
   \widetilde{\sigma} \overset{X}{\sim}
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  Kustu S.G.;
Submitted (MAR-1995) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: NTRB ACTS AS A SIGNAL TRANSDUCER WHICH RESPONDS TO THE
  Gaps
  Gaps
  Utatsu I., Sakamoto S., Imura T., Toh-E A.; Yeast plasmids resembling 2 micron DNA: regional similarities and diversities at the molecular level."; J. Rarreriol 169:5537-5545(1987).
  Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
  Eukaryotű, Fungi, Ascomycota: Saccharemynntina; Sancharomycetes;
  0;
   ċ
   0.5%; Score 59; DB 1; Longth 260; 61.9%; Pred No. 51;
0.5%; Schure 59, DB 1, Length 243; 29.2%; Pred No. 47;
  982 EELQREKKLKSHQKLSETLKNIJSCVYSCPSYTAKDIMKVIQGVNGEM 1029
   Saccharomycetales, Saccharomycetaceae, İygesaccharomyces.
  6; Indels
   21: Indels
   30438 MW; OB68E5BA7073C13D CRC64;
   UI-NOV-1995 (Rel. 32, Cleated)
OI-NOV-1995 (Rel. 32, rast sequence update)
OI-NOV-1995 (Rel. 32, Last annotation update)
NITPOSEN PERHIATION PROTEIN NR(II) (EC 2.7.3.-).
  01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel 15, Last annotation update)
HYPOTHETICAL PROTEIN A.
  2; Mismatches
   13; Mismatches
   MEDLINE=B8U58763; PubMed=308U169;
   EMBL, M18275; AAA15276.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 260 AA; 30438 MW;
   979 TLFEELQREKKLKSHOKLSRT 999
   204 TLFEELVREKRSQETQKTSST 224
  2ygosaccharomyces fermentati
  STRAIN-NAGANISHI IFO 0021;
              Query Match 0.5%
Best Local Similarity 29.2%
Matches 14; Conservative
   Conservative
   STANDARD;
  STANDARD;
   Best Local Similarity
   SECTIFINGE FROM N A
   SEQUENCE FROM N.A.
  NCBI_TaxID=4955;
  NCBI_TaxID=602;
  GLNL OR NTRB.
  J. Banteriol
  Plasmid pSM1.
   NTRB_SALTY
   Query Match
  YA_ZYGFE
  RESULT 105
   Matches
   NAME OF COLOR OF STANK OF COLOR OF STANK OF COLOR OF STANK OF COLOR OF COLOR OF STANK OF COLOR OF COLO
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   this SWISS Performential comparight. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way meditted and this statement is not removed. Usage by and for commercial entities requires a license marement (See http://www.isb.sib.ch/armonner/or send an email to license-isb-sib.ch).
   Ċ
   WHILE IN NITHOGEN EXCESS NIRC IS DEPROSPRORYLATED AND CONSEQUENTLY
   "Sequence analysis of the Bacillus subfills chromosome region between the serA and Kdq forl cloned in a yeast artificial chromosome.";
Mirrobiology 142:2505-2016(1996).
   Saps
  SIMILARITY: 10 OTHER PROKARYOTIC SENSORY TRANSBUCTION HISTIDINE
NITEGER LEVEL OF CELL AND MODILATES THE ACTIVITY OF NIKE, IN
                 NITROGEN LIMITATION NERB ACTIVATES NTRO BY PHOSPHORYLATING IT,
  Sorokin A.V., Azevedo V., Zumstein F., Galleron N., Fhrilich S.D.,
   oftes Tibus (Rel. 44, Created)
oftes Tibus (Rel. 44, Last sequence update)
15-080 (1908 (Rel. 37, Last annotation optate)
HYPOTHETICAL 40.7 KDA PECTEIN IN PER-PECT INTERGENIC PESTON.
  Sensory transduction: Transletase; Kinase; Phosphorylation; Nitropen lixation; AFP-binding. (FAMEMITTE LAMAIM CENTRELY)
  0.5%; Score 59; 68 l; Length 40;
6.4%; Pred, No. 72;
   a Mismatches 12: Indels
  ATP (BY SIMILARITY).

A105F131E4018733 CRC64;
  40709 MW; 97EDDF7A247E223E CRC64;
   Marteria: Firmicutes: Barillas/Clostridiam group;
  1241 IPQEQONMEYIEQLILSHINDMYSPESTRI 1233
   228 LTELLHOPEQIECVELNIVENALQALGREGGET 269
   send an email to licerse disb-sib.ch).
  Bacillos/Staphylococous group; Bocillus
   STRAIN 158 / MARRORS);
MEDLINES 96 44 (105); Pubmed 8760912;
  14 1 AA; 1844 - MW;
  EMB13 X851043 "AA59424.13 -..
   EMBL: 147648; AACB3946.1; -.
EMBL: 299115; CAB14219.1; -.
  16.48;
  EMBL: 299116; CAB14235,1; -
  Local Similarity (6.4)
es 12; Conservative
   Subtilist; BG11429; ypbB.
Hypothetical protein.
   Ptam: PFO0512: Signal; 1
   STANDARD;
  INATIONALED BY NIEB.
   ...
  Stydency Solusies, nirs.
  6.73
   TERDSO4 10;
  152 AA:
   SECUENCE FROM N.A.
   Martillus subtillis
  N. B.L. . 1 1 8 7 1 1 1 4 7 4
   KINASES
   YPBB, BACSO
   InterPro:
  SEQUENCE
  SEUTENCE
  guery Match
   M C RES
  HINDIN:
  150728;
   Matches
  RESULT 167
YPBB BACSU
  YPBBB.
  Hist
   5
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   ÷
   Fraser C.M., Gocayne J.D., White D., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Gerlavage A.P., Suffon G., Kelley J.M., Fleischmann R.L., Weidhard J.E., Sandli R.V., Sandusky M., Puhrmann J.L., Wighen D.T., Weidhard J.E., Sandsky E.M., Fhilligs C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Butt K.F., Hu P.-C., Lucier T.S., Feterson S.N., Smith H.G., Hulchison C.A. III, Venter J.C., Free minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
  Sides
   Science
  1197 QEVOGSYNQRVILLLELLQHKKKI PSPQILVPTLFNILSPCTFF9 PQFQSNMEYIKQL 1254
   113 QQAAGVEWKELSTI VQVI,SHKQQQSSPQVTPVTKTHETEHWVKRYESEBTEHTEMAKST, 170
   Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes; Saccharomycetales; Saccharomycets. Saccharomyces.
   ..
C
  Bacteria, Firmicutes, Bacillus/Clostridium group; Mollicutes;
                     0.5%; score 59; DB 1; Langth 45z; 25.9%; Pred. No. 73;
  0.5%; Score 59; DB 1; Length 384;
  29; Indels
   3; Indels
   Hypothetical protein.
SEGUENCE 384 AA; 42795 MW; 3274EH60H5EE94AB CRC64;
  035819;
15 JUL 1999 (Rei . 38, Created .
15 JUL 1999 (Rei . 38, Last sequence update)
30-MAY-2000 (Rei . 34, Last annotation update)
  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
  14; Mismatches
  Query Match
Best Local Similarity 42.9%; Pred. No. 81;
Matches 9 Mismatches
  PRI;
  SEQUENCE FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE:96026346; Pubmed-7559393;
   Saccharomyces douglasii (Yeast).
  1613 PSVRRKALDLINNKLQQNISW 1633
   355 PATAKRAVELLNIJKIJKKKINW 375
  Mycoplasmataceae; Mycoplasma.
  EMBL; U39683; AAC71255.1; -.
  RYPOTHETICAL PROTEIN MG039.
query Natoh
Best Local Similarity 25.77.
For 15, Conservative
  STANDARD;
  STANDARD;
   Mycoplasma genitalium.
   01-OCT-1996 (Rel.
   NCBI_TaxID=2097;
  Mitochondrion.
  FIGE; MG039; -
  CYTOCHROME B.
  COB OR CYTB.
  YOAS_MYCGE
   CYB_SACDO
   RESULT 108
   RESULT 109
  CYB_SACDO
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   entities requires a license agreement (Sec http://www.isb sib.ch/announce/
  COFACTOR: TWO HEME GROUPS (B562 AND B564) WHICH ARE NOT COVALENTLY
                                     MEDLINE-91218158; PubMed-1708831; Tian G.L., Michel F. Macadre C., Slonimski P.P., Lazowska J.; Tian G.L., Michel F. Macadre C., Slonimski P.P., Lazowska J.; Inforpitent mitochondrial evolution in yeasts IT The complete acquaence of the gene coding for cytachrome bis Succintronyces adouglastic reveals the presence of both new and conserved introns and discloses major differences in the fixation of mutations in
  Mitochondrion; Electron transport; Respiratory chain, Transmembrane;
   RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.
   SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-CL ARE: CTTCCHROME B, CYTOCHROME CL AND THE RIESKE PROTEIN.
  J. MOJ. BIOI. 218:747-769(1991).
-!- FUNCTION: COMPONENT OF THE UBIGUINOL-CYTCCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-CI COMPLEX), WHICH IS A
   Nobrega F.G., Taagoloff A.; "Assembly of the mitochondrial membrane system. DNA sequence and
  Eukaryota, Pungi, Ascompouta, Saccharompoutina, Saccharompoutus,
Saccharomycetales, Saccharomycetaccae, Saccharomyces,
  Ö
   IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AX:AL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
   IRON 1 (HEME B562 AXIAL LIGAND).
   0.5%; Score 59; DB 1; Length 385;
45.2%; Pred. No. 82;
tive 5; Mismatches 12; Indels
   35418407D7784DD2 CRC64;
  SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
   100163, 010807, 010301, 010802,
21-JUL-1986 (Rel. 01, Created)
10-JUL-1988 (Rel. 36, Last sequence update)
01-07T-2000 (Rel. 40, Last sequence update)
   385 AA.
  1929 PKPPILTFYNLAD TAEKLKGLFTLFAGHLV 1959
   Saccharomyces cerevisiae (Baker's yeast).
   or send an email to licensewisb-sib.ch).
  271 PEWYLLPFYAILRSIPDKILGVITMFAAILV 301
   РКОSITE: PS00192; СТБСНКОМЕ_В-НЕМБ: 1.
PROSITE: PS00193; СТГОСНКОМЕ_В_ОО; 1.
   PRT,
   Pfam, PF00032, cytochrome_b_C; 1. Pfam; PF00033; cytochrome_b_N, 1.
  MEDLINE-81046788; Pubmed-6253454;
   82 82 IRC
96 JHC
183 183 IRC
197 197 IRC
385 AA, 43631 MW;
   EMBL; X59280; CAA41971.1; -.
   Best Local Similarity 45.2
Matches 14; Conservative
   BOUND TO THE PROTEIN.
   STANDARD,
   InterPro; IPR000179;
   STRAIN D273 16B, A21,
                             SEQUENCE FROM N.A.
   SEQUENCE PROM N.A.
   NCBI_TaxID 4932;
   Mitochondrion.
   CYTOCHROME B.
   COB OR CYIB.
  CYB_YEAST
   Query Match
  SEQUENCE
  RESULT 110
  ŝ
  qq
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Ricinformatics and the EMRL outstation o
  COUPLED TO ATP SYNTHESIS.
-!- COFACTOR: TWO HEME GROUPS (BS62 AND BS66) WHICH ARE NOT COVALENTLY
   Labowska J., Jacq C., Slonimski P.P.;
"Sequence of infroms and flanking exons in wild-type and box3 mutants
of cytochrome b reveals an interlaced splicing profess coded by an
   The case of a cytoplasmically synthesized apocytochrome
  "Revision of the mucleotide sequence at the last intion of the mitochondrial approximation by gene in Saccharomycos cerevisiae."; Praz. J. Med. Biol. Res. 17-17-20(1984).
  COMPLEX (COMPLEX 111 OF CYTOPHEGME RECLOOMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
  Claros M G., Peried I , Shu Y . Samatey F A . Popot J E . Jacq C., "Limitations to in vivo import of hydrophobic proteins into yeast
  -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
organization of the cytochrome b gene in Saccharomyces cerevisiae
  Privar-Charillote P., di Rado 3.-P.;
Brivar-Charillote P., di Rado 3.-P.;
"Electron transfer restaration by vitamin K3 in a complex
III deficient mutant of S. cerevisiae and sequence of the
corresponding expoorneme b mutation.";
PFRS lett 255-5-q (1989)
-!- PRINCTION: COMPONENT OF THE HRIQHINOL-CYTOCHPOME C PEDUCTASE
   MEDLINE-ROll=256; PubMod-7034963;
Lazowska J., Jacq C., Slonimski P.P.;
"Splice points of the third intron in the yeast mitochondrial
  -:- SIMILARITY: BELONGS TO THE CYLOCHROME B FAMILY
  EMBL, J01476; AAA99924.1; ALT_SBQ.
PMRL, WA4042; CAASRES1.1:
EMBL, VOOGR6; -, NOT_ANOTATED_CDS.
EMBL, J01473; AAA32151.2; -, OINED
EMBL, J01475; AAA3717.12; IOINED
EMBL, J01475; AAA37152.2; -, EMBL, J01475; AAA37152.2; -, IOINED
   Biol, chem. 255-9828-9847(1980).
   J. Biechem. 228.762-771(1995).
   MEDLINE=95255283; PubMed=7737175;
   MEDI.INE-90005972; PubMed=2551731;
   MEDLINE 81088336, PubMed 7004642;
  STRAIN=D273-10B/A21;
MEDLINE-ASOCOG73, PURM=d-6383504,
   Bonjardim C.A., Nobrega F.G.;
   SECUENCE OF 144-169 FROM N A.
  SPOTTENCE OF 20-143 FROM N A
   BOUND TO THE PROTEIN.
   Interpre: IPR000179; -.
  Cell 22:333-348(1980).
   cytochrome b gene.";
  Cell 27:12-14(1981).
   PIR; A00159; CBBY. SGP; SANN7270; COR
   SECUENCE FROM N A
  SECUENCE FROM N A
   STRAIN=777-3A;
   STEAIN=777-3A;
  mitochondria
   STRAIN-WR200;
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.; =

Gaps

: :

Indels

Mismatches

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Conservative

10;

Matches

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  entities requires a fire se attendent (see http://www.isb sib dyatmonner;
or send an email to firerse isb sit eb)
  S (IN MUTANI W7 WHICH IS RESPIRATORY
Ptams PPDD032; cytochromo_L_s: 1,
Ptams PPD0033; cytochromo_L_s: 1,
PROSITE: PSD0132; cypcHHOME_B_BENES: 1,
PROSITE: PSD0193; cytocHHOME_B_C's: 1,
Election transport; Mitochoudrion; Bospiratory chain; Iransmembrane;
   Gaps
   ot-AST (1999) [Berl, 15, Last Sepanne apdate)
91-FEB 1995 (Rel, 31, Last annotation update)
OKANAIPTN POLYKETINE PUTATIVE BETA KETGACYL SYNTHASE 1 (EC. 2.3.1.+)
  Bacteria: Firmicates: Actinobacteria: Actinobacteridae;
Actinomycotales: Streptonycineae: Streptomycotaceae; Streptomyces.
   Sherman L.H., Malpartida F., Bibb M.J., Kieser H.M., Bibb M.J.,
  polyketide synthase gene cluster of Streptomyces violaceoruber
  LEON 1 (HEME B562 AXIAL LIGAND).
LEON 2 (HEME B566 AXIAL LIGAND).
LEON 2 (HEME B562 AXIAL LIGAND).
   IRON 2 (HEME B566 AXIAL LIGAND).
IRON 2 (HEME B562 AXIAL LIGAND).
IRON 1 (HEME B566 AXIAL LIGAND).
   "Structure and deduced function of the granaticin-producing
  0.5%; Score 59; 108 l; Length 485;
45,2%; Pred. No. 82;
   DB 1, Langth 421,
   12; Indels
  T - + 1 (IN REF. 1 AND 2).

D - + V (IN REF. 3).

2 03416148712A790 CRC64;
  Antibootic biosynthesis; Transferase, Acyltansterase,
ACT_SITE 169 169 BY SIMILARITY.
SEQUENCE 421 AA: 44.92 MW; 5012DEREA59412D6 CRC64;
   5: Mismatches
   1929 PROBLEITEYNLAW TAEKLKGLETLEAGHEV 1959
   PROSITE: PSOUGOG: B.KELOZNI.SYNIHASE: 1.
   271 PEWYLLEFYALLESTEDKLUGVITMFAAILV 301
  DEFICIENT)
   MEDITINE PROFESSION 41: PLEAMED 2584128;
  ol-A98 (oro (Ro), 15, created)
ol-A98 (oro (Ro), 15, Last sept
ol-FEB 1995 (Ro), 3, Last anno
  Ptamp PEssilvia Kertorryl synta
   4.465 J. MW.
   Streptomyces violaceoruber.
   EMBL: X15 (0.); (TAN 64 659.1);
EMBL: X16144; (TAN 64264.1);
  Similarity 45.2
   STANDARD;
   ž [2
  Interpres 1PR000734;
  PIR: S05493; S05494.
   185 AA:
  SHOTHIN'TE PROM K.A.
   NCB1_Tax1D=1935;
   Hopwood D.A.:
  / Mas.
Local Sim.
14:
  STRAIN THZZ
   KASI STRVN
  Query Match
Best Local S
   1. ... 1.1N
  O NFLLOT
   SECORN
  VARIANI
  (ORE1)
   MEIAL
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   Mathibas
   Heamer
   N TALEBERT N TELEVISION N
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   -i- SUBUNIT: BOMOPOLYMER.
-i- PTM. ONE OF THE MOST PROMINENT PHOSPHOPROTEINS IN VARIOUS CELLS OF MESENCHYMAL OKIGIN. PHOSPHORYLATION IS ENHANCED DUKING CELL.
DIVISION, AT WHLCH TIME YIMENTIN FILAMENTS ARE SIGNIFICANTLY REDEGANIZED (BY SIMILARITY).
   2061 IMMERINIGILIANI HUSSENVEFAALITVIALAEKIRINTIVULEEGIITTAADINHOH VIR
   o daps
  Gene 140:257-259(1994).
-!- FUNCTION: VIMENTIN ARE CLASS-111 INTERMEDIATE FILAMENTS FOON: IN
VARIOUS NONEPITHELIAL CELLS, ESPECIALLY MESENCHYMAL CELLS.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodaetyla; Buminantia; Peeera; Bovoidea;
  SHOSPHORYLATION (BY CAM-KINASE 11) (BY SIMILAKITY).
   PHOSPHORYLATION (BY CAM KINASE 11)
   Hess J.F., Casselman J.T., Fitzgerald P.G.: "Nucleotide sequence of the bovine vimentin enrodima cDMA.";
   -1 - SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
  Intermediate filament; Coiled coil; Heptad repeat pattern;
   0.5%; Score 59; DB 1; Length 465;
25.3%; Sred. No. 1e+02;
   42: Indels
  (BY SIMILARITY).
119E126778BF5801 CRC64;
   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01 FEB 1996 (Rel. 33, Last annotation update)
  17: Mismatches
  3Y SIMILARITY.
   JOIL 18.
THYTE 12.
  LINKER 1.
   TOIL 1A.
  PRJ:
   HEAD.
   MEDLINE-94193008; PubMed-8144034;
   465 AA; 53545 MW;
                    62 ESPREVERMPRATOFAVACE 81
  EMBL; 1.13263; AAA53661.1; -.
  25.3%;
  InterPro; IPR001664; -.
Pfam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
31 FOPKEAATIDRDTAFAIGGT
   20; Conservative
  STANDARD;
  Bowidae: Rowinae: Bos.
   Bos taurus (Bovine).
  Query Match
Best Local Similarit\gamma
   HSSP; P03069; 1SW1
  SEQUENCE FROM N.A.
   NCB1_Tax1D=9913;
   Phosphorylation.
  95
131
153
245
   268
   ු
ස
  3
  VIME_BOVIN
  VIMENTIN.
   SEQUENCE
   P48616;
   DOMAIN
DOMAIN
DOMAIN
DOMAIN
  MOD_RES
  MOD_RES
  DOMAIN
DOMAIN
  DOMAIN
   VIME_BOVIN
   Matches
   RESULT 112
   S
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State 5a. Pred. No.

Party Match Nest foral Similarity 50.0%;

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  60 PSFEOFEAPLFSQLAKTLERSVOTKAVNKGLDENTSLFLIHLSPYFLLKPAQKCLEWLIH 119
   Gaps
   184 TREKTOPPMIQEPFARSTLOSPRODVONASIAPLDI EPKVESTORETAFLIKKUHDARIQE 243
   papillomaviruses by polymerase chain reaction amplification.
   ringses, on PNA stage: Paperaviridae: Papillomavirus
  Guery Match n 5%. Score 59: DB 1: Length 501; Best Local Similarity 25.4%; Pred No 1.1e+02; Matches 17; Conservative 11; Mismatches 39; Indels
  SEQUENCE OF 312-462 FROM N.A. MFDLINF=65052821: PubMed-7964668; MEDLINF=65052821: PubMed-7964668; Manos M.M., eng c' K , Viila L.L., Bolius H.J., Chan S.Y., Manos M.M., Wheeler C.M.; Polius H.J. Peyton C.L., Bauer H.M., Wheeler C.M.; "Identification and assessment of known and novel human."
   submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
   Coat protein; Late protein.
SEGHENCE 501 AA: 55787 MW: 0DBC4D47E552E968 CRC64;
  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NICMFI HINDING PEPIPLASHIC PROTEIN PPECURSOR
   Last annotation update)
   p50820; 080940;
01-00T-1996 (Rel. 34, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update
   phylogenetic algorithms.";
J. Infect. Dis. 170:1077-1085(1994).
   PRT;
  PRT;
  Pfam, PF00500; late_protein_L1; 1.
PRINTS; PR00865; HPVCAPSIDL1.
                                  2121 VEHQCOPTIQQUETVIGEP 2139
   Human papillomavirus type 55.
  244 LQAQIOPOHVQIDMDVSKP 262
   EMBL; U31791; AAA79484.1; -
  U12494; AAA67238.1;
   STANDARD:
  STANDARD;
   MAJOR CAPSID PROTEIN L1
   IFEC02219;
   SECUENCE FROM N.A.
  NCBI_TaxID: 37114;
   120 RFHIHLY 126
   64 GPOYRVE 70
   J.F.RA
   NIKA_ECOLI
  VI.1_HPV55
   InterPro,
  SHOUFINGE
   Delius H.
  RESULT 114
   NIKA.
  VI.1_HPV55
   5
  X X X
   \stackrel{\circ}{\sim}
   X X X X
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   REPRESENTS THE NICKEL BINDER.
--- SUBCELLULAR LOCATION: PERIPLASMIC (PROBABLE).
--- SIMILARIIY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-RINDING
  STRAIN-K12 / MG1655;
MEDLINE-44316500; Pubmed-8041620,
SOFIA H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
"Analysis of the Escherichia coli genome. V. DNA sequence of the
   Gaps
   Navarro C., Wu L.-F., Mandrand-Berthelot M.-A.; "The nik operon of Escherichia coli encodes a periplasmic binding-protein-dependent transport system for nickel."; Mol. Microbiol. 9-1181-1191(1993).
  Viruses; dsDNA viruses, no RNA stage, Tailed phages; Fodoviridae;
T7-like phages,
  NICKEL-BINDING PERIPLASMIC PROTEIN.
               Bacteria; Proteobacteria, gamma subdivision, Enterobacterionan;
Escherichia.
   ċ
  Nucleic Acids Fos. 22:267h-25m6(1994).
-i- FUNCTION: INVOLVED IN A NICKEL TRANSPORT SYSTEM, PROBABLY
   Score 59; DB 1; Length 524;
Fred. No. 1.26+02;
   21; tadels
   524 AA, 58719 MW; CB2E3CHCE42396 CRC64;
   222 STIVSALVAAELVSENLIAKLEPYIQKGIKSSIEDYRAATYMI 264
   299 SLIDNALYGTQQVADTI.FAPSVPYANLGLKPSQYDPQKAKALL 341
  Last annotation update)
   Query Match 6 58; Score 59; DB 1. Best Local Similarity 34.98, Fred. No. 1.2046
   536 AA.
   P03728;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Tast sequence update)
   PROSITE; PS01040; SBP_BACTERIAL_5; 1.
Transport; Nickel; Signal; Periplasmic.
  region from 76.0 to 81.5 minutes.",
Nucleic Acids Res. 22:2576-2586(1994).
   PRT;
  MEDLINE-83241725; PubMed 6864790;
  MEDLINE=95020649; PubMed=7934931;
  EMBL; AP000423; AAC76501 1; -. PIR; S39594; S39594. Froncene; EG12075; nika.
   HEAD-TO-TAIL JOINING PROTEIN.
  EMBL; X73143; CAA51659.1; -.
   AAB18451.1; -.
  Pfam; PF00496; SBP_bac_5; 1.
  STANDARD;
   PROTEIN FAMILY 5.
  1 PPOOO914;
  SEQUENCE FROM N.A.
  (Rel.
   NCBI_TaxID=10760;
  SECUENCE FROM N.A.
  SECTIENCE FROM N A
   Bacteriophage T7
Escherichia coli.
  NCBI_TaxID=562;
   1100039;
  01-FEB-1991
   VHTJ_BPT7
   SEQUENCE
  STRAIN-K12
  InterPro;
  SIGNAL
  CHAIN
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   0
   1551 LETVIOYISAVAJSMERNAJKIJAKEMKALLSKATIJLIJAKANĀLIPIETETPIKGLV 1508
  STRAIN KIZ / MSEGS;
MEDLINE 97426617; Folded 9278603;
Whitther E.R., Plunkert 5, 111; Bloch C.A., Perna N.E., Burland V.,
Willey M., Allad Punkert 5, Glasher 7.10, Folde 7.K., Maybow G.P.,
Stepot J., Lagis N.W., Kirkpattick W.A., Goslon M.A., Pose P.E.
   448 TEARLSFARMINSAVQRIGGRATAFFTRYVASFLEDTLGBVYSTLSGELQLDBVRVLL. 405
   Trobe T., Aiba H., Baba T., Pujita K., Bayashi K., Inada F., Issooo K., Esso. M. Kilanaka M., Kilanaka M., Kilanaka M., Kilanaka M., Martus K., Mari H., Nishio Y., Oshima T., Santo N., Sampa J., Santo N., Sa
  Berteils Professarie jamma subdivisions Enterobacteriaceaes
  varresponding to the 40.1 for 0 min region on the linkage map.";
Genn 1919. Stidiet F.W.;
"Complete incleation sequence of bacteriophage 17 DNA and the
Lowethous of T. aratic demonts.";
L. Mol. Rich. Polish 75 66 (1918).
  0.5%; Score 59; DH 1; Length 536;
24.1%; Pred, No. 1.2e+02;
ev. 16; Mismatthes 26, Indels
   The complete acrown sequence of Escherichia coli R 12.", Science 277:1453-1474(1997).
  STRAIN KLZ / WSTRU,
al Mamour A.A.M., Tominasja A., Enomoto M.;
Submitted (JAN-1997) to the PWRG/Asempank/ffRT databases
   5912 J. MW: - (TJE87892)#(1486065 CR054)
  File 67 4.1 State And true, the AA. Piscobe PASSOBE PASSOBE PASSOBE PASSOBE TO MAY EVEL (Red., 22, Created) of MAY TOO (Red., 24, created) of the TOO (Red., 14, last sequence update) FIAMELIAR M RINS PROFEEN.
   MEDLINE 97251458) PubMed 9097040;
   EMBL: V 11145; (AAZ4425.1) -. PIR: A04354; JOBPT7.
  ELIF OF FLA BLOR FLA ALL.L.
Escherichia coll.
  24.18;
  Oberg Match
Rest Local Similarity 24.18
Matches 14, Conservative
   1:174 (92(1)16).
  TELS FROM N.A.
  P1R; S42424; S42424.
  Structural protein.
SEQUENTE 5.6. AA:
  SECTEN'E PROM N.A.
   SECUENCE FEW N.A.
  SECUENTE FROM N.A.
   Shar Y.
  N'HILLIAXIN 552:
   Eschertichia.
  SECUENCE OF SIRAIN JAIL
   STRAIN KIL
  NA Pris.
   Man B.,
   *: 1 1 1:538 #
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  between the Swiss Institute of Bioinformatics and the EMBL outstation
  Ligition of the
  -!- SUBGUIT: THE BASAL BODY CONSTITUTES A MAJOR PORTION OF THE FLAGELLAR OFGANELLE AND CONSISTS OF FOUR KINGS (1, P. S. AND M) MOUNTED ON A CENTRAL ROD. THE M RING IS INTEGRAL TO THE INNER MEMBRANE OF THE CELL. AND MAY BE CONNECTED TO THE FLAGELLAR KOD VIA THE S KING. THE S (SUPRAMEMBRANE RING) LIES 1057 DISTAL TO THE M RING. THE L AND P FINGS LIE IN THE OUTER MEMBRANE AND THE PERIPLASMIC SPACE, RESPECTIVELY.
   J
  SIGNUNCE OF 532-552 FROM N.A. MINITARY 94040702; FURMA R23408):
Roman S.J., Frantz B.R., Matsumura P.;
"Jone Sequence, .Zerproduction, partitionion and determination of wild-type level of the Escherichia coli tlagellar switch protein PhiG."
                Muclier V. Jones G.J., Kawagishi I., Aizawa S.I., Machab R.M.; "Characterization of the fill genes of Escherichia coli and Sanouellat typhimurium and icentification of the FliE protein as component of the flagellar hock-basal body complex."; J. Bactericl. 174:2298-2304(1992).
   30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last aminotation update)
HYALURONAN SYNTHASE 2 (E. 2.4.1.-) (HYALURONAIE SYNTHASE 2)
(HYALURONIC ACID SYNTHASE 2) (HA SYNTHASE 2).
  1- FUNCTION: THE M RING MAY BE ACTIVELY INVOLVED IN ENERGY
   Innerth 552;
  Indels
  1243 QEQGNMEYTKQLILSCLINIÇÖKI SPIGGKIPKPIDITIFFKFNV 1285
  78 FASGATEVPADKVHELRIRLAQQGLPRGGAVGFELLDQEKFGI 120
   0.5%; Score 59; DH 1: 15
27.9%; Pred. No. 1.4c+02;
ivc. 10; Mismatches 21;
  SIMILARITY: BELONGS TO THE FLIF FAMILY.
   Loval Similarity 27.9%; Fred. Mo. 1.46 es 12; Conscruative 10; Mismatches
  PRT;
  EMBL: M84992; -: NOT_ANNOTATED_CUS.
EMBL: L13248; -: NOT_ANNOTATED_CUS.
PUR: D42376; D42376.
ECOGONO: EG11347; FLIE.
MEDI.INE=92202159; PubMed=1551848;
   30-MAY-2000 (Rel. 39, Created)
   EMBL; D89826, BAA14029.1; -.
EMBL; AE000286; AAC75005.1; -.
   Pfam; PF01514; YSCJ_FliF; 1.
PRINTS; PR01009; FLGMKINGFLIF.
   EMBL; D90833; BAA15761.1; -
EMBL; D90834; BAA15763.1; -
  STANDARD:
   Gene 133:103-108(1993).
   InterPre: IPR002920; -
  InterPro; IPR000067;
  Flagella; Membrane
  TRANSDUCTION.
  HAS2_BOVIN
097711;
  CONFLICT
   Query Match
  STOUENCE
   CONFLICT
  Matches
  HAS2_BOVIN
  DE DE CE
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Hos taurus (Bovine).

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   entities requires a license agreement (See http://www.isb.sib.ch/announce) or send an email to license@isb.sib.ch).
   "Hyaluronan synthase expression in bovine eyes.";
Invest. Ophthalmol Vis Sci 40-563-567(1999).
-!- FUNCILON: PLAY A ROLE IN HYALURONAN/HYALUKONIC ACID (HA)
SYNTHESIS (BY SIMILARITY).
-!- PATHWAY: HYALURONANE SYNTHESIS, WHICH HAS A REPEATING UNIT
CONSISTING OF GLUGHRONIC ACID (GLCA) AND N-ACETTLGALACTOSAMINE
  {\tt Glycosyltransferase}; {\tt Transmembrane}, {\tt Multigene family}.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Rovoidea;
Boyidae; Rovinae; Ros
   Einspanier R., Patzner K., Lauer B., Berisha B.;
"Hydiatonan synthase is expressed during cumulus-oocyte complex
maturation in the cow.";
  SUBCECLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE). TISSUE SPECIFICITY: EXPRESSED IN CORNEAL ENDOTHELIAL CELLS. SIMILARITY: PELONGS TO THE NODC/HAS FAMILY.
  MEDLINE=99165281; Purmed=10067958;
Usui T., Suguki K., Kaji Y., Asanet S., Miyata K., Heldin P
  Submitted (MAP-194%) to the EMBL,/GenBank/hub. databases.
   Submitted (SEP-1998) to the EMBL/Genbank/DDBJ databases
   EXTRACELLULAR (POTENTIAL).
  EXTRACELLULAR (POTENTIAL).
   EXTRACELLULAR (POTENTIAL).
  EXTRACELLULAR (POTENTIAL)
  85AD256435A5EB64 CRC64;
  CYTOPLASMIC (POTENTIAL).
  CYTOPLASMIC (FOIENTIAL).
  CYTOPLASMIC (POTENTIAL).
  CYTOPLASMIC (POTENTIAL)
  E > 1 (IN REF. S -> C / IN ...
  3 (POTENTIAL)
  4 (POTENTIAL)
   5 (POTENTIAL)
  6 (POFENTIAL)
   1 (POTENTIAL)
   2 (POTENTIAL)
   (POTENTIAL)
  Zamashita H., Usui T., Suzuki K.;
   EMBL; AJ004951; CAA06239.1; -. EMBL; AB017804; BAA76547.1; -.
   63459 MW;
  SECUENCE OF 267-469 FROM N.A.
   45
9374
3395
402
423
450
  510
  406
425
552 AA;
   FISSUE SPECIFICITY
   SEQUENCE FROM N.A.
  NCBI_TaxID=9913;
  403
  Yamashita H.;
   Transferase,
   CONFLICT
   TRANSMEM
   TRANSMEM
  TRANSMEM
  TRANSMEM
  TRANSMEM
   PRANSMEM
   TRANSMEM
   SEQUENCE
  DOMAIN
   DOMA I N
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Transferase; Glycosyltransferase; Transmembrane; Multigene family.

EMPL, U54804, AACSOR92 1; -

601636;

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CYTOPLASMIC (POTENTIAL).

(POTENTIAL)

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL) 3 (POTENTIAL) EXTRACELLULAR (POTENTIAL).

375 396 403

TRANSMEM

TRANSMEM

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4 (POTENTIAL)

5 (POTENTIAL) 6 (POTENTIAL)

424 430 451 476

TRANSMEM

DOMAIN DOMAIN

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

510

TRANSMEM TRANSMEM SEQUENCE

DOM'A IN DOMAIN

(POTENTIAL)

EXTRACELLITIAR (POTENTIAL). EEFF58D978131F9D CRC64;

63566 MW;

552 AA;

Watanabe K., Yamaquchi Y.; "Molecular identification of a putative human Byaluronan synthase.";

Riol. Chem. 271:22945-22948(1996).

SYNTHESIS.

MEDLINE-96394371; PubMed=8798477;

SEQUENCE FROM N.A. NCBI\_TaxID=9606;

TISSUE=Brain

Eukaryota, Metasoa, Cherdata, Cramiata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

Homo sapiens (Human)

30-MAY-2000 (Pel 39, Last sequence update)
30-MAY-2000 (Pel 39, Last annotation update)
HYALURONAN SYNTHASE 2 (EC 2.4.1.-) (HYALURONATE SYNTHASE 2)
(HYALURONIC ACID SYNTHASE 2) (HA SYNTHASE 2).

30-MAY-2000 (Rel. 39, Created)

STANDARD;

HAS2\_HUMAN

CONSISTING OF GLOCHRONIC ACTO (GLA) AND N-ACETYLGALACTOSAMINE

-i- PATHWAY: HYALURONATE SYNTHESIS, WHICH HAS A REPEATING UNIT -1- FUNCTION: PLAY A ROLE IN HYALUKUNAN/HYALUKUNIC ACID (HA)

SUBCELLULAR LACATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).

-;- TISSTE SPECTFICITY: EXPRESSED IN FIBROBLASTS. -;- SIMILARITY: BELONGS TO THE NOUC/HAS FAMILY.

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Gaps
  .;
``
   973 VIQDLATLFEELQREKKLKSHQKLSETLKNLLSCVYSCPSY1AKDLMKV 1021
  0.5%; Score 59; DB 1; Length 552; 28.6%; Pred No. 1.30+02;
   58 11QSLFAFLEHRKMKKSLETPIKLNKTVALCIAAYOEDPDYLRKCLOSV 106
  24; Indels
   #IAS2_MOUSE STANDARD, PPT; 5:52 AA P70312; P70411; Q62405; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last sequence update)
   11; Mismatches
ouery Match
Best Local Similarity 28:59
Walches 14; Conservative
   RESULT 119
   HAS2_MOUSE
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Length 552, 24; Indels

0.5%; Score 59; DB 1; 1 28.6%; Pred. No. 1.3c+02;

11; Mismatches

Conservative

Local Similarity es 14, Conserv

Matches

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HAS2\_HUMAN

RESULT 118

Ouery Match

973 VIQDLATLEBELQREKKIKSHQKISPTI:KNILISCVYSCPSYTAKDI.MKV 1021 

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   This SWISS PROT entry is enepyrique. It is produced through a collaboration
   Spicer A.F., Angustine M.L., McDonald J.A.; ** ** Motecular cloning and characterization of a printive mouse Lyaluronan
  Fulop C., Salustii A., Hascall V.C.;
"Codding sequence of a hydluronan synthase homologue expressed during
expansive of the merge require complex."
Arch. Biochem. Biophys. 337:261-266(1997).
  SUBTELLULAR DOTATION: INTEGRAL MEMBRANE PROTEIN (PROBALLE).
TISSUE SPECIFICITY: EXPRESSED IN HEART, PRAIN, SPLFEN, LUNG AND
   PATHWAY: HYALIF MALE SYNTHESTS, WHITH HAS A PEPEALING UNIT PURSIBLE OF REPORTING ONLY
  Approxyltransferase: Transmembrane: Multigene family.
   Mus musculus (Mouse).
Enkaryotis Metazoas Choratas Craniatas Vertebratas Enteleostomis
Mammalias Entherias Eodertias Scieroquathis Moradaes Marinaes Mass
   orbinish and mouse and are involved to versymbolsky if Mai like childs on knosaccharides during early embryogenesis. Ty
Proc. Natt. Acad. Sci. U.S.A. 944548-4554(1996).
  semino 2 8., Specht C.A., Raimondi A., Roabins P.W.;
Homelous of the Xeropis developmental grove DA42 are present in
  1 - FURTION, BLAY A ROLE IN HTALSBONAN/BRALDRONIC ACID (HA)
HYALUE-MAN SYNTHASE 2 (ET 2.4.1.) (HYALUE-MAIE SYNTHASE 2) (HYALUE-MA), ATID SYNTHASE 2) (HA SYNTHASE 2).
  EXTRACELLOLAR (POTENTIAL).
  EATERCELLOLAR (POTENTIAL).
  EXTRACELLULAR (FOTENTIAL)
  EXIRACELLULAR (POTENITAL)
  B840BABC6D2260D5 CRC64;
  2 (POTENTIAL).
CYTOPLASMIC (POTENT(AL).
   'YIOPLASMI' (POTENTIAL).
   'F' TENT AL).
   PYTOPLASMIC (POIENTIAL).
7 (POIENTIAL).
  DEVELOPMENTAL STAGE: EXPRESSED AT DAY 7.5. SIMILARITY: BELONGS TO THE NOCE/HAS PAMILY.
   1 (POTENTIAL)
  (POTENTIAL)
   * (POFENTIAL)
  (POTENTIAL)
  (POTENTIAL
   "YIOPLASMI"
  Biol. chem. 271:23400-23406(1996).
  MEDILINE 96209769; PabMed 8643441;
   MEDICINE PERSONALING PUIDMED 8798545;
  STRAIN SWISS (201)
MEDGINE 97169014; Pubmed+9016821;
  FELTO MW.
  SECUENCE JE 215 1446 FROM N.A. SIRAIN SWISS WEBSTER;
   EMBL: UK9/95; AABI7609,11; 5.
   EMBL: 05 4222: AA352: 51.1;
Mate: Mat:107821; Basz.
   ÷ ;
   SKELEIAL MUSCLE.
  SECUENCE FROM N.A.
  55.2 AA;
   SECUENCE FROM N.A.
   N'BI_IaxII lare90;
  STRAIN PS7BL/EU;
   SYNTHESIS.
  (::1::.NV:.)
  Pransterasar
  synthase.";
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   N. AM.
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   Enkarycta, Metassa, Chordata, Craniata, Vertetrata, Enteleostomi;
Mammalia; Eutheria; Rodentia; Seiurognathi; Muridae; Murinae; Rattus.
   Sdpt
                                    Gaps
  CONSISTING OF GLUCURONIC ACTO (GLCA) AND N-ACETYLGALACTOSAMINE
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O
   -!- SUBCELLULAR LOCATION: INTIGRAL MEMBRANE PROTEIN (PROBABLE).
   92 × VILIHARI EFEL VESEEN FERGELALLENGLESVISSTEST IAFRAMAV (102)
   30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
3YALISCANA SYNTHASE 2 (E. 2.4 l. ) (BYALISCANA SYNTHASE 2)
(HYALGRONIC ACID SYNTHASE 2) (HA SYNTHASE 2)
  973 VIQDLAITHEELQREAKLKSEQRISELILANILSCVYSCPSYIAKDIMKV 1021
Query Match 0.5%; score 59; UR 1; Length 952; Best Local Similarity 28.6%, Pred. No. 1.6-92; Matches 14; Conservative 11; Mismatches 24; Indels
  58 IIQSLFAFILEHRKMKKSLFTPIKLAKTVALCIAAFQEDDPYLRKCLQSV 106
   24; Indels
  58 IIQSLFAFLEHRKMKKSLFTPIKLNKTVALCIAAYQEDPDYLRKCLQSV 106
  0.5%; score 59; DB 1; Length 552;
   EXÍRACELLULAR (POTENTIAL).
  EXTRACELLULAR (POTENTIAL).
   EXTRACELLULAR (POTENTIAL).
  EXTRACELLULAR (POTENTIAL)
  1DCAA244E4A4E9BC CRC64;
  CYTOPLASMIC (POTENTIAL).
  2 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
   CYTOPLASMIC (POTENTIAL).
   Fred. No. 1.4e+02;
   -1- SIMILAPITY: RELONGS TO THE NOFCZHAS FAMILY.
   Conservative 11, Mismatches
   4 (POTENTIAL).
   ( (POTENTIAL)
  (POTENTIAL)
  (POTENTIAL)
   7 (POTENTIAL.)
   PKI;
   30-MAY-2000 (Rel. 39, Created)
  63534 MW;
   FMRI; AF008201; AAR63209.1; -
   Best Local Similarity 28.6%;
  STANDARD;
  Rattus norvegious (Rat).
  4 4 2 3
4 4 2 9
4 4 5 0
4 4 7 5
4 9 6
  510
   374
395
402
  552 AA;
   SEQUENCE FROM N.A.
  NCB1_TaxID=10116;
  (GECNAC)
   lansferase,
   14;
   HAS2 RAT
   TRANSMEM
  SECUENCE
  Query Match
   TRANSMEM
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   IRANSMEM
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   NIVWOK
  DOMAIN
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   DOMAIN
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   DUMAIN
   Matches
  RESULT 120
  qq
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   ċ
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   Sdr
  Nagase T., Scki N., Ishikawa K. T., Chira M., Elwurubuyasi Y., Chara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Prediction of the coding sequences of unidentified human genes. VI. The coding sequences of 80 new genes (KIAAurel-KIAAUreu) deduced by analysis of CDNA clones from cell line KG-1 and brain."; DNA Res. 3-321-329(1996)
   "A DNA polymerase from the archaeon Sulfolobus solfatarious shows sequence similarity to family B DNA polymerases."; Nucleic Acids Res. 20:2711:7716(1992)
   Bukanyola, Metacoa, Cherdata, Cranjata, Vertrebrata, Buteleostemi;
Mammalia: Butheria, Primates, Catarrhini, Hominidae, Homo.
  Archaea, Cremarchaecta, Sulfolobales, Sulfolobaceae; Sulfolobus.
NCBL_TaxID-2287;
   ó
   Sensen C.W., Klenk H.-P., Singh R.K., Allard G., Chan C.C.-Y.,
  0.5%; Score 59; DB 1; Length 635;
29.5%; Fred. Mo. 1.5e+02;
  11, Mismatches 20; Indels
   Hypothetical protein.
SEQUENCE 635 AA: 70128 MW: 34182DUACZEFISE9 CRC54;
   953 YELTDHLISKAEELISDAATVIQDLATLEBELÜREKKLASHÖKL 296
  01-NoV-1997 (Rel. 35, Created)
01-NoV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PRT;
   Pisani F.M., Martino C., Rossi M.;
  SEQUENCE FROM N.A.
STRAIN-ATCC 49255 / MT4;
MEDLINE-92310905, Fubmed 1614458,
   STRAIN+DSM 1617 / P2;
MEDLINE+97055432; PubMed+8899719;
  TISSUE-Bone marrow;
MEDLINE-97191544; FubMcd: 9039502;
   DNA POLYMERASE I (EC 2.7.7.7).
  HYPOTHETICAL PROTEIN KIAA0256.
  EMBL; D87445; BAA13386.1; -.
  13, Conservative
   Sulfolobus solfataricus.
STANDARD;
   Homo sapiens (Human).
  Best Local Similarity
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  NCB1_TaxID-9606;
Y256_HUMAN
  Query Match
   KIAA0256
   093073;
   RESULT 122
   Matches
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   Buchmera aphidicola (subsp. Acytthesighen pisum) (Acyrthesiphon pisum symbiotic bacterium).
Bacteria: Proteobacteria; gamma subdivision; Buchmera.
   Charlebois P. L., Singh P. K., Chan-Weither C.C.-Y., Allard G., Chow C., Confalonieri F., Curtis B., Duguet M., Erauso G., Faquy D., Gaasterland T., Garrett P.A., Gordon P., Jeffries A.C., Kozera C., Kushwata N., Zafleur E., Mediaa N., Peng X., Penny S.L., She O., St Jean A., van der Cost J., Yeung F., Zivanovic Y., Doolittle W.F.,
   "Gene content and organization of a 281-kbp contig from the genome of the extremely thermophilic archaeon, Sulfolobus solfatarious P2."; genome 4:4.116-18.6(2000)
i principal prize Polimberase Possesses TWO ENZYMATIC ACTIVITIES:
  DNA SYNTHESIS (POLYMERASE) AND AN EXONUCLEOLYTIC ACTIVITY THAT DEGRADES SINGLE STRANDED DNA IN THE 3' TO 5' DIRECTION.
-!- CATA:YTIC ACTIVITY: B DEGXYMINITEGRIDE TRIPHOSPHATE *
  01-0CT-2000 (Pel 40, Created) degree of control of control of the control of control of control of control of control of control of control of control of control of control c
Liu Q.Y., Penny S.L., Young F., Schenk M.E., Gasterland T., Doolittle W.F., Ragan M.A., Charlebois R.L.; "Organizational characteristics and information content of an arrhapal genome- 156 kb of sequence from Sulfolobus solfataricus
  ..
.
  67 APLESOLAKTLERSVOTKAVNKOLDENISLELIHLSPYFILIKPAQKOLEWLI 118
   622 APAVAESVTALGRYVITSTVEKAPFEGLTVITGETESIFILINPPKNSLENII 673
  Interpro; ippn02064;
PERMIN PR00136; DNA_pol_B; 1.
PRIMIN: PR00104: PROMOTO:
PROSTEE: PR00116: DNA POLYMERASE_B; 1.
PROSTEE: DNA-directed DNA polymerase; DNA replication:
DNA birding, Rydrolase: Exonuclease.
CONFLICT 139 139 L -> H (IN REF. 1).
  0.5%; Score 59; DB 1; Length 882;
30 8%; Pred No. 2.2c+02;
Live 8; Mismatches 28; Indels
  N PYROPHOSPHATE + DNA(N).
  139 139 L -> H (IN REF. 1).
624 624 A -> R (IN REF. 1).
882 AA; 101223 MW; 7755E0975AALC81A CEC64;
  940 AA.
  PRT;
  STRAIN-DSM 1617 / P2;
MEPLINE 20145948; PubM~d-10701121;
  Mirrobiol 22.175-191(1996).
  EMBL; X64466; CAA45795.1; -. EMBL; U92875; AAB53090.1; -. EMBL; Y18930; CAR57747.1; -
  Conservative
   S'rANDAED;
   Ragan M.A., Sensen C.W.;
   Best Local Similarity
  PIR; $23019; $23019
  NCB1_Tax1D=118099;
  SEQUENCE FROM N A
  HFS OF BU149.
  16;
  SY1_BUCA1
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                      STRAIN FORYO 1999.
MEDLINE 20445174; PubMed 10994077;
Mildern Edwin St. Watanabe H., Hartori M., Sakaki Y., Ishikawa H.;
Shider dou S., Watanabe H., Hartori M., Sakaki Y., Ishikawa H.;
Shider dou S., Watanabe H., Hartori M., Sakaki Y., Ishikawa H.;
Burhmeta Sp. Afs.";
Mature do A. Ed. Selectori The endocellular bacterial symbication of aphids
Mature do A. Ed. Selectori J., The endocellular TRNA(ILE) AMP +
PYROPHOSPHATE + I. ISOLEUCYL-FRNA(ILE).
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SUBMITARIIY: MELONGS POCIASSI: AMINOACYL-IRNA SYNIHFIASE FAMILY.
  Amireary! *PNA symbotime; Protein biosymthecis; Danse, ATP binding,
  MELLANE 92.02814; FatMod 16.0427, Didomentoo B., Chakraburtty K.; Didomentoo B., Lupisella J.A., Sanshaken M.C., Chakraburtty K.; Issolation and Sequence analysis of the dence encoding translation element for lattoom Candida albicans."; Peast 81.477-352(1992).
   Eskaryota, Entati Ascomprota, Saccharomycotina, Saccharomycotes, Sacrharomycetales, candida.
   Myers K.K., Fourthwid., sypherid P.S.,;
"Isolation and Sequence and yes so of the gene for translation
electron letter 4 from Candida albinans.";
Nucleur Aride Dee, 200725-51720 (1902)
  Score 59, 08 1; Length 940; Prod. No. 2.4e+02;
9; Mismatches 10; indel:
  607 + 67 ATP (BY SIMILAKITY).
340 AA: 11:455 MW: 769F5D01504F6496 GR054).
   MEDLINE-92261319; Pubmed 1584022;
Collourst D.R., Schander B.S., Hyaes M.V., Fulte M.F.,
  61 MAY 1902 (Rel. 22, Created)
ol-MAY 1902 (Rel. 22, Last Sequence update)
15-DEC 1998 (Rel. 47, Last annotation update)
  "KMSKS" RESTEAN
  PRT: 1049 AA
   "HIGH" REGIEAN.
   72 GLARTERESVUIRAVARGULBATSUFUTH 190
   820 BINKFLEBALQNKLINNSLLTSILLIXVSH 848
  EMBL: Aroulle: BAB12867.1; -.
FROSIE: PSOO178: AA_IRNA_LIGASE 1: 1.
   STRAIN (S05314)
MEDLINE (1225337), FubMed-1573403;
   Good Similarity 44,58;
  SEQUENCE OF 83 148 FROM N.A.
  ELONGALION FACTOR 4 (RF-5).
  andida albicans (Yeast).
   end the losting
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  Metal binding: Zinc.
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  Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badvock K., Basham D., Brown D., Chillingworth T., Connor R.,
   1,4158
  Actinomycetales, Corprehactor.neae, Mycobarterlaceae; Mycobacterium.
NCHI_TaxID-1773;
   11 SIMILARITY: BELÖNGS TO THE ATE-BINGING TRANSPORT FROMEIN PAMILY
  01-0XI-2000 (Ref. 40, Last sequence update)
01-0XI-2000 (Ref. 40, Last annotation update)
CARBAMOYL-PHOSPHAIE SYNTHASE LARGE CHAIN (Ε΄ Ε΄ 6.3.5) ("ARBAMOYL
             structural and functional similarity to \mathrm{EF}^{-1} from Saccharomyces corevisiae.";
  PROSITE: PS00251; ÄBC_TRANSPOCIER; 2.
PROSITE; PS50077; HEAT_REPEAT: 1.
Protein biosynthesis; Elongation factor: Repeat: ATP binding;
"Elongation factor 3 (EF 4) from Candida albicans shows both
   0.5%; Score 59; DW D. Length 1049;
32.7%; Pred. No. 2.7c+02;
ive 8 Mismatches 25; Indois
  2081 RFAALITVIJALAEKLKENYIVIJJPSTPFIJAEIMEDECEEVEHQCQKTT 2129
   149 KVAILRAVSQLVDTAKAQIALRMPELIPVLSESMWDTKKEVKEAATAIM 197
  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
   ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
::YS-KICH (RASIC).
  HEAT REPEATS DOMAIN.
   CARB OR BV1384 OR MICYQDB12.18 OR MICY21B4.01.
Mycobacterium imberculosis.
   PRT; 1115 AA
  -!- SIMILARITY: CONTAINS TO HEAT REPEALS.
   (ABC TRANSFORTERS), EF: 4 SUBFAMILY
   DOMAIN 11
   OF AMINOACYL-TRNA TO THE KIBOSOME.
-1- PATHWAY: PROTEIN BLOSYNTHESIS.
  PHOSPHATE SYNTHETASE AMMONIA CHAIN)
  MEDLINE-98295987; Pubmed=9634230;
  116872 MW:
  01-0CT-2000 (Rel. 40, Created,
  EMBL: Z11484: CAA77567.1: -.
EMBL: Z12822: CAA78292.1: -.
FTE, S25363, 025363.
   32.78;
   InterProj IPR001617;
Ptam, PF00005; ABC_tran,
PROSITE: PS00211; ABC_TRA
   Best Local Similarity 32.79
Matches 16; Conservative
   STANDARD;
   2446
712
1035
111
7292
7293
  325
  299
729
729
1049 AA;
   SEQUENCE FROM N.A.
   1014
  677
465
705
   STRAIN=H37RV;
   RNA-binding.
  CARB_MYCTU
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   0
              Hornsby T., Jagels K., Krogh A., McLean J., Monle S., Murphy L., Cliver E., Csterne T., quail M.A., Fajandream M.A., Regers J., Stelton S., Squares S., Squares J., Taylor K., Whitehead S., Barrell B.G.; Taylor K., Whitehead S., Barrell B.G.; Complete genome sequence."
   THE LARGE (OR AMMONIA) CHAIN TO SYNTHESIZE CARBAMOYL PHOSPHATE (BY
  SUBUNIT: COMPOSED OF TWO CHAINS, THE SMALL (OF GLUTAMINE) CHAIN PRONOTES THE HYDROLYSIS OF GLUTAMINE TO AMMONIA, WHICH IS USED BY
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
   Caps
   Arginine biosynthesis, Pyrimidine biosynthosis, Ligaso, Duplication;
ATP-binding, Manganese.
   -t- PATHWAY: INVOLVED IN BOTH AEGININE AND FYRIMIDINE BIOSYNTHESIS.
-t- SUBUNII: COMPOSED OF TWO CHAINS, THE SMALL (OR GLUTAMINE) CHAIN
   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eufeleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
  MEDLINE=96199216: PubMed-8621630;
Chen G., Guy C.T., Chen H W. Hay N. Lee-F Y H P., Lee-W H.,
Molecular cloning and developmental expression of mouse p130, a
inember of the retinoblastoma gene lamily.",
J. Biol. Chem. 271:9567-9572(1996).
   30-MAY-2000 (Rel. 39, Last sequence update)
C1-OGT-2000 (Rel. 40, Last annotation update)
RETINOBLASTOMA-LIKE PROTEIN 2 (130 KLM FETINORIASTOMA-ASSOCIATED PROTEIN) (PHB2) (P130) (RBR-2).
   0;
   MEDLINE-96192345; Pubmed-9019172;
Pertile P., Baldi A., de Luca A., Virgilio L., Pisano M.M.,
  0.5%; Score 59; DR 1; Length 1115; 33.3%; Fred. No. 30.02;
   H-CATALYTIC ACTIVITY. 2 ATH H-GIUTAMINE H-CO(2) H-H(2) \theta ORTHOPHOSPHATE H-GIUTAMATE H-CARBAMOYL PHOSPHATE.
   20; Indels
  -!- COFACTOR: BINDS THREE MANGANESE IONS (BY SIMILARITY).
  293PhA (SEDÉNIMA) PECE4,
  1729 AIPQLPSLMPSLLTTMKNTSELVSSRVYLLSALAALQKVVET 1770
   367 AFEKEPGADPTLTTTMKSVGFAMSLGRNEVEALGKVMPSLET 408
   ATP (POTENTIAL).
ATP (POTENTIAL).
  PRT; 1135 AA
   8, Mismatches
   or send an email to ilcensewisb-sib.ch).
   Fred. No.
   EMBL; Z81011; -; NOT_ANNOTATED_CDS.
  NOT_ANNOTATED_CDS
  1115 AA, 118961 MW,
   30-MAY-2000 (Rel. 39, Created)
   PROSITE; PS00866; CPSASE_1; 1. PROSITE; PS00867; CPSASE_2; 2.
   33.38,
   Best Local Similarity 33.3
Matches 14; Conservative
   Nature 393,537 544(1998).
  STANDARD;
   215
  358
   1115
   Mus musculus (Mouse).
   Tuberculist; Kvi384;
   SECUENCE FROM N.A.
   SEQUENCE FROM N.A.
  NCB1_TaxID=10090;
   559
  SIMILARITY)
  280108;
  RBL2_MOUSE
Q64700;
   Query Match
  SEQUENCE
   NP_BIND
  NP_BIND
   REPEAT
   REPEAT
  Matches
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           "Molecular cioning, expression, and derelopmental characterisation of the murine retinoblastoma related gene Rb2/pl30 "; cell Growth Differ, 6-1659-1664(1995).
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                                                                                                                                                                                                                                               oneogene 12:1433-1440(1996)
-i- FUNCTION: MAY HAVE A FUNCTION IN CELL CYCLE REGULATION. BINDS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding, Nuclear protein; Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE RETINOBLASTOMA PROTEIN (RB) FAMILY.
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O
                                                                                                                                                                                         Teconter J.E., Whyte P.F.M., Rudnicki M.A.; "Figning and expression of the Pb-related mouse p130 mRNA.";
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S -> A (IN REF. 2 AND 3).
V > I (IN REF. 1).
XW; 0555449998ArrAdh CPC44;
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A -> F (IN PEF. 3).
A -> T (IN REF. 1).
T -> S (IN REF. 1).
G -> T (IN REF. 1).
O -> R (IN REF. 2).
MISSING (IN REF. 2).
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P -> A (IN PEF. 3).
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                                                                                                                                                              MFDLINE=96203998; PubMed-8622859;
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1135 AA, 127472 XW;
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DOMAIN 414 1021 PC
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Best Local Similarity 28.8%;
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Pfam; PF01857; RB_B; 1
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MGP; MGI-105085; Pb]2
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                                                                                                                                         SEQUENCE FROM N A.
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484
768
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Y195_HUMAN
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Deaven L.;
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          between the swiss fastilate of bisinformalise and the EMME contained the European Bisoinformatics institute. Increare no restrictions on its use by compretit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a hierare agreement (See http://www.isb-sib.ch/announce/or send an email to licensedish-sib.ch/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PEOF entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagles E., Soki N., Ishikowo K. E., Panaka A., Nemura N., **
**Prediction of the coding Sequences of unidentified human across. V. The coding sequences of the measures (FISA 27. FISA 
                                                                                                                                                                                                                                         Eukaryotas Metasoas (Nordatas Staniatas Vertebratas Esteleossomis
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Mammallas Estherias Primutes, Satarchinis Hominidaes Homos
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                                                                                                                                                                                                                                                                     Mammalia: Entheria; Primates: Catarrhini; Hominidae; Homo.
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$12707;
of NV 1997 (Ref. 35, Freated)
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THREKIN (TOHER ADS STIERCEIS 2 PROTEIN).
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Nellist M., Janssen B., Frook-Parter P.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Soki N., Tshikowa K., I.,
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                                                                                                                                  HYPOTHETTO'AL PROTEIN KIAAU195.
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                                                                                                                                                                                                       Homo sapiens (Human).
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Best Local Similarity
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Sampson J.E.:
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P49815; +75
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"The GAP-related domain of tuberin, the product of the 1802 dene, is a target for missense mutations in tuberous sciencesis.";
Hum. Mol. Genet. 6:1941-1946(1997)
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RECKE D.G., Brace D., Mandf M., Boatett N., Mank C., Stonders F.,
Robinson D., Jones M., Bucktudham J., Chasteen L., Thompson S.,
Goodwin L., Bryant J., Tesmer J., Mohreke L., Fondmire J., White S.,
Denq S., Tatum O., Campbell C., Fawcett J., Maltbie M., Misra M.,
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"The tuberous selectorsis 2 deno product, Tuberin, functions as a Rab5
GTBase activating protein (GAP) in modulating endocytusis.";
J. Biol. Chem. 272:6097-6100(1997).
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MEDLINE-96422264; PubMed-8824381;
                                                                                                                                                                                                                                                          Xu L., Sterner C., Maheshwar M.M., Wilson P.J., Nellist M., Short M.P., Haines J.L., Sampson J.R., Kamesh V.; "Alternative splicing of the tuberous selerosis z (TST2) gene in human and mouse tissues.";
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Smell R.G., van den Duweland A.M.W., Fenser A., Sampson J.K.,
Halley D.J.J., van der Sluijs P.;
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"Germ-line mutational analysis of the 1802 quee in 90 tuberous
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Kwiatkowski D.J., Short M.P., Haines J.L.;
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Submitted (DEC-1998) to the EMBL/Surmark/DUBS databases.
                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hum. Mol. Genet. 7:1053-1057(1998).
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MEDLINE: 20054445; Pubmed: 10583443;
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MEDLINE-97197768; PubMed=9045618;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Senomics 27:475-480(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  familial TSC patients.";
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Am. J. Med. Genet. 90:124-126(2000)

-i.- FUNCTION: IMPLIFATED AS A TUMOR SURPRESSOR, MAY HAVE A FUNCTION IN VESTIGULAR TRANSPORT, BUT MAY ALSO PLAY A ROLE IN THE REGULATION OF CELL GROWTH APPREST AND THE PEGULATION OF TRANSPRIPTION MEDIATED BY STEROID PECCEPTORS INTERACTION BETWEEN HAMARTIN AND TGBERIN MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Superiority of denaturing high performance liquid chromatography over single-stranded conformation and conformation sensitive gel electrophoresis for mutation detection in TSC2.";
                                                                                                                                                                                                                                                                                            "Mutation and polymorphism analysis in the tuberous sclerosis 2 (TSC2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS TSC R-137; L-320; Q-611; N-547; P-717; E-759; M-963 w L-1657.
MEDLINE-20637501; Pubmed-16570911,
Chang H., Namba E., Yamamato T., Ninomiya H., Ohno K., Mizuquchi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Mutational analysis of 1SC1 and TSC2 genes in Japanese patients with tuberous sclerosis complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS TSC W-611;W-505;P-1744 & H 1746 - F 1751 DEL, & VARIANT L 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang H., Yamamoro T., Nanba E., Kitamura Y., Terada T., Akaboshi S., Yuasa I., Ohtani K., Nakamoto S., Takeshita K., Ohno K.; "Novel Tsiz metation in a policent with pulmonary Luberous selerosis: lack Ann. J. Med. Genet. 82:364-370(1999).
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                                                                                                                                                                                                                                       VARIANTS TSC.
Gilbert J.R., Guy V., Kumar A., Wolpert C., Kandt R., Aylesworth A.,
Koses A.D., Pericak-Vance M.A.;
                                                                                                Beauchamp R.L., Banwell A., McNamara P., Jacobsen M., Higgins E., Northrup H., Short M.P., Sims K., Ozelius L., Ramesh V., "Exon scanning of the entire TSC2 gene for germline mutations in 40 unrelated patients with Luberous sciencisis.", Hum. Mutat 12:408-416(1998)
                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=99223423; FubMod*10.05.61;
Jones A.C., Shyamsundar M.M., Thomas M.W., Maynard J.,
Jones A.C., Shyamsundar M.M., Thomas M.W., Maynard J.,
Jones A.C., Shyamsundar M.M., Thomas M.W., Maynard J.F.;
Comprehensive mutation analysis of TSC1 and TSC2-and phenotypic
correlations in 150 families with tuberous scherosis.",
Am. J. Hum. Genet. 64:1305-1315(1999).
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Kasprzyk-Obara J., Beeve M.P., Kwiatłowski D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE-2000454; probled-10533067: Mida Y., Lawrence-Smith N., Batwell A., Hammer E., Lewis J., Beatwell A., Lawrence-Smith N., Batwell A., Callus L.; Sims K., Ramesh V., Ozelius L.; Analysis of both Tstl and 1802 for germline mutations in 126 munclated patients with tuberous sclerosis."; Hum. Mutat. 14:412-422(1999).
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MEDLINE=20076217; Pubmed=10607950;
                    Hum, Genet. 62:286-294(1998).
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                                                                                    MEDLINE-99045375; Pubmed 9829910;
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sclerosis patients.";
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                                                                  VARIANTS TSC
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1323 IMSTETEMGANVMELDETYSFOVINKTVKMVIPALIGSDSGDSIEVSENVEETVVKIISV 1382
                                                                                                                                                                                                               -!- ALTERNATIVE PRODUCES: A NUMBER OF FORMS CAN BE DERIVED FROM ALTERNATIVE SPLICING OF THE TSC2 GENE.
-!- TISSUE SPECIFICITY: LIVER, BRAIN, HEART, LYMPHOCYTES, FIBROBLASTS, BILLARY EPITHELIUM, PANCREAS, SKELETAL MUSCLE, KIDNEY, LUNG AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liang J., Choi J., Clardy J.;
*Pelined Structure of the FKBFlZ-rapamycin-FKB ternary complex at 2.2
                                                                                                                                                                                                                                                                                                                         1. DISEASE. DEFECTS IN TSC2 ARE THE CAUSE OF TURFFOUR STIFFGSIS COMPLEX (TSC), THE MOLECULAR BASIS OF WHICH IS A FUNCTIONAL INPAIREMENT OF THE TUBERIN "HAMARINE STIFFGSIS OF WHICH IS A FUNCTIONAL DOWINANT WILTT-SYSTEM DISORPRE THAT AFFECTS ESPECIALLY THE BRAIN. KIDNEYS, HEART, AND SKIN. TSC IS CHARACTEKIZED BY HAMARIDAMS CHENIGN OVERGENOWINS PREPONINANTLY OF A CELL OR TISSUE TYPE THAT OCCURS NORMALLY IN THE ORGAN AND HAMARITAS (DEVELOPMENTAL ARNORMALITIES OF THE ORGAN AND HAMARITAS (DEVELOPMENTAL FOR BRAINING MITCH AND MOLECULAR SKIN TO PROFOUND MENTAL FOR AND MATTER THAT OF PROFOUND MENTAL FOR AND MATTER SKIN TO PROFOUND MENTAL
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              INTRINSIC GTPASE ACTIVITY OF THE RAS-RELATED PROTEIN RAPIA AND RAB5. SUGGESTING A POSSIBLE MECHANISM FOR ITS ROLE IN REGULATING CELLULAR GROWTH, MUTATIONS IN TUBERIN LEADS TO CONSTITUTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKBP-PAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN TARGET PROTEIN).
                                                                                                     SUBDNIT: INTERACTS WITH HAMARTIN. MAY ALSO INTERACT WITH THE ADAPITED MOLECULE PARAPTIN 5 THE FINAL COMPLEX CONTAINS TUBERIN AND RABAPTIN 5 LINKED TO PAR5 (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RETARDATION WITH INTRACTABLE SELZURES TO PPEMATURE DEATH FROM A
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=96279639; PubMed=8662507;
Choi I., Chen J., Schreiber S.L., Clardy J.;
Structure of the FRRPIZ-rapamycin complex interacting with the binding domain of human FRAP.";
                                                                                                                                                                       -!- SUBCELLULAR LOCATION: CYTOPLASMIC, AT STEADY STATE FOUND IN ASSOCIATION WITH MEMBRANES.
FACILITATE VESICULAR DOCKING SPECIFICALLY STIMULATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brown E.J., Albers M.W., Shin T.B., Ichikawa K., Roith C.T., Lane W.S., Schreiber S.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 59; DB 1; Length 1807;
25.8%; Pied. No. 5.3e+02;
1Ve 17; Mismatches 32; Indels
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01-NOV-1995 (Kel. 32, Last sequence update)
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                                                                                         ACTIVATION OF RAPIA IN TUMORS.
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                                                                                                                                                                                                                                                                                                                         this SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS INSTITUTE of Bioinformatics and the EMBL outstailon. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way mobilized and this statement is not removed. Usage by and for commercial entities requires a licement (see http://www.isb.sib.ch/announce/or send an email to licenserisb sib.ch).
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Mammalia: Entheria: Rodertia: Sejarequathi: Maridae; Morinae; Pattus
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01 N.V. 1955 (Ref. 42, Created)
01 N.V. 1995 (Ref. 42, Last Sequence update)
01 Oct 2000 (Ref. 40, Last annotation update)
01 Oct 2000 (Ref. 40, Last annotation update)
FKBF RAPMMYTH ASSOCIATED PROTEIN (FKAP) (FARAMYTH IAMSET PROTEIN).
PAFIL:
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Sabets 713., Martin M.M., Brunn G.J., Williams J.M., Dumont F.J.,
Wiederrecht G., Abraham F.T.;
                              Acta Orystallodr. D 55:746-744(1999).

-! FUNCTION: ATTS AS THE TARGET FOR THE CELL-CYCLE ARREST AND IMMONOPERESIVE REPETING OF THE FKBF12-KAPAMYCIN COMPLEX.
-! SIMILARITY: BELOANS TO THE PI3/PI4 KINASES FAMILY.
-! SIMILARITY: ALLONIS & HEAT REFEALS.
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2; Mismatches 12, Indels
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Sabatini D.M., Erdjument-Bromage H., Lui M., Tempst P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2070 ULETRISSPEVPEAALITVLALAELKENYIVULE 2104
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POB; 1NSG; 18+MAR-98;
POB; 1AHE; 18-NOV-98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2544 AAS
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www.commonated E.E. Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Property Common Pr
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Richinormatics and the PMBL outstallon the Broopean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in to way modified and this statement is not removed. Usage b_T and for commercial
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or send an email to licensedisb-sib.ch).
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01-AUG-1992 (Rel. 23, Last sequence update)
15-Jul-1999 (Rel. 23, Last sequence update)
15-Jul-1999 (Rel. 23, Last sequence update)
15-Jul-1999 (Rel. 23, Last sequence update)
16-Jul-1999 (Rel. 23, Last sequence update)
16-Jul-1999 (Rel. 26, Rel. 27, Rel. 
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Viruses, ssENA positive-strant viruses, no DNA stage; Flavivitidae;
                                            "RAPT1: a mammalian protein that binds to FKBP12 in a rapumyein-
dependent fashion and is homelogous to yeast ToRs.";
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Choo O.-L., Richman K.H., Han J.H., Herser K., Lee C., Fond C.,
Callegos C., Coit D., Medina-Asiby A., Barr P.J., Weiner A.J.,
Bradley D.W., Kuo G., Houdhlor M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic organization and diversity of the hepatitis C virus.";
Proc. Natl. Acad. Sci. U.S.A. 88:2451-2455(1991).
                                                                                                                                                                                             -i- FUNCTION: ACTS AS THE TAKGET FOR THE CELL-CYCLE ARREST AND IMMONSOPERENSIVE EFFCUS OF THE PRACT FARMANTIN COMPLEX.
-i- SIMILARITY: HELONGS TO THE PLEYF14 KINASES FAMILY.
-i- SIMILARITY: CONTAINS 8 HEAT REPERTS.
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1109 1148 HEAT 6.
1150 1186 HEAT 7.
2193 1970 HEAT 8.
2198 2549 PTR/P14K.
2549 AA; 288791 MM; BEB41EA7E99086F99 CRC64;
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PROSTE: P800915; P13_4_KinAsE_1: 1
PROSTE: P800916; P13_4_KINASE_2: 1.
PROSTE: P550240; P13_4_KINASE_3: 1.
Transferase; Kinase; Repeat.
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HEAT 5.
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                                                                                                                                                      Cell 78:35-43(1994).
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Snyder S.H.;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute of State of the Forestrictions on its ase by non-profit institutions as loss as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           CARSID PROTEIN C (FOTENTIAL).
MAJOR ENVELOPE PROTEIN (POTENTIAL)
MAJOR ENVELOPE PROTEIN E (POTENTIAL).
NONSTRUCTURAL PROTEIN NSL/EZ (POTENTIAL).
NONSTRUCTURAL PROTEIN NSZ (FOTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-DIRECTED FOR POLYMERASE (POTENTIAL).
                                                 HSB AND NSS MAY REAT A ROLE IN THE VIRAL RNA REPLICATION.
SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Follytectin, Gijopietein, Transferase, RRA-directed RNA polymerase;
Core protein; Goat protein; Envelope protein; Helicase; ATP-binding;
Transmembrane, Neustrectural protein, Hydrelase, Serine protease
INIT_MET 1 1 REMOVED FROM (ARSI) PROTEIN ? PT 1HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NONSTRUCTURAL PROTEIN NS4A (POTENTIAL)
NONSTRUCTURAL PROTEIN NS4B (POTENTIAL)
                                                                                                     LIPOPROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSTO OF TWO PROTEINS: PROTEIN MAND GLYCOPROTEIN E. THE NUCLEOCAPSTO IS A COMPLEX OF
                    HYDROPHOMIC, SUGGESTING A POSSIBLE MEMBRANE RELATED FUNCTION.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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(GLCNAC...) (POTENTIAL).
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-!- FUNCTION: THE SMALE PROTEINS MEDA, MEDB, MEAA AND MEAB ARE
                                                                                                                                                                                            SIMILARITY: THE PROFENSE BELONGS TO PEPTIDASE FAMILY $25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELLULAR AMINOPEPTIDASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M62321; AAA45676.1; -.
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Pfam: PF01560; HCV_NSI; 1.
Pfam: PF01538; HCV_NS2; 1.
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MERCOPS; U39.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnston M., Andrews S., Brinkman R., Couper J., Ding H., Dover J., Pu Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hiller L., Jier M., Johnston L., Langslon Y., Louis E.J., Macri C., Mardis F., Menezes S., Mouser L., Nhan M., Fifkin L., Files L. St Potor H. Trevastis E. Vaurhan R., Vignati D., Wilson R., Wehldman P., Walerston R., Wilson R.,
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                                                                                                                                                                                                              Gaps
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N-LINKED (GLONAC ) (POTENTIAL).
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01-FEB-1995 (Rel. 31, Last sequence update)
01-FEH-1996 (Rel. 33, Last annotation update)
HYPOTHETICAL 433.2 KLA PECTEIN IN HXT5-NFK1 INTERGENIT PEGION.
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                                                                                                                                                                             Length 3011;
                                                                                                                                                                                                            10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 1.3e+03;
5; Mismatches 8; Indels
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                                                                                                                       HERRIGA47PCR5AF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 265:2077-2082(1994).
-! SIMILARITY: STRONG, TO S.POMBE SPACIF5.11C.
-! SIMILARITY: BELONGS TO THE PI3/PI4-KINASES FAMILY.
                                                                                                                                                                           0,5%; Score 59, DB 1; 3
34,5%; Pred Nn 9,8e+02;
                                                                                                                                                                                                                                                                                                                                                                   PRT; 3744 AA.
                                                                                                                                                                                                            9; Mismatahes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Raker's yeast)
                                                                                                                                                                                                                                             1821 VLLPAIKKTYKQIEKNWKNHMGPFMSILQ 1849
                                                                                                                                                                                                                                                                             1745 VIAPAVQTNWQKLETFWAKHMWNFISGIQ 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PI3K/PI4K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1341 YSFQVINKTVKMVIPALIQSPSGDSI 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2907 HAFQVINNAYLPLIPALQQSNSNSNI 2932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed=8091229;
                                                                                                                         4.27147 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, UC0060; AAB68923.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Conservative
                                                                                                                                                                                                              Ponservative
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0001141; YHR099W.
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                  645
2041
2077
2240
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2364 23
2789 27
3011 AA,
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                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4932;
                                                     2077
                                                                                                                                                                                                                                                                                                                                                                 YHP9_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vaudin M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                     CARBOHYD
   CAPROHYD
                      CARBOHYD
                                      CAPROHYD
                                                                         CARROHYD
                                                                                        CARROHYD
                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                    P38811;
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EMBL; AE003512; AAF48985.1;

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the European Ricinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no war
                                                                                                                                                                                                                                                                                                                                     Ruper M.E., Bronner M., Hofmann S.;
"Coming and mapping of the Timilo/Tob gene family encoding small zing times proteins involved in mitochondrial carrier import."; stabilited (MAY 1772) to the tamogiveness's leaf detects.
                                                                                                                                                                                          Bukaryota; Metazea; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterydota; Neoptera; Endopterydota; Diptera; Brachycera; Muscomorpha;
                                                                                                               MITOTHONDRIAL IMPORT INNER MEMBRANE TRANSLOCASE SUBJUIT TIM9B.
                                                olowir-zobo (Rel. 45, Created)
olowir 2000 (Rel. 45, Last Sequence update)
Olowir-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                          Ephydroidea: brosophilidae; brosophila.
                                                                                                                                                                    brosophila melanogaster (Fruit fly).
     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seleuce 247:2185 2195(2000).
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     STANDARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               SECUENTE FRAM N.A.
                                                                                                                                                                                                                                                               NCBL TaxID 7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN BERKELEY;
  IMORO DE ME
                           SALAKON
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a livewer appearance of the commercial content.
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                                                                                                                                                                                                                           1143 GAQIVSSVERGISVNAEQVPIELFPPPRAFPCCIVQQFPPQKMQQFRSQUESVQFVGGS 1202
                                                                                                                                                                                                                                                                 42 CVBRCVTKFARFNONMMKVYVDVCTTINAKHMEEMEENARKAFOOOREOEKEKLKEAAAT 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence analysis of the non-structural NSI (10) and NS2 (1b) protein genes of boyine respiratory syncytial virus."; J. Gen. Virol. 76:193-197(1995).
                                                                                                                                                                                      0; daps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151 FWLLPVKQSGVPLAKGTLITHCYKNLGPMPFIGSLVTKSVKVFAEYPGSSAGLRVLL 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 FTSMPTTQNGGYTWELMETTHGFQ+NGCTTU-NFETTH-5KPLSOSFT AKYSNGLSTTL. 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus spretus (Western wild mouse).
Fabaryota, Metakoa; Chondata; Craniata, Vertebiata, Eutrieostomi;
Mammalia; Eutheria; Rodentia; Sciuroquathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::
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INTERLEMEIN-2 PRECURSOR (IL-2) (T-CEIL GROWTH FACTOR) (TGGF).
                                     Transport; Protein transport; Translocation; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 0.5%; Score 58; DB 1; Longth 136; Local Similarity 28.1%; Pred. No. 31; reds 16; Conservative 11: Mismatches 30; Indels
                                                                                                                                         0.5%; Score 58; DB 1; Length 117;
                                                                                                                                                                                 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bovine respiratory syncytial virus (strain A51908) (BRS).
Viruses: ssRNA negative-strand viruses: Mononegavirales:
                                                                           117 AA; 13520 MW; 3327A332075A57E5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         136 AA; 15246 MW; AEB6A89D7BED2D24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 15-UUL-1998 (Rel. 36, Last sequence update)
15-UUL-1998 (Rel. 36, Last annotation update)
NONSTRUCTURAL PROTEIN 1 (NONSTRUCTURAL PROTEIN 1C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
                                                                                                                                                             Pred. No. 26;
18; Mismatales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95146950; Pubmed=7844532;
Pastey M.K., Samal S.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                  5 JUL-1598 (Eel. 36, Created)
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                                                                                                                                                           Best Local Similarity 20.0%;
Matches 12; Conservative 1
                 FlyBase; FBgn0027358; Tim9.
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QORRA7; P70462; P70463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonstructural
                                                                                                                                                                                                                                                                                                                                                                            VNS1_BRSVA
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Best Local S
                                                                                                                                              Query Match
                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                            065694;
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                                                                                                                                                                                                                                                                                                                                  RESULT 134
                                                                                                                                                                                                                                                                                                                                                        VNS1_BRSVA
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32.78;
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                                                                                                                                                                              Plasmid 19:134-150(1988).
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                                                                                                                               r., Cole S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S00869: S00869.
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                                                                                                                                                                                                                SEQUENCE FROM N A.
                                                                               SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  RECOMBINASES.
                                             NCBI_TaxID=1502;
Plasmid pIP404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSb; PO3012:
                                                                                                                                                                                                                                STRAIN-CPN50;
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                               Clostridium.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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between the Swiss Institute of Robinformatics and the EMBL outstation the European Bioinformatics on Robinformatics and the EMBL outstation is see by one profit institute. There are no restrictions on its mast by one profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communications requires a former operator of seed to statement (see the profit of some processes).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 LASCVTLTLVLLVNSAPTSSPTSSSTABAGGGGGHLEGILMDLGELLSRMENYRNL 6.5
                                                                                                                                                                                                                   ) (BY SIMILAPITY)
                                                                                                                                                                                                    "Gintamine and tetrapeptide repeat variations affect the biological activity of different gouse interleded alleles.",
                                                                                                                                                                                                                                                                                              IMMUNE RESPONSE, CAN STIMULATE B CELLS, MONCYTES, LYMEBOKINE ACTIVATED KILLER CELLS, AND GLIOMA CELLS. SUBCELLULAR LOCATION: SECRETED
                                             Matesanz F., Alcina A., Pellicer A., matesanz F., Alcina A., Pellicer A., mouse of at least five interleukin-2 molecules in different mouse strains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytokine: Giyroprofesin Smane tesponse, Signai, Growth Gotton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 166;
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164 INTERPLENCE.

23 LINEED (AGLING) (BY

137 HY SIMILARITY.

43 POLY-GLN.

27 MISSING.

18763 MW; C11055622938AAR CPC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 KLPRMLIPKFYLPKGATELKHQCLEDELGPLGSVLDLT 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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PROSITE, PSOC424, INTERLAURINLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     041398; AAB39205.1; ALT_SEQ. 041495; AAB39207.1; ALT_SEQ.
                                                                                                                                                                      MEDLINE:96:50482; PubMed:8765005;
                                     MEDI,INE-94307791; PubMed-8319981;
                                                                                                    Immunogenetics 38:300-303(1993).
                                                                                                                                      SHOUFINGE OF 21-166 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L07575; AAA39327.1; -.
   SEQUENCE OF 1-60 FROM N A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                    Matesanz F., Alcina A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:96548;
                   STRAIN SPRET/EL;
                                                                                                                                                         STRAIN-SPRET/EI;
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P07945;
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ACT_SITE 9 9 TRANSIENT COVALENT LINKAGE TO DNA DUKING STRAND CLEAVAGE AND REJOINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- FUNCTION: A LIKELY SOLE FOR THE RES PROTEIN WOULD BE TO STABILIZE PIP404 BY REDUCING THE NUMBER OF PLASMID MULTIMERS RESULTING FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garnier T., Saurin W., Cole S.T.)
"Molecular characterization of the resolvase gene, res, carried by a multicopy plasmid from Chastridium perfilingens. common evolutionary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMOLOGOUS PECOMPINATION
-!- SIMILARITY: BELONGS TO THE "RESOLVASE" FAMILY OF SITE-SPECIFIC
                                                                                                                                                                                                                                                                                                  "Complete nuclectide sequence and genetic organization of the barreringingenic plasmid, pIP404, from Clostridium perfringens.";
Bacteria, Firmicutes; Bucilius/Clostridium group, Clostridiaceae;
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189 AA; 21427 MW; B1781±8A11450784 7PG64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human herpesvirus (type 6 / strain 229) (HHV6).
Viruses; dsDNA viruses, no kNA stage; Heipesvilidae,
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Mol. Microbiol. 1:371-376(1987).
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PROSITE; PS00397; RECOMBINASES_1; 1.
PROSITE; PS00398; RECOMBINASES_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 88201675; PubMcd-2896291;
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                                                                                                                                                                                                                               MEDLINE-88336297; PubMed-2901768;
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01-AUG-1988 (Rel. 08, Created) 01-AUG-1988 (Rel. 08, Last sequence update) 01-MAY-1992 (Wel. 22, East annotation update)

RESP CLOPE

clostridium perfriugens.

RESOLVASE (ORF8).

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SEQUENCE FROM N.A.
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FUNCTE NO READSCRIPTEN FACTOR THAI BINDS TO THE OCTAMER MOTIF
("ATTIGEATED"). PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL
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"Homen set Cores tability connasses, alternative splicing gene ordering a less changes what location, and expression at low levels in order tissues."
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FINALD ASS WIALED WILL GLAT OPPOTED H (6H) TO FORM A COMPLEX
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Enkaryota: Meticous Teordata: Tamintas Vertebratas Enteleostomi.
Aimmalia: Entheria: Primates: Satarrhini: Hominidae: Homo.
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N. HINKED (CAPANA). ...) (POTENTIAL).
N. HINETE (CT. MAY. ...) (POTENTIAL).
ODE/724P55194104 CRC54;
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P. SIMILARITY: TO OTHER HERPESVIRUSES CLYCOPROTEIN I...
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OF N.W. 1965 (Rel. 42, Last sequence apdate)
OF OCT-2006 (Pel. 40, Last annotation update)
OCTAMER HINDIN'S TRANSCRIPTION FACTOR 38 (OCT-38).
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                                      MINISTER SERVING N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAX SSEED CONTRACTOR AND ENDER
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between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Livrelli V., Peduzzi J., Joly B.;
"Sequence and molecular characterization of the ROR-1 beta-lactamase
gene from Pasteurella haemoly.ica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reslit, Psactas, Pad_z, 1.
PROSITE; PS50071; HOMBOBOX_2; 1.
Homeobox; DNA-binding; Transcription requlation; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Flasmid RKob, and Flasmid pAB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 0.5%; Score 58; DB 1; Length 265; Local Similarity 44.0%; Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41C21E136EFBCBB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae, Pasterrella haemolytica, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequence analysis and evolutionary perspectives of beta-lactamase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-P.haemolytica; STRAIN-INPR 51; PLASMID-FROD;
MEDLINE 91221591; PubMed-2024356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPECIES-H influenzae: STRAIN**940; PLASMID*RROb;
MEDLINE 90351123; FubMed-2201253;
Juteau J.-M., Levesque R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antimicrob. Agents Chemother. 34:1354-1359(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrob. Agents Chemother, 35:242-251(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTIG=VAR_003774.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FFB-1944 (Fel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1FF-LACTAMASE FOR-1 PRECUFSOR (FC 3.5.2.6).
ROBI OR BLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FT I d=VAR_003775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                           or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   622 AIYI,SKSGICSI,HPLI,RGWEEALEN 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 ALOLSFKNMCKLRPLLOKWVEEADN 118
                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0028; POUDOMAIN.
PROSITE; PS00027; HOMFOROX_1; 1.
PROSITE; PS00035; POU_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30084 MW:
                                                                                                                                                                                                     HMBL; 211899; CAA77952.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727, 75985, 715;
                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF00046, homeotox, 1.
Pfam; PF00157; pou; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                  InterPro; IPR000327; -. InterPro; IPR001356; -.
                                                                                                                                                                                                                                HSSP, P20263; 10CP.
TRANSFAC; T01872; ..
MIM; 164177; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [2]
Sequence from N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           асмарфая
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P33949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Pfsm, PP00191: annexin; 4.
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                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00196; ANNEXIN.
                                                                                                                                                                                                                                                                                             MCD; MG1:88030; Anxa4.
InterPro; 1PR001464; -
                                                                                                                                                                                                                                                                                                                               InterPro; IPR002391;
                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                           1ANN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCB1_Tax ID=28985;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADH2_KLULA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P49383:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Rioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no way modified and this statement is not removed. Base by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to licensewisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                  -+- CATALYTIC ACTIVITY: A HETA-LACTAM + H(2)0 - A SUBSTITUTED BETA-AMING ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniala, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciuroquathi, Maridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C3H/HEJ;
Sable C.L., Shannon J., Riches D.W.H.;
Submitted (JAN-1997) to the EMM, Journamy ZubbJ databases.
-!- FUNCTION: CALCIOW/PHOSPHOLIPID-BLWING PROFEN WHICH PROMOTES
MEMBRANE FUSION AND IS INVOLVED IN EXOCYTOSIS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE CLASS-A BETA-LACTAMASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.5%; Score 58; DB 1; Length 305; 28.8%; Pred. No. 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches 27; Indels
                                                                                                                       Chang Y.F., Shi J., Shin S.J., Loin D.H.; "Sequence analysis of the RGB-1 beta lactamase gene from Actinobacillus pleuropneumoniae."; Vet. Migrobiol. 32:879-325(1992).
                     Wood A.R., Lainson A.F., Baird D.G.;
Submitted (FER-1993) to the EMBLysienHenkin/Autholdslabases.
   SPECIES P.harmolytica, STRAIN SERCIYEE A1, FLASMID PAB2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBSTRATE (BY SIMILARITY). 6145E12B76507422 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BETA-LACTAMASE ROB-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1957 (Rel. 35, Greated)
01-NOV-1957 (Rel. 35, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKT; 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0118; BLACTAMASEA.
PROSITE; PS00146; BETA_LACTAMASE_A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase: Antibiotic resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ptam; PF00144; beta-lactamase; 1.
                                                                                                          MEDLINE-93088532; PubMed-1455627;
                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: X52872; CAA37652.1; -.
EMBL: AF02211; AA87205.1; -.
EMBL: 22124; CAA79823.1; -.
EMBL: S51028; AA824384.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33869 HW,
                                                                                            SPECIES A.pleuropneumoniae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5% Guery Match 6.5% Best Local Similarity 28.8% Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANNEXIN A4 (ABMEXIM IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000871;
InterPro; IPR001466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A60680; A60680.
PIR; A61156; A61156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; $31923; $31923.
HSSP; P00810; lTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 2
305 AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCB1_Tax10-10090;
                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANXA4 OR ANX4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANX4_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACT_SITE
BINDING
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                       SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS MAY FORM ONE RINDING SITE FOR CALCIUM AND PROSPHOLIPID.
                                                                                     -!- MISCELLANEOUS: SEEMS TO BIND ONE CALCIUM ION WITH HIGH AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eluyveremyees lactis (Yeast).
Eukatyota: Fangi; Ascongrecta, Saccharomyeetis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITURE-SCROOMS TO Denis C.L.;
Shain D.H., Salvadore C., Denis C.L.;
"Fouristion of The alcohol delydrogenase (ADH) genes in yeast:
characterization of a fourth ADH in Kluyveromyces lactis.";
MACL Gen Genet 272.479 488(1992).
-1- DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 58; DB 1; Length 318; 25.0%; Pred. No. 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    982 LEF GPEPELE SHQELSE DJENEL SIVVSI PSVI APDIMEVLOGV. 1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53FAC7AD8006BC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 KDIEQSIKSETSGSFEDALLAIVKOMPSKPSYFAEPLYKSMKGL 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PROGOO; ANNEXINIV.
PROSITE; PSOG23; ANNEXIN; 4.
Annewin- Calcium/phospholipid-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61-FEB-1996 (Rel. 33, Cleated)
01-FEB-1996 (Rel. 37, Lest sequence update)
145-DEC-1998 (Rel. 37, Last annotation update)
ALCOHOL DEHYDPGFENASE II (EC 1 1 1)
                                                                                                                                                            -i- SIMILARITY: BELONGS TO THE ANNEXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CBS 2359 / IFO 1267 / NPRL Y-1140;
MEDLINE=92269769; PubMed=1588917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANNEXIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANNEXIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANNEXIN 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 82 ANN
94 154 ANN
178 238 ANN
253 313 ANN
318 AA; 35858 MW; <sup>1</sup>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U72941, AAB40697.1; -.
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use by ten profit institutions as busy as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a from the analysis of the interference of send as email to increase as both.
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-kind over of thirding trins siphier factor is differentially expressed in mass embryonic certs."
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Etaurpota: Metas at Postata: Praniatus Vertebrata: Enteleostomi:
Mammalia: Eutberia: Rodentia: Seinrequath: Moridae; Murinae; Mus.
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- I. FIRE: Of (Ref. 17. Tolated)
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- OffIAMER BINDING FRANSCHIFFOR FACTOR (COTT) (COTT) (RF A1).
- P.0DSFI OF OFFICE OF TEXTS FOR OUT 4.
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helween the swiss Institute of Bioinformatics and the BMBL outstation. The European Bioinformatics Latitute. There are no restrictions on its ase by real profit institutions as iong as its content is in no way modified and this statement is not randoved. Usage by and for commercial entities repaires a license attenuent. (See http://www.ish.sib.ch/announce/or send an email to license/lish-sib.ch).
                                                                                                                                                                                                                                 this SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                          +! SIMILARITY: STRONG TO OTHER "POU" TRANSCRIPTION FACTORS. BELONGS
                                                                                                                        ('ATTTGCAT'), PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL
           MEDLINE 93238934; Pubmed-8097478;
Morita E.H., Shirakawa M. Hayashi F., Kmadawa M., Kyoqoku Y.;
"Secondary structure of the oct-3 POU homeodomain as determined by
                                                                                                     1. FUNCTION: TRANSCRIPTION FACTOR THAT BINDS TO THE OCTAMER MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homeobox; DNA-binding; Transcription regulation; Nuclear protein;
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O03860, 905167, Q35168, U16422;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 40, Last annotation update)
07-OCT-2000 (Rel. 40, Last annotation update)
07-MARKER HIMDIAG TRANSCRIFTION FACTOR 3A (OCT-4).
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Y -> M (IN REF. 2).

P -> S (IN REF. 4).

757E41DF52286714 CRC64;
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EMBL; X52447; CAA36682.1; -.
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EMBL; S58423; AAB19896.1; JOLNED.
EMBL; S58424; AAB19896.1; JOLNED.
S58424; AAB19896.1; JOLNED.
EMBL; S58424; AAB19896.1; JOLNED.
                                                                                                                                                       -!- SUBCELLULAR LOCATION: NUCLEAR
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PROSITE; PSO0027; HOMEOHOX_1; 1.
PROSITE; PS50071; HOMEOHOX_2; 1.
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1 28 M1
29 29 7
31 31 P
352 AA; 38216 MW;
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STRUCTURE BY NMR OF POU DOMAIN
                                                                 1H-15N NMK spectroscopy.";
FEBS Lett. 321:107-110(1993).
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Best Local Similarity 44.0%,
Morobes 11; Conservative
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PDB; loCP; 15-SEP-95.
TRANSFAC: T00651; -.
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PIR; A34672; A34672.
                                                                                                                                                                                             FO CLASS-5 POU.
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CONFLICT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: 2 1SOFORMS; OCT-3A (SHOWN HERE) AND OCT-3B (AC P31359); ARE PRODUCED BY ALTERNATIVE SPLICING. SIMILARITY: STRONG TO OTHER "FOU" TPANSCRIPTION FACTORS. HELONGS
                                                                                                                                                                                                                                                                                                                                                                              Wey F., Lyons G.E., Schaefer B.W.;
"A buman PGV domain gene, mPOU, is expressed in developing brain and
enablific adult tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ('ATTTGCAT'), PRIME CANDIDATE FOR AN EARLY DEVELOPMENTAL CONTROL
                                                                                                                                                  Takeda J., Seino S., Bell G.I.;
"Human oct? gene family. cOMA sequences, alternative splicing, gene
organization, chromosomal location, and expression at low levels in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION. TRANSCRIPTION PACTOR THAT BINES TO THE OCTAMBE MOTTE
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Homeobox; DNA-binding: Transcription regulation; Nuclear protein;
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V = 1 (IR REF. 2; #21963).
V = 5 G (IR REF. 2; #21964).
R => 0 (IR REF. 2; #21964).
O = 1 R (IR REF. 2; #21964).
O = 2 R (IR REF. 2; #21964).
934C58DABAOCS358 CRC64;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE 56160538, EuDMed 8567814,
Abdel-Rahman B., Piddler M., Rappolee D., Pergament B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of transcription regulating genes in human
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                                                                                                                                                                                                                                                   Nucleic Acids Res. 20:4613-4620(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eur. J. Biochem. 220:753 762(1994).
                                                                                                                                                                                                                                                                                                                             TISSUE-Heart, and Skeletal muscle;
MEDLINE 94192665; PubMcd-7908264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBJETTUTAR LOCALION: NUCLEAR
                                                                                                                          MEDLINE 93027160; Pubhed 1408763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSTIE; PS00027; HOMEOBOX_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10:2787-2792(1995).
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                                                                                                                                                                                                                                                                                                        SEQUENCE OF 188-274 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 212-283 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL: Z11898: CAA77951.1;
EMBL: Z21964: CAA7974.1;
EMBL: Z21964: CAA79975.1;
EMBL: S81255; AA835990.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam; PF00157; pou; 1.
PRINTS; PR00028; POUDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS00035; POU_1; 1. PS00465; POU_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preimplantation embryos.
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220
                                                                                                                                                                                                                                                                                                                                                                                                                                   specific adult tissues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 825561; 825561.
; P20263; 100P.
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251
276
360 AA;
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                                                                          SECUENCE FROM N.A.
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                             NCB1_TaxID=9606;
                                                                                                  TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00157;
                                                                                                                                                                                                                                   adult tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM: 164177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
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This SWISS-PPOT entry is depyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities regains a lieural outsewed. See the profit of commercial or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hu R.-J., Lee M.P., Johnson L.A., Feinberg A.P.;
"A novel hyman hymalogue of yeast nucleosome assembly protein, 65 kb
                                                                                                                                                                                                                           01-NeV-1997 (Rel. 35, Created)
01-NeV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
NUCLEGSOME ASSEMBLY PROTEIN 1-LIKE 4 (NUCLEGSOME ASSEMBLY PROTEIN 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             centromeric to the p57KIP2 gene, is biallelically expressed in fetal and adult tissues ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- TISSUE SPECIFICITY: URIQUITOUS, BIALLELICALLY EXPRESSED IN FETAL AND ADULT TISSUES, HIGHEST LEVELS IN TESTIS.
-i- SIMILAPITY: BELONGS TO THE NUCLEOSOME ASSEMBLY PROTEIN (NAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEAR LOCALIZATION SIGNAL (POTFNTIAL)
                                    Gaps
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukarysta, Metassa, Cherdata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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O
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0.5%; Score 58; DB 1; Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 VPSPSVFAAKNASNTEKLIDOVMONPPVLAALQERLDNVPHTPSSYIE 57
                                    10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.5%; Score 58; DB 1;
31.2%; Pred. No. 1.1e+02;
                    le+02;
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                                    4; Mismatches
                     Pred. No.
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                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-1743-1748(1996).
                                                                       622 AIYISKSGICSLHPLIPGWEEALEN 646
                                                                                                        189 ALOISEKNMOKLEPILOKWVEKAPN 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHRCELLHLAR LOCATION - NICLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDITINE 97081759; PubMed-R923002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
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Pfam; PP00956; NAP_family; 1.
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                    44.08;
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 Query Match 0.5%
Best Local Similarity 44.0%
Matches 11; Conservative
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                                                                                                                                                                                              STANDARD:
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310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genet
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                                                                                                                                                                                                                                                                                                                 NAPIL4 OR NAP2.
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                                                                                                                                                                                              NPL4_HUMAN
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055145;
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                                                                                                                                                             RESULT 144
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This PWISS-Peol entry is capyrill. It is produced through a collaboration between the Swiss Institute of Rechnormalies and the EMML outstailon. The European Rechnormatics institute, There are no restrictions on its same use to account to the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the cont
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                                                                                                                                                 Entrop a growling (Ent).
Enking for Metazon: Todania: Tributal Vertebrata: Enterestemi)
Mammalon: Entheria: Redertia: Scrutognathi: Muridae: Muridae: Rattus.
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SCHWARDINE POSSESS FORCE SCHALL SCHALL TOUR PARTEMENT FOR PARTEMENT AND PARTEMENT.
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Pres. Nati. Acad. Sci. U.S.A. 95:10896-10901(1998).
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Newtonal expression of tractalkine in the presence and absence of
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PS JUL. LOGO (Foll. 99, Last September spate).
PS JUL. LOGO (Foll. 38, Last annotation update).
FRACTAININE PREPUBSIDE (NUDECIALINE) (SXS) MEMBRANE-ANCHORED SPRING (SMALL BIOCHDIE, YEARINE DI).
SCYLL P. PRINGE ANCHOLE.
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27346; Pred, No. Liberozi
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EXTRACELULAR (POTENITAL).
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7E403828688E4BBA CRC64;
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FUNCTEONS THEM LATER FASTER BINGS TO CXACKEL
STRUMBER MONOMER (BY SEMILARITY).
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BY STMILARITY.
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Plant Procedas (Ext. 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORM THE FUNCTIONAL COR. OF THE ENZYME COMPLEX. SUBJUIT 2 IRANSFRS IN B. ELECTH WINS FORM OTTCOMPENDED TO 18 FUNDLEAR CHPER CALIFOR TO THE HIMBERLIP CHNIER OF THE CATALYTIC SUBJUIL 1. CATALYTIC SUBJUIL 1.
                                                      01-0C1-1993 (Rc1, 27, Creates)
01-0C1-1993 (Rc1, 27, Last Sequence update)
30-MAY-2000 (Rc1, 39, Last annotation update)
CYPOCHROME COXIDASE POLYPEPTIDE II PRECURSOR (EC 1.9, C.1) (FRACHENT).
                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER, SUBGNITS 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1 SIMILARITY: BELONGS TO THE CYTOCHROME COXIDASE SUBURIT 2 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOTENTIAL.
HITOSHORBATAL INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHORDLAL INTERREMERANE (POTENTIAL)
                                                                                                                                                                    Enkaryota, Viridiplantae, Embryophyta, Trackeophyta: Spermatophyta;
Magnoliophyta; endicotyledons: core endicots; Kosidae; enrosids I;
Enhales; Fabaceae; Papilionoideae; Glycine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION, INTIGRAL MEMBRANE PROTEIN, MITORIONDRIAL
                                                                                                                                                                                                                                                                                                                                              "Silent mitochondrial and active nuclear genes tor subunit 2 of eytochrome \sigma exiduse (evx2) in soybean; evidence for RNA-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIPSTRONDERES (FESTRATIAL).
CYLCHROME C EXIDASE ESTYPETHUE II.
MITSTRONDERAL INTERNEMBRANE (FOTENIA
POTENITAL
HITSCHONDERE MATRIX (FOTENIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCHONDRIAL MAINIX (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Obery Match 0.5%; Score 58; Dit 1; Length 494;
Hest Local Similarity 40.5%; Pred. No. 1.1e+02;
Matches 15; Conservative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Prom. PE00116, CoX2; 1.
PROSITE, ESOGOR: CoX2; 1.
Oxidoreductase: Copper; Mitochondrios: Indusmembranc: H
Electron transport; Respiratory chain: Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDEZAEGODABENDOB ORC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CATALYTIC ACTIVITY, 4 FERNATTOCHRAMENT (2)
4 FERRICYFOCHROME C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COPPER A (PROBABLE).
COPPER A (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COPPER A (PROBABLE).
COPPER A (PROBABLE).
                                                                                                                                                                                                                                                                                 SIRAIN-CV. WILLIAMS; TISSUE S 1001, and Leat;
MEDIANE-93010975; PubMed-1342,779;
                      - KI
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InterPro; IPR001505; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: 211980; CAA78032.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       11:3815-3820(1992).
                      STANDARD,
                                                                                                                                                                                                                                                                                                                              Covello P.S., Gray M.W.;
                                                                                                                                                     Glycine max (Soybean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1PR002429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S28027; S28027.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INNER MUMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00404; locc
                                                                                                                                                                                                                                                                       SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      qene transfer.";
                                                                                                                                                                                                                                NCBL_TaxID 3847;
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ANAMOREA
DOMAIN
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METAL
SCXT_SOYEN
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457 CELETIOPVSLSTSOGKYOFLADSDISLMLSLNGPLAPVRILAMN 500 #7 KHIJH, FAAT IPN TIKFEKRVINVITERI ISAIRGI SPITALOSI,S 13-03

1519 SPMSQLLSSNNFLKKVVESGGPETLKGLEERLLETVL 1555

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01-NoV-1997 (Rel. 35, Created)
30-MRY-2000 (Rel. 39, Last sequence update)
30-MRY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL 45.9 KDA PROTEIN C47E12.7 IN CHROMOSOME IV.

Caenorhabditis elegans.

C47E12

SEQUENCE FROM N.A. STRAIN BRISTOL NZ

NCBI\_TaxID-6239;

397 AA.

PRT;

STANDARD;

YXX7\_CAEEL 018674;

Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.

Submitted (NOV-1998) to the FMRL/AbenkyTeak (Balabases -!- SUBCELLOLAR LOCATION: NUCLEAR (POTENTIAL). -!- SIMILARITY: BELONGS TO THE NNP-1 FAMILY.

STRAIN-BRISTOL N2;

Durbin R.; REVISIONS

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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-L., Town C.D.,
Fujii C.Y., Mason T.M., Howman C.L., Rarnstead M.E., Peldblyum T.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Magnoliophyta, eudicotyledous, core codients, Residac: eurosids II;
Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The aspartate aminotransferase gene family of Arabidopsis encodes is nonlymens localized to three distinct subsellular compartments.";
      Kornstein L.B., Gaiso M.L., Hammell R.L., Bartelt D.C.; "Cloning and sequence determination of a cDNA encoding Asperqillus nidulans calmodulin-dependent multifunctional protein kinase."; Gene 114-75-82(1942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam: PF00069; pkinase; 1.
PPOSITE, PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108 : FROTEIN_KINASE_ST; 1.
PPOSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
                                                                                                                                             -i - CATALYTIC ACTIVITY: ATP + A PROTEIN - ADP + A PHOSPHOPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASPAPITATE AMINOTPANSFERASE, MITOCHONDPIAL PPECTIFSOR (EC 2.6.1.1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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ງວາດງ;
9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1E8D58A1C0R2F18C CPC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.5%; Score 58; DB 1; 48.0%; Prod No 1 20402
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40, Tast annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 LKMQEEDEEDIPSAVDVQASFASDK 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE 95201829; Pubmed 7894512;
Schultz C.J., Coruzzi G.M.;
MRDLINE-92225350; PubMed-1563634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M74120; AAB97502.1; -.
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Plant J. 7:61-75(1995).
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nes 12; Conserv
                                                                                                                                                                                                                             CAMK SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Nematoda, Chromodoroa, Phabditida, Phabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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0.5%; Score 58; DB 1; Length 397; 21.5%; Pred. No. 1.1e:02; Live 16; Mismatches 35; Indels

Rest Local Similarit $_T$  21.5% Matches 14, Conservative

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Query Match

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EMBL; Z68882; CAA93111.1; -.
Wornhep; C47E12.7; CE20571.
Hypothetical protein; Nuclear protein:
Expothetical protein; Nuclear protein:
SEQUENCE 397 AA; 45870 MW; 03E91E2D26D7D6BC CRC64;

Emericella nidulans (Aspergillus nidulans). Enkaryota; Pungi; Ascomyecta; Perizomyecties; Eurotiales; Trichocomaceae; Emericella.

SECTENCE FROM N.A.

NCBI\_TaxID:5072;

Eurotiales;

JOSEPH (1998 (Rel. 3b, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update)

414 AA.

PRT,

STANLARD,

KCC1\_EMEN: 000771;

KCC1\_EMEN1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..
Audin C.E., Ketchem K.A., Love J.E., Fernand C.M., Koo H., Mattat K.S., Yendin L.A., Stein M., VanAken S.E., Bmayam L., Dallo, L.J., Sill J.B., Adams M.C., Saltera A.J., Sreavy J.H., Goodman H.M., Soleryille C.K., Sperbarder L.E., Prosss J., Nietman W.C., White C., Elsen J.A., Salzbert S.E., Fraser C.M., Venter L.C.,
                                                                                                                       NATURE 40-2 PER (1999).
U. PHANTENE IMPORTANT ACIDS, IN PLANTS, IT IS INVALVED IN NITROGEN METARS LICE ARE IN ASTRONOMY ACIDS. IN PLANTS, IT IS INVALVED IN NITROGEN METARS LICE ARE IN ASTRONOMY ACIDS. IN ARE ENRICH METARS LICE ARE IN ASTRONOMY.
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                                                                                                                                                                                                                                                                                          SIMILAKITY: RELEGINGS TO CLASS-I OF PYPITESXAL PHOSPHATE-DEPENDENT
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PROSITE: PSOOLOS: AA_HEANSFEE_VIASS_): 1.
HIRSTOLIS: ASHL Fansferase: Pyridoxai Plosphate: Mitochandiion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yuassius aurris (Boldfush).
Eukaryota: Motazoa: "Fordata: "Tinnata: Vertobrata: Eutoiewstomi:
Actinopheryon: Respecty II, Felcostei, Eateleostei, Ostariophysi,
"Yprinitormes: "Yprinidae: Cypritinac; Carassius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYKLESZAL PHOSPHATE (BY SIMILAKITY).
A6525B958F0249EF CRO64:
                                                                                          "Sequence and analysis of chromonome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schockter N., "Thompson coldrish vimentia: differential expression in PMS.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Massow E., bruger R.K., Fuchs J., Levine E.M., Mordano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 58; LB 1; Longth 430; 41.3%; Pred. No. 1.30+02;
                                                                                                                                                                                                                                                        SUBUNTE: HOMODIMER (OF SCHILDRETTY).
SUBCRILLOLAR LOCATION: MIDOTHONORIAL MATRIX (POTSNEIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8: Mismatches 20; Indels
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LMANSIE 1 28 MITSCHENDERM (POTINITAL).
                                                                                                                                                                                                   -- ASPARTATE + 2-0X00L0TARATE
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44 Last annotation update)
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                                                                                                                                                                                                                                       OR: PYRIDOXAL PRISPHALE.
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23 440 AS
277 277 PY
440 AA; 47757 MN; 2
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ol FEB-1996 (Rel. 35 Last Segue
ol FEB-1996 (Rel. 34 Last anno
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Best Local Similarity
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                                                                           Suitherd S.E.
                                   Adams M.C.,
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SELUEN'E
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PUNCTION: VIMINITA AND CLASS THE INTERMEDIATE CHIAMBREE CORD IN VARIOUS NOMBERTHELIAL CELLS.
PARTOUS NOMBERTHELIAL CELLS.
PERFORMENT: HOMOPOLYMER (FY SIMILARITY).
PERSON TISSUE SPECIFICITY: EXPRESSED IN LOW AMOUNTS IN RETURNA, 1910'S HINCE SPECIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S 1 5
                                                                                              -i- PTM: ONE OF THE MOST PROFINENT PHOSEBEPR LEINS IN VAREOUS CHILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE optic nerve; MEDLINE-920985; PubMed-1661917; Cohen I., Shani Y., Blaugrund E., Schwartz M.; Shani Y., Blaugrund E., Schwartz M.; Sequence and sequence to sequence of sequence of two intermediate filament cDNA clones from tish optic nerve.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eŭkaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Actinopterygii, Neopterygii, Teleostei, Enteleostei, Ostariophysi;
Cypriniformes: Cyprinidae: Cypriniaec, Cyprinus.
                                                                                                           MESCACHYMAL JEGGIN, PROSTIGATION IN CARRAMMED DUKING CELL
DIVISION, AT WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
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                                                                                                                                     REGARDIED (BY SIMILARITY).
F. SIMILARITY: BELONGS TO TEE INTERMEDIATE FILAMINI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.5%; Score 58; DB 1; Lenath 450; 50.0%; Pred. No. 1.30:02;
                                                                                                                                                                                                                                                                                                                                                        Intermediate filament; Coiled will Heptad report pattern.
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. DESCHEZBACGOILEE CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Greated)
40-MAY-2000 (Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LINKER 12.
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                                                                                                                                                                                                                                                                                                                            Přamy Průčovsky filament; l.
PROSITE: PSO0226; IF; l.
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232
255
450 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                          82
118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIME_CYPCA
Q92155;
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EMBL, p14694; BAA03520.1; -.
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181
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                                                                                                         PIR; A41680; A41680.
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P48651;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ol-JUL-1993 (Rel. 26, Created)
Ol-JUL-1993 (Rel. 26, Last sequence update)
Ol-GUL-1993 (Rel. 40, Last sequence update)
PHOSPHATIDYLEBRIHE SYMTHASE I (SHRINE-EXCHANCE ENZYME I) (PC 2 7 R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: COMMITTED STEP IN THE SYNTHESIS OF PHOSPHATIDYLSERINE. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -t- FUNCTION: BASE-EXCHANGE REACTION BETWEEN FREE L-SERINE AND THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus longicandatus (Long-tailed hamster) (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enkaryota; Metázoa; Chordata; Craniata, Vertebrata, Enteleostemii,
Mammalla; Entheria; Bodentia; Scintognathi; Muridae, Clicetinae;
  DIVISION, AI WHICH TIME VIMENTIN FILAMENTS ARE SIGNIFICANTLY
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C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2090 ALAEKUKENYIVLIPESIPPIAEIMEPPPVFHQOQMFIQQIPTVIGEP 2139
                                                    SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 SLARLHILDTRVESLQEEIAFLYRIJHDRELAELQUQUQUPMBVARP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Intermediate filament; Colled coil; Heptad repeat pattern. \begin{array}{ccc} & & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ & & \\ & & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & \\ & & 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 58; DB 1; Length 455; 30.0%; Pred. No. 1.4c+02;
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                                   REORGANIZED (BY SIMILARITY).
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PRINTS; PR01248; TYPELKERATIN.
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                                                                                                                                                                                                                                                                                                                                            EMBL; S76850; AAB20706.2; -.
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Matches 15; Conservative
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entities requires a library appropriate [Sochet] (fow the sib chimmenous send an email to license@lsb sib.ch).
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IT CAN ALSO CATALYZES
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01-org-2000 (Rel. 40, Last annotation update)
PHOSPHATIDYLSERINE SYNTHASE I (SERINE-EXCHANCE ENZYME I) (EC 2.7.8.-).
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-i- FUNCTION BASE-EXCHANGE REACTION BETWEEN FREE L SERINE AND THE POLAH HEAD GROUPS OF PRE-EXISTING PHOSPHOLIPIDS. IT CAN UTILIZE PHOSPHATIDYLCHOLINE AS A PHOSPHATIDYL DONGR. IT CAN ALSO CATALYZ THE CHOLINE AND PHANDLAMINE BASE-EXCHANGE REACTIONS.

-i- PATHWAY: COMMITTED STEP IN THE SYNTHESIS OF PHOSPHATIDYLSERINE.
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L'Similarity 22.5%; Pred No 1 40+02;
18; Conservative 19; Mismatches 43; Indels
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                                                                                                                                                                                                   Transferase; Phospholipid biosynthesis; Transmembrane.
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                                                                                                                       EMBL; D10234; BAA01084.1; -.
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*** Mismatches 43; Indels
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Counsternse; Phosphelipid blosynthesis; Transmembrane.
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CHEGE-SAMI, ESCLIVITER ENTITALSE PROFEED DAYA.
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J. Barteriol, 176:401:408(1994).
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es (8) Conservative (
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TO SITE: PSULODE: DNAA: 1.
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-1- CATALYTIC ACTIVITY: TELRADEGANOVI.-COA + GLYCYL, PEPTIDE - COA + N
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J. Biol. Chem. 273:6595-6598(1998).
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35.7%; Pred. No. 1.58(02)
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                                                Salmonella typhimurium.
Bacteria: Protrobacteria: qamma subdivision: Enterobacteriaceae;
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                                                                                                                                                                                                        Jones C.J., Homma M., Marciab R.M.;
"I., P-, and M-ring proteins of the flagellar basal body of Salavarella t.phimurium. gene sequences and deduced protein somerons "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol, 174:2298-2304(1992).
-i- FUNCTION, THE M RING MAY BE ACTIVEDY INVOLVED IN CHERCY
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36.0%; Pred. No. 1.70402;
Uye 9; Mismatches 19; Tadhis
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                                                                                                                                                                                                                                                                                                                    Bacteriol, 171:3890-3900(1989).
                                                                                                                                                                                                MEDITAE 89291739, PubMed 2511561,
                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE 92202159; PubMed-1551848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1009; FLGMRINGFLIF.
                            FLIF OR FLA BI OR FLA AII.1.
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                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1 26 FROM N.A.
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Matches 12; Conservative
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  FLAGELLAR M-RING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; C42376, C42376.
StyGene; SG10118; flik.
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                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                           NCB1_Tax1D=602;
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                                                                                                    salmonella.
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P00893: P78045; 21-JUL-1986 (Rel. 0], Created) 01-NOV-1997 (Rel. 35, Last sequence update)

PRT;

STANDARD;

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the European Richnformatics Institute. There are no restrictions on its use by non-profit institutions as long as its scontent is in no way multiply and the statement is not removed "mand by and for commercial entities requires a license autrement (See http://www.isb.aib.cb/aim.out.cc/
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I CATALYTE ACTIVITY: 2-ACEPCLACTATE + CO(2) - 2-PYRUVATE (THIS ENCYME ALSO CATALYZES FORMATION OF 2 ACEPO-2-HYPPSYKUTANOATE).
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1. PATHWAY: FIRST STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.

1. SHHUNIT: DIMER OF LARGE AND SMALL, CHAINS.

1. SHHUNIT: DIMER OF LARGE AND SMALL, CHAINS.

1. MISCELLANDOUS: E.COLI CONTAINS GENES FOR 3 AHAS ISOZYMES: ILVBN,
15-DEC-1998 (Rel. 37, Last annotation update)
ACETGLACTATE SYNTHASE ISOZYME III LARGE SUBUNIT (EC 4.1.3.18) (AHAS-
III) (ACETGHYDROXY-ACID SYNTHASE III LARGE SUBUNIT) (ALS-III).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STPATR-K12, / Morross, MEDITRE-97426617; PubMed-9278503; MEDITRE-97426617; PubMed-9278503; Blattner F R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Filey M., Collado-Vides J., Glasner I D., Rede C K., Mayhew G.F., Filey M., Collado-Vides J., Glasner I D., Rede M A . Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
Isono K., Misobuchi K., Nakata A.;
"Systematic sequescing of the Escherichia coll genomo: buslysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Squires of H., Defelies M., Demorsons J., Calvo J.M.; "Molecular structure of ilvIH and its evolutionary relationship to
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                                                                                                                                                                                             Bacteria: Proleobacteria; gamma subdivision, Enterobacteriaceae: Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome Sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- COPACTOR THIAMINE PYROPHOSPHATE, AND MAGNESIUM ION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 11:5299-5313(1983).
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EMBL; D10483; BAA01345.1; -.
PIR; A01113; YCEC31.
PIR; S14385; S14385.
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20.3305-3308(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilvG in Escherichia coli K12.";
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BEZDEPGARRYOFBO CROSA;
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ACL SIDE 51 51 7 A - + G CIN DUE 55
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Mycopiasmalaceae: Urcaplasma.
N'HI TaxID 2103:
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Pred. No. 1.8e+02;
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MEDLINE FOR 072; PURMED 19558-072;
MEDLINE FOR 072; PURMED 195404 S., Wang B., Gilbert 04.L.
Edgi enterin anniysis of Greaplasma neasyticum suppor establishment of a new species, Ureaplasma parvua.";
Ult. J. Syst. Bacteriol, 19:1879-1889(1999).
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01-ADG-1000 (Ref. 15, Created)
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01-AT_2000 (Ref. 4) Last sequence update)
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DPEASE ALERA SCROWLI (RC 0.5.1.5) (DREA AMIDOHYDROLASE).
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J. Harteriol. 178:647-655(1996).
-!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; A FRAMESHIFT WAS
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Barteria: Firmicutes: Barillus/Clostridium group: Mollicutes;
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7, Mismatches 9, indels
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Q60008: Q9PQ56; Q9R3U4:
01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last Sequence update)
01-0CT-2000 (Rel. 40, Last anneation update)
01-0CT-2000 (Rel. 40, Last anneation update)
UREASE ALPHA SUBUNIT (EC 4.5.).5) (UREA ANIPOHYDROLASE).
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MEDLINE-96146510; PubMed 8550495;
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EMBL, AP085725, AAND28121-11-
EMBL, AP085727, AND28124-11-
EMBL, AP085727, AAND28122-11-
EMBL, AP085727, AAND28127-11-
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РКОSTIE; PS00145; UREASE_2; 1.
PROSITE; PS01120; UREASE_1; 1.
                         CORRECTED IN POSITION 581.
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NCBI_TaxID:134821;
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Local Similarity 40.7%;
tes 11, Conservative
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EMBL; M36190; AA
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                                                                                                                                                                                                                     STRAIN VARIOUS SERVVARS,
MEDIATOR SERVARS,
MEDIATOR SERVING CONTROL TO SERVING B., CIIDERT C.L.;
MEDIATOR E., James G., Ma. E., Gorden S., Wang B., Cillbert C.L.;
"Phylogenetic analysis of Breaplasma urealyticum -- support for the establishment of a new species. Ureaplasma parvum.";
Int. J. Syst. Barteriol. 49:1879-1889(1999).
-- CATALITIC ACTIVITY. SKIA * H(2)9 (CC(2) * 2 HH(3).
--- CATALITIC ACTIVITY. SKIA * H(2)9 (CC(2) * 2 HH(3).
--- COPACTOR EACH BRIDS TWO HIGHEL TORS.
--- SUMMULT: BELOWS TO THE URBASE PAMILY.
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01-APE-1993 (Rel. 25, Last sequence update)
01-APE-1993 (Rel. 25, Last annotation update)
01-APE-1993 (Rel. 25, Last annotation update)
01TER CAPSID PROTEIN UP4 (HEMAGGIUTININ) (00TER LAYER PROTEIN VP4)
[CONTAINS: 00TER CAPSID PROTEINS VP5 AND VP9].
                                                                            Letkowits B.J., Glass J.S., Heiner C.P., Chen B.Y.,
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NICKEL 2 (BY SIMILARITY).
NICKEL 1 AND 2 (BY SIMILARITY).
NICKEL 1 (BY SIMILARITY).
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NICKEL 2 (BY SIMILARITY).
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                                                                                                                 "The complete sequence of the mucosal pathogen Greaplasma urealyticum.";
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H -> A (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF085731, AAD28139.1, -.
AF085732, AAD28142.1, -.
AF085733, AAD28145.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFam: PF00449; urease; 1.
PROSITE; PS01120; UREASE_1; 1.
PROSITE; PS00145; UREASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AE002140, AAF30844.1; . AF085730; AAD28136.1; -.
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                                                                                                                                                                                                    SECURINGE OF 1-135 PROM N.A.
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Matches II, Conservative
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                                                                                                                                                               Nature 407:757-752(2000).
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EMBL; AF085732; AAD2
EMBL; AF085733; AAD2
HSSP; P18314; 1FWE.
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[2]
SEÇJENTE FROM N.A.
                                       STRAIN SEROVAR 4;
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                                                                                                    Cassell G.H.;
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                                                                               MEDINE-87127560, PubMed-3028337;
Kantharidis P., Dyall-Smith M.L., Holmes L.H.;
"Marked sequence variation between segment 4 genes of human RV-5 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Taniquchi K., Urasawa T., Kobayashi N., Gorziglia M., Urasawa S.:
"Nucleotide sequence of VP4 and VP7 genes of human rotaviruses with
subgroup I specificity and long RNA pattern: implication for new G
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01-AR-1993 (Rel. 25, Last amoutation update)
00TER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
(CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8).
                                                                                                                                                                           -!- PTM; VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         OUTER CAPSID PROTEIN VP4.
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35 6%; Prod. No. 2.6e+02;
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Humman rotavirus (scrotype 2 / strain RV-5).
Virusca; dsEMA viruscs: Proviridac; Pertavirus.
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T Virol 64:5640-5644(1990).
-!- SUBCELLULAR LOCATION: OUTER CAPSID.
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MEDLINE-91012813; PUDMAd-2170690;
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                                                                                                                             simian SA 11 rotaviruses.";
Arch Virol 93-111-121(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000416; -. Pfam; PF10426; VP4; 1
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195
324
583
589
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es 16: Conserv
                                                                 SEQUENCE FROM N A.
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599
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Barditidier Pelakerinaes Trematkabditis,
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KITIKE H., SCRIPS K., MCLECHIR A.D., Premner S., Karn J.)
"Paramaposin open (encels) of Cambridahdiris elequas Molecular
cloning, nuclearide sequence and madels for thick illument
                                                         THEF PROJUCT IS VEC. SIMILARING RECEED FAMILY.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a factor attached. (See http://www.ish.sik.ch.one.coll.).
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                                                                  Schriefer L.A., Waterson K.H.; "Phosphorylation of Caenothabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil; Heplad repeat pattern; Muscle protein; Thick filament;
Myosin; Phosphorylation.
1 47 NONHELICAL REGION (POIENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM. FROSFBORYLATES ON SERVINE RESIDUES IN THE BON-ALPHA-HELICAL
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C1 APE 1993 (Rel. 25, Last sequence update)
C1 OCT 2000 (Rel. 40, Last annotation update)
TYEESENE-PROTEIN KINASE RECEPTOR UPD PRECURSOR (EC 2.7.1.112) (AXE, ONCYGENE).
                                                                                                                                                                                                                                                                                                                       -1- DOMAIN: FOR MOST OF ITS LENGTH, PARAMYOSIN APPEARS TO FORM AN ALPRILICAL COLLED COLL. AND SHOWS THE HEITOR REPEAT OF HYDROPHOBLE AMINO ACID RESIDUES AND THE 28-RESIDUE REPEAT OF CHARGED AMINO ACIDS CHARATTERISTIC OF MYOSIN HEAVY CHAINS. HOWEVER, PARAMYOSIN DIFFERS FROM MYOSIN IN HAVING NOW-HELLCAL EXTENSIONS AT BOTH FERMINI AND A MADDITIONAL "SKIP" KENDUE THE 28-RESIDUE REPEAT. THE DISTRIBUTION OF CHARGED RESIDUES IS ALSO DIFFERENT FROM MYOSIN HEAVY CHAINS.
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Enkaryota: Metazoa: Chordata: Craniara: Vertebrata: Enteleostomi:
Mammalia: Eutheria: Primates: Catarrhiai: Hominidae: Homo.
                                                                                                                                                          MOT. BIOL, 207:451-454(1989).
PURCTION: PARAMYOSIN IS A MAJOR STEUCTURAL PURPONENT OF MANY THICK FILAMENTS ISOLATED FROM INVEKTERRATE MUSCLES.
                                                                                                                                                                                                                                                            -i-SUBUNIT: HOMODIMER (BY SIMILARITY).
- i-sullar tolar between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between the between th
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ROBBLICAL REGION (POTENTIAL).
INTERCHAIN (POTENTIAL).
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33.0%; Pred. No. 3e+02;
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89404BFF4A67005F OR064:
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                                   MEDIINE=89329036; PubMed:2754743;
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882 AA; 101949 MW;
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Pfam; PF01576; Myosin_tail; 1.
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143
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PHOSPHORYLATION.
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                                                                                                                                     paramyosin.";
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P 405 40;
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DOMAIN
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                                                                                                                                                           putative tyrosine kinase receptor with oncogenic potential.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- ALTERNATIVE PROJUCTS: 2 ISOPORMS: A LONG FORM (SHOWN HEPB) AND A SHORT FORM, AME PRODUCED BY ALTERNATIVE SHLICING.
-1- DISEASE, HAS LAMASOMHINS POTENTIAL IN PATIENTS WITH CHECKET MYBLOCHALLERATIVE DISNABLE OR CHRONIC MYBLOCYTIC LEUKEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94067751; PubMed 8247543;
Lee S.-T., Strunk K.M., Spritz R.A.;
"A survey of protein tyrosine kinase mRNAs expressed in normal human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OBCOGORGE 8:3403-3410(1993).
-!- FUNCTION, MAY PURCTION AS A SIGUAL TRANSBUCER BETWEEN SPECIFIC CELL TYPES OF MESODERMAL ORIGIN.
-!- CALL TYPES ACTIVITY: ATP - A FROTEIN TYROSINE - ADP - PROTEIN
                                                                    Janssen J.W.G., Schulz A.S., Steenvoorden A.C.M., Schmidberger M., strehl S., Ambros P., Bartram C.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINE-PROTEIN KINASE RECEPTOR UFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMITABILY, CONTAINS 2 IMMORGGOODLIM CIRC C2 TYPE DOMAINS. SIMILARITY; CONTAINS 2 FIBRONECTIN TYPE III LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MPDI INF-201777; Pubmod 1654220;
MPDI INF-201777; Pubmod 1654220;
MPDI INF-201777; Pubmod 165420;
MPDI INF-201777; Pubmod INF-2017 B., Prokop C., Espinosa R., Le Beau M.M., Earp H., Liu E.T.,
"AXL, a fransforming gene isolated from primary human myeloid
"AXL, a fransforming gene isolated from primary human myeloid
"AXL, a fransforming sene isolated from primary human myeloid
"AXL, a fransforming senesion in the second second in the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second se
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Transferase, Phosphorylation, Transmembrane, Signal, Repeat,
Immunoglobulin domain, Proto-oneogene, Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE TYR FAMILY OF FROTEIN KINACES.
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1G-LIKE C2 TYPE DOMAIN.
1G-LIKE C2 TYPE POMAIN
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PROSITE; PS00109; PROTEIN_KINASE_LIFF; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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EMBL, M76125, AAA61243.1, ALT_INIT.
EMBL, S65125, AAAE0305.1, ALT_INIT.
HSSP, P11362: IFGI.
                                         MEDLINE:92050809; PubMed-1834974;
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                                                                                                                                                                                                         meogene 6:2113 2120(1991).
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Interpro; IPR001245; -.
Interpro; IPR001777; -.
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SECUENCE FROM N.A.
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This SWISS-PROT catry is everyight it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics That in There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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-i - FUNCTION: IF-2, ONE OF THE ESSENTIAL COMPONENTS FOR THE INITIATION OF PROTEIN SYNTHESIS IN VITRO, PROTECTS FORMYLMETHIONYL.-TRNA FROM SPORTANEOUS HYDROLYSIS AND PROMOFES ITS BINDING TO THE 30S RIBGSOWAL SUBUNITS, IT IS ALSO INVOLVED IN THE HYDROLYSIS OF GIP DURING THE PORMATION OF THE 70S RIBGSOMAL COMPLEX (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stablens R.S., Kalman S., Lammel C.J., Fan J., Marathe E., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                     751 IYDYLPQCNPLKQPADCLOGLYALMSRCWELNPQDRPSFTELREDLENTLKALPPAQEPD 810
                                                                                                                                                                                                                                                                                                                        0; Caps
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Are 30; Indels
                                                                                                                                                                                                                                                                   inilarity 25 00; Prod No Asimi
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DOMAIN 400 548 G-DOMAIN.
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Bocteria: Chlamydiales: Chlamydiaceae: Chlamydia.
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E > K (IN REF. 2).

G \rightarrow D (IN PEP. 2).
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(Rel. 39, Last annotation update)
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-!- SIMILARITY: BELONGS TO THE IF-2 FAMILY.
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This PWESTER; entry is equipment in the project through a collaboration between the SWESTER Institute of Michiformatics and the FMEL outstain and the Encyclab Richinformatics Institute. There are no restrictions on its use by non-profit institut ons as long as its content is in no way
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MEDIINE-9500489; PubMed-7548215;
Sage J., Martin L., Cuzin F., Rassoulzadegan M.;
"GDMs sequence of the murine synaptenemal complex protein 1 (SCP1).";
Biochim. Biophys. Acta 1263:258-250(1995).
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Mammalia, Eutheria, Bodentia, Sciurognathi, Muridae, Murinae, Mus.
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Saqe J., Li Y., Martin L., Martei M. G., Susnet J. L., Lia J.G.,
Hooq C., Cusin F., Rassoulpadeqas M.;
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-!- FUNCTON, RAJOR COMPCHURT OF THE TRANSVERSE FILAMBERS OF STARPFORMEAL COMPLEXES (SSS), FORMED RETWEEN HOMOLOGOUS CHROMSCARED LOURING MELOTIC PROPHASE.
-!- SUBCELLULAR LOCATION: NUCLEAR, IN TRIPARTITE SEGMENTS OF
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Transferance, SerineyThrowine protech Kinase, ATF Linding,
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Best Local Similarity 23.7%; Pred, No. 3.46.02;
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Kerr S.M., Taggart M.H., Lee M., Cocke H.J.,
Submitted (APR-1995) to the EMBL/Genbank/UbbJ databases.
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This SWIGS PROT entry is copyright. It is produced through a collaboration
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-!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
- SIMILARITY RELAKES TO CLASS-I AMINCACYL TRNA SYNTHETASE FAMILY.
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Dietrich F.S., Allen E., Araujo E., Aparicio A., Carpenter J.,
Cherry J.M., Chang E., Davis E., Dancan M., Honlybe-Smith S.,
Hyan F., Kalmus E., Kong C., Kurdi A., Caskari D., Fow H.,
Lin A., Lin D., Marathe R., Mirtipati S., Namath A., Oefner P.,
Petel F.X., Roberts D., Schramm S., Schroeder M., Botstein D.,
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Matches 17, Conservative 19: Mismatches
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FMBL: FG2864; AAC53335 1; -.
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U62861; AAC53335.1; JOINED.
U62862; AAC5335.1; JOINED.
U62863; AAC5335.1; JOINED.
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                AN IMPORTANT STRUALING TRIDEMEDIALD MEDIMERA HUDROFFICIDE AND THE BECEPPORS OF NEUROTRANSMITTERS THAT INCREASE CALCIUM FILK AND THE DOWNSTRIAM SIGNALS THAT FEDULATE NEURONAL ACTIVITY.

CATALITY SATIVITY AT 1 A THE TERM TYPE-SINE. AD4 .

PROTEIN TREASINE PROSPHERE.

-1. SUBCELLULAR LOCATION. CYTOPLASMIC (POTENTIAL).
AME AND VALUE OF THE MAY REMAKE OF CHARLEM PATHWAY, MAY PERPERSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHARILATION (ATTO-) (BY SIMITARITY).
A -- G (IN MEF. 3).
G --> P (IN MEF. 2).
F -- L (IN MEF. 2).
R --> G (IN MEF. 2).
We --> G (IN MEF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase, AIP-binding, Phosphorylation.
                                                                                                                                                                                                                                              1. SIMILABILTY: TO OTHER PROTEIN TYBUSINE KINASES IN THE VALARIES?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryola, Metazoa, Chordata, Craniata, Vertebrata, Eufeicostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yaseen N.R., Blobel G.;
"Clonian ind characterization of Lomer Maryopherin betas.";
Proc. Ratl. Asad. Sci. U.S.A. 94.4451 4456(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.5%; Score 58; DB 1; Length 1809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1203 YWQRVILLILLILLILDHKKKLRSPGTI VPILFNILSEN EPLPQEG 1245
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HY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plam: PF00069; pkinase; 1.
PROSTIE: PS00109; PROTEIN_KINASE AIF: 1.
PROSTIE: PS00109; PROTEIN_KINASE_IYE: 1.
PROSTIE: PS00119; PROTEIN_KINASE_LOGE: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE Rone marrow:
MEDLINE 97.272244; PubMed 9114010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115874 FW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL: 034284; AAT50203.1;
EMBL: 149207; AA847217.1;
EMBL: 04352; AAT05330.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosine-protein kinase:
E'MAIN 425 682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPRG00719; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1PK001245;
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Matches 10; Conserv
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780
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                                                                                                                                                                                                                                                                                 D. MAIN.
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SINDING
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                                                                                                                                                                                                   1- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR, FOUND PARTICULARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enkarysta: Metazoa; Nematoda; Chromadorea; Ehabditida; Ehabditoldea;
Ehabditidae, Peloderinae, Caenorhabditis.
                                                                                 "Ran binding protein 5 (KamBF5) is related to the nuclear transport
factor importin-beta but interacts differently with RanBPL.";
Mol. Cell. Biol. 17:5087-5096(1997).
                                        Deane K., Schaeffer W., Zimmermann H.-P., Mueller U., Goerlich D.,
Prehn S., Ponstingl H., Bischoff F.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2075 DSCHAVRIMALLIMIZALARELERATIVICH ESTITILAELMEGETEVVVVCCOMT 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MAY BE INVOLVED IN THE NUCLEAR IMPORT OF REPEAT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAN CTP BINDING (BY SIMILARITY). POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.5%; Score 58; DB 1, Length 1097;
25.9%; Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Palmer S., Suiston J.,
Submitted (MoV-1994) to the EMBLyGenBank/DOBG databases.
-!- SIMILARITY: TO C.ELEGANS 28666.1 AND 28666.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               009459; 009513;
01-nvv-1997 (Rcl. 35, Created)
01-nvv-1997 (Rcl. 35, Last sequence update)
01-nvCT-2000 (Rel. 40, Last, annotation update)
HYPOTHETICAL 130.5 KDA PROTEIN C09G5.8 IN CHROMOSOME 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ES -> GF (IN REF. 1).
W, 1864AD23513F2DFT CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat; Nuclear protein.
BEAT 1.
                                                                                                                                                                                                                                                   !- SIMILARITY: BELONGS TO THE IMPORTIN BETA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Mismatches
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                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 6 HEAT REPRATS.
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                                                                                                                                                                                                                           IN THE NUCLEAR RIM AND NUCLEOLUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEAT 4.
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                                                                                                                                                                              CONTAINING RIBOSOMAL PROTEINS.
                     MEDLINE-97415587, PubMed-9271386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123629 MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIM; 602008; -.
Transport, Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL: 072761; AAC51317.1; ·. EMBL: Y08890; CAA70103.1; ·.
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1357 AA,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a lacense appeared. (See Mith. 1998 and for commercial entities a lacense appeared. (See Mith. 1998 and for commercial entities a lacense above.).
Usage by and for commercial
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PROBABLY CONTAINS THE CATALYTIC DOMAIN (BY SIMILARITY), WHILE THE
PRESENCE OF SLIGHT DIFFERENCES SUGGEST A DIFFERENT ROLE FOR
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01-0cT-1996 (Rel. 34, Last sequence update)
3n-MAY-2000 (Rel. 39, Last annotation update)
YFROGINE FROTEIN KINASE JAKI (EC 2.7.1.112) (JANUS KINASE 1) ('AK-1).
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Chang M.S., Chang G.D., Leu J.H., Huang F.L., Chou C.K., Huang G.J.,
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-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
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Actinopteryaii; Meopteryaii; Teleostei; Euteleostei; Ostariophysi;
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                                    entities requires a librage agreement (Abbilly [ www.i.b.sii or send an email to license@isb-sib.ch).
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EMBL, US3868; AAB38256.1; JOINED.
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"Tonicity-responsive enhancer binding protein, a rel like protein that
eliminists transcription in response to hyperforicity.";
Proc. Nail, Acad. Sci. H.S.A. 96;25:48-2542(1999).
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"HRAIS, a constitutively nectean HPAL protein that does not coopedate
with Fos and Jun.";
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1079 1095 NOCLEAR DEVALIZATION SIGNAL (POTENTIAL).
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054916: 095893: 090018:
004-0071-2000 (Rel. 40, Fast sequence update)
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PRINTS, PROD853 XPGRADSUPER.
PROSITE, PSOU841: XPG_1: 1.
PROSITE, PSOU842: XPG_2: 1.
PROSITE, DRA binding, Nærlear protein, Hydrolase, Nuclease:
Endonuclease.
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Best Local Similarity 24.4%: Prod. No. 4.40002
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Mammalia, Eutheria, Primates, Cafarribini, Hominidae, Homo
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SEQUENCE FROM N.A. (ISOFORM B).

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TISSUE Brain;

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This SWISS-PROT entry is copyright, it is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licensefisb-sib.ch).
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TISSUE SPECIFICITY, HIGHEST LEVELS, IN SKRIETAL MUSCLE, BRAIN,
HEART AND PERIPHERAL HIGHEST LEVELS, ALSO EXPRESSED IN PLACENTA,
LUNG, LIVER, KIDNEY, PANCHEAS, SPLEEN, THYMUS, PROSTATE, TESTIS,
OVARY, SMALL INTESTINE AND COLON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBDITE: DOES NOT BIND WITH FOS AND JUN TRANSCRIPTION FACTORS. RITMINGHT BE CAPABLE OF FORMING STABLE DIMICKS WITH DNA BLEMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELANGS TO THE REL/DOKSAL FAMILY.
CAUTION: REP.S SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 1165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ISOFORMS; A, B AND C (SHOWN HERE); MAY RE
                                                                                                                                                                                                                                              MEDINE 20029268; FabMrd 19565538;
Saudike G. Kill R. Johannsmeyer A., Graschik K.H., Schwinger R.;
"Isolatica and characterization of novel CAG repeat centaining genes
expressed in human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro: IPM000451; -.
PROSITE; PSS0254; REL_2; I TALSE_NEG.
PROSITE; PSS0254; REL_2; 1.
Transcription regulation; Activator; Auclear protein; DNA-binding;
                               Gilbert D.J., thomas S., Disteche C., Jonkins N.A., Rao A., "NPAT5: The NP-AT tamily of transcription factors expands in a new
                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, PLAYS A ROLE IN THE INDUCTBLE EXPRESSION OF DENES, REGOLATES HYPERFOUNCILY INDUCED CELLUIAR ACCOMULATION OF
Pakeman A S , Copeland N G ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E > D (IN REF. 5).
MW: A68C68088DABF69E CRC64;
                                                                                                                     Cold Spring Harb. Symp. Quant. Biol. 64:517-526(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MISSING (IN ISOFORM A). MISSING (IN ISOFORM B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLY-GLN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: NUCLEAR.
   Lopec-Rodriquez C., Aramburu F.,
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                                                                                                                                                                                 SEQUENCE OF 675 1531 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                      DNA Seq. 10:1-6(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative splicing.
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EMBL: 297015; CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSMOLYTES.
                                                                                                                                                                                                                    TISSUE-Brain;
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                                                                                               direction.
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123 THEATHGOSELACVETHETE ETVPVEQUEETUNCEHEWPWEDPVECSOVPLANOTEETING 192
                                                                                                                                                      496 MELFHÖNHLIVKVPPYHDÖH ITLIPVSVGIYVVTNAGKSHDVQPFTYTPDPAAAGALNVNV 555
                                                          n; daps
0.5%; Score 5%; DB 1; Length 1531;
26.4%; Pred. No. F.Ge+02;
                                                        39; Indels
                                                          14; Mismatches
                                 26.495
                                   Rest Local Similarity 26.4
Matches 19; Conservative
            Querry Match
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This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no no way modified and this statement is not removed. Usage by and for commercial or send an email to licensewish-sib.ch).
                            01-Nov-1991 (Pcl. 20, Last sequence update)
GENOME POLYPROTEIN (CONTAINS: COAT PROTEINS VP1 TO VP4: CORE PROTEINS P2A TO P2C. P3A: GENOME-LINKEN PROTEINS VP1 TO VP4: CORE PROTEINS (P7 3 4 22 28) (PROTEASE 3C) (P3C); RNA-DIRECTED RNA POLYMEKASE P4D (PC. 27.7.48)].
                                                                                                 Poliovirus type 2 (strain W-2).
Vitubos, ssRNA positivo strand viruses, no DNA stage, Dicornaviridae;
Enterwirus
                                                                                                                                                                             PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polyprotein; Coat protein; Core protein; Transferase;
EMA linested BNA polymetase; Epstedase Thist protease; Myristate.
CHAIN 2 69 COAI PROTEIN VP4 (PIA).
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                                                                                                                                                                                                                                                                                                           -! - SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C3.
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PROTEASE (POTENTIAL).
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CORE PROTEIN 2B.
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        PPT: 2205 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00548; Cys protease-3C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COAT
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D00625; RAA00516.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00447; Pico_P2A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01552; Pico_P2B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           interpro; IPROUO081; -.
Interpro; IPROUO199; -
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1746
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2205 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        P03299; 1POV.
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                                                                                                                                                                       SECTIONS FROM N A
                                                                                                                                                                                                                                                                                        VP3, AND VP4.
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ACT_SITE
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POLG_POL2W
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the Burgeau Biolanormatics fastitute. There are no restrictions on its aby new footh instructions as its centent is in no way modified and this stremment is not removed. Usage by and for commercial entities reprint a new secondary commercial or send an email to hearselish spice).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Mapping of Sequences required for mouse neurovirulence of poliovirus in year. In a Lansing."

1 VIDEL 1021818 525(1985).

1 FUNCTON: FOR EXTREMEDIA IS A FOOTBASE THAT CLEAVES AT CHAIN VAIG. 2018 IN THE POLYBORINE. IN MAY BE A SYSPERIAL BECTASE.

2 SHEARTH FOR PARTIES OF MOUSED OF 60 FOOTBASE. INTIE, EACH FOR MAY BE A SPERIAL PARTIES.
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of JAN 1999 (Rott, 05), Last sequence applate)
is LECTRON (Rott, 07), Last annotation update)
Obeyon (Rott, 07), Last annotation update)
                                                                                                                                                                                                                                                                                                                             6.2. TAVISTGATBI GZYEST GYGTERY JERTRESTS VIGETTARGAS VALITIVISK AFTREASKL, 68.2
                                                                                                                                         01 02018
                                                                                                                                                                                                                   451 GUMUSOMBOM VNIGAMBBETAELSED VEGFEREAVIAED GAG VOORDAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses: ssPNA positive-strand viruses, no DNA stage; Picornaviridae;
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PIME SPECIFIC ENCYMALITY CLEAVAGES IN VIVE YIELD MATSRE PROTEINS.
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PNA directed FNA pelgmerase; Hydroluse; Thiol profess; Myristale,
CHAIN 2 - See See Seat BEOTEIN VIA (PIA).
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                     (*M. Schre Sm. 18 D. Length 2205;
hitty waster Prod. No. naeroz:
hasernature (%) Mismatches 48; Indols
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PIRO ALOSOTO INNYSE.
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InterProj IPPOSISAZ; -
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This SWISS PKGT entry is copy iddt. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation .
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                                                                                                                                                                                                                                                                                                                      481 TSLALSLEHHTAFVRILAMMHTKKIMKTSKEDVEDEFIKBAVLAKLIBANIDVVLSAISA 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Titus M.A., Kuspa A., Loomis W.F.; "Discovery of myosin genes by physical mapping in the typestellum."; Proc. Natl. Acad. Sci. U.S.A. 91:9444-9450(1994).
-!- FUNCTERN MYOSIN IS A PROJEIN HALL BINDS TO ACTIN AND HAS ALFASE ACTIN. THAT IS ACTIVATED BY ACTIN.
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J. Muscle Res. Celi Motil. 17:412-424(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           novel, dimexic, unconventional myosif with a feery chain molecular mass of 258 Kha.";
J. Biol. Chem. 271:7120-7127(1996).
                                                                                                                           FICCREATIN 3C, RNA POLYMERASE 3D,
                                                                                                                                                                                                                                                      0.5%; Score 58; DB 1; Length 2207;
22.2%; Fred. Bo. 9.2e+02;
ive 15; Mismatches 48; Indels
                                                                                                                                                                        CORE PROTEIN 20.
CARL FROTEIN 3A.
SENOME-LINKED PROTEIN VIG.
COAT PROTEIN VP2 (FIB).
COAT PROTEIN VP3 (FIC).
COAT PROTEIN VP1 (FID).
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Eukaryota: Mycetozoa: Dietyostellidu: Dietyostellum.
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40, Last annotation update)
                                                            NAME PROTEIN 2B.
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                                             PROTEASE ZA.
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01-00T-2000 (Rel.
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modified and this statement is not removed. Usage by and for commercial
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Ephydroidea: Drosophilidae; Drosophila.
WGB:_raxib 7244,
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-!- FUNCTION: RECEPTOR FOR AN EXTRACELLULAR SIGNAL REQUIRED TO INSTRUCT A CELL TO DIFFERENTIALE INTO A R7 PHOTORECEPTOR. THE LIGAND FOR SEVIEW SEVERIESS. (PRIDE OF SEVENLESS) PROTEIN.
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Myosin; Repeat; ATP-binding; Calmodulin-binding; Actin-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%; Score 50; DB 1; Length 2245; 20.7%; Pred. Rc. 9.30-02; Lize 20; Mismatches 49; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
SEVENLESS PROTEIN (EC 2.7.1.112).
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Pfam; PE00612; IQ; 3.
Pfam; PE00063; mycx:h_head; 2.
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PROSITE, PS50096; 10; 1.
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UMBL: U35322; AAA79858.1; ··
HSSP; P08799; IMNE.
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Gs 18; Conservative
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                                                                                 -!- SIMILARITY: CONTAINS 7 FTRHONETTIN TITE THE STANDING RECTON -!- CAUTION: SHOLEAF WHETHER THE POTENTIAL HEMBRANE DOMAIN IN THE NEEP THE N-TEPMING IS PRESENT AS A TRANSMEMBRANE DOMAIN IN THE NEEP THE N-TEPMING IS PRESENT AS A STRANGE, SHOUGHUE.
                                         SIMILARITY, BELONGE TO THE INSOLIN PEREFTOR FRACEY OF TYPOSINE-PROTEIN KINASES, SEVENLESS SUBFAMILY.
SIMILARITY: CONTAINS 7 FIRRONECTIN TYPE III-LIKE DOMAINS.
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BOMAIN 1 2139 EXTRACELLULAR (POTENTIAL).
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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-:- FUNCTION: PROTEASE NS3 IS RESPONSIBLE FOR THE CLEAVAGE OF NS2-NS4A, NS4A-NS4B, NS4B-NS5A AND NS5B.
-:- FUNCTION: NS4A FORMS A COMPLEX WITH NS3 AND IS ESSENTIAL FOR THE
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-1- FÜNCTION: NSSA TA ENAA-NPERNDENT FANA POLYMERASE THAI PLAYS AN
ESSEMILAL ROLE IN THE VIRUS REPLICATION.
-1- SUBGNIT: THE VIRION OF TH'S VIRUS IS A NUCLEOCAPSID GOVERED BY A
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"Hepatitis C virus NS3 RNA he lease domain with a bound
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MEDLINE-97331322; Pubmed-9187654;
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BAY ACTOR OF P. Olson P.F. (North M. Froll I H M. Taylor R., Actor D. Olson P.F., Olson B.R., Burgeson R.E., Actor D. P. Olson P.F., Olson B.R., Burgeson R.E., Actor D. Chappillad M.P.F., Olson B.R., Burgeson R.E., Actor D. Carrock D. P. Olson B.R., Burgeson R.E., Actor D. Carrock D. P. Olson B.R., Burgeson R.E., Complete primary structure of two splice variants of cellaqon XII, and alpha 1(XI) collaqon (COL12AI), alpha 1(IX) and alpha 1(XII) collaqon (COL12AI), alpha 1(IX) cellaqon (COL12AI), alpha 1(IX) cellaqon (COL19AI) in buman chromosome 6d12-413."; and alpha 1(XIX) cellaqon (COL12AI), alpha 1(IX) cellaqon (COL12AI), alpha 1(IX) cellaqon (COL12AI), alpha 1(IX) cellaqon (COL19AI) in buman chromosome 6d12-413."; and alpha 1(XIX) cellaqon (COL12AI) in buman chrominer The Firm Collagon Interaction of the Associate May be controlated to the Firm Collagon North Firm Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Collagon North Coll
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EXTERNEL; PSSOCAL VINCENDENTIAL BALFIX; Connective tissue; Pepcat; Hydroxylation; Cell adhesion; Collagen; Signal; Glycoprotein, Alternative splicing STGNAL.
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                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PAPITAL SEQUENCE (LONG AND SHORT FORM).
                                                                                                                                                                                                Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                       COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.
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(5) Syste (6) 10k D. Dougth (5) 60;
(6) Prod. No. 1140(40)
(10) Mismatches (5) [146]8
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Prime Protocol, AIP-synt_DE: 1.
Hydroldso: AIP-synt_DE: 3.
Hydroldso: AIP-synthesis; CF(1): Hydroden fon Itansport.
SEQUENCE 121 AA: 13135 MW: ZAESCCASSMTHCRDO CRO54:
                                               01-071-1996 (Rel. 34, Greated)
63 087-1996 (Rel. 34, Hast sequence update)
80 MAY 2000 (Rel. 34, Last amotation apdate)
81 SYNTIAGE EFFICEN CHAIR (BC 3.6.1.44).
ATPC OR EVI311 OR MICY373.31.
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01-NeW-1995 (Ref. 42, Last annotation update)
Alt STATHASE EFSILON CHAIN (EU 5.6.1.34).
ATPC:
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                                                                                                                                                                                                        Mycrobacterium tuberculosis.
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                                                                                                                                                                        SCHUMTT F TYPE ATPASKS HAVE 2 COMPONENTS, CF(1) THE CATANYLE. CORE - AND CF(0) - THE MEBRANE PROTON CHANNEL, CF(1) HAS FIVE SUBUNITS ALPHA(3), HETA(3), GAMA(1), DELTA(1), EPSTLON(1), CF(0) HAS THEE MAIN SCHAUTS, A, B AND C. SIMILARITY - RELOADS TO THE ATPASE EPSTLON CHAIN FAMILY.
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                          Smith D.R., Robison K.;
Submitted (SEP-1994) to the EMBL, Abertamb, April databases
-!- FUNCTION: PRODUCES ATP FROM ADE IN THE PRESENCE OF A PROTON
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Venter J.C.;
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Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.5%; Score 57; DB 1; Length 124; 30 0%; Pred Nr. 20
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Hydrolase: ATF synthasis, CF(1), Hydrogen ion transport.
SEQUENCE 124 AA: 13685 MW; 0596F88E83DE6078 CRC64;
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RRMJ OR FTSJ OR HI1334.
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01-N:V-1995 (Rel. 32, Last sequence update)
01-0CT-2000 (Rel. 40, Tast annetation update)
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MEDLINE 95350630, PUBMUJ 7542800,
                                                                                                                                      GRADIENT ACROSS THE MEMBRANE
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Matches 10, Conservative
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Science 269:196-512(1995).
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SPOURNCE PROM N.A.
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P45162;
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Eukaryota, Fongi, Ascomycota, Saccharomycotica, Saccharomycotes;
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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Rel. 38, Last amondation update)
24.5 KEA PEOPEN IN 17V2 ARRIT INTERSENIC REGION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FP 1- Length 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             na 1; lemyth 214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hunt S., Rowman S., Barrell B.G., Bajandroam M.A.;
Submittel (MAY-1995) to the EMBL, Genkonk, Dubkl databases.
                                                                                                                                                                                                                                                                                                                                                                                                                    8BE4B961900408FP (*P064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                   TRNA processing, Transferase, Methyltransferase.
Segunnes วิติศี AA, 234ติพี MW, กานโรโคคน112คคิด
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1940, Source 7 Feb. Local Similarity 52.5%; Pred. No. 71; Pred. No. 71; Pred. No. 71; Pred. 10: Conservative 6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE 213 AA, 24604 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             518 IKEAVLARLGDDNIDVVLS 536
                                                                                                                                                                                                                                                         EMBL; U32812; AAC22978.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 VINALLAFVGEDKVDVVMS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.68;
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                                                                                                                                                                                                                                                                                                                 Interpro: IPR002877; -
Pfam; PP01728; FtsJ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STFAIN-S288C / AP972;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_Tax1D-4932;
                                                                                                                                                                                                                                                                                          TIGR; HI1334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL
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Q04477;
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this SWISS-PPOL outry is expyright. It is produced through a collaboration between the SWISS Institute of Holintommatics and the EME, outration on the burdens of Holintommatics and the surface are no restricting in its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for examercial outlities of the examercial or send an email to licensee isb sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choisne N., Robert C., Brottier P., Wincker P., Cattollog L.,
Attinction F., Surin W., Weissenberg L., Mowes H.-W., Endd S.,
Attinction F. Mayor F. Y. Lordine L. Mowes H.-W., Endd S.,
Schmitted (Mak good) to the EMBL, Serson Attinction Control of the PROTEIN SAMELY BOUNTION: THE PROTEIN SAMELY TO ANDITIONAL PROTEINASE COMPLEX
WHEN IS CHRANCERIZED BY ITS ABILITY TO CLEAVE PEPTINGS WITH ARG,
PHE. 178. LED., AND GJ. AND GJ. AND GJ. AND ALE AND MESTINGS GROUP AT BEING GROUP AT BUTCH AND ALLAND MESTINGS AND AND ALSO AND A PROTEIN BESTINGS AND AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A STREET HEAD AND A ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Molecular characterization of a beta-type proteasome subunit from Arabdopsus thallons co-expressed at a high level with an alpha-type proteasome subunit carly in the cell cycle."; else of the cell cycle.";
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11 DEVELOPMENTAL STATE: EXPRESSED AT MAXIMAL LEVELS AFTER FIRST DAY
                                  of oct 2000 (Ref. 40, fast annotation update)
PROTEAS WHI PERSONE BUTA TYPE 1 (B) 3.4-55.46) (203 PROTEASOME ALPHA
SHRINL F) (PROTEASOME COMPONENT C5) (TAS-F22ZFAFP98).
PRET OR 140.21_2.00.
                                                                                                                                                                Arabidopsis thaliana (Monse-ear cress).
Enkaryota: Viridiplantae: Embryophyta: Fracheophyta: Spermatophyta:
Magnollophyta: eudicotyletons: core endicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIJNE 98278790, pubmed 9611183;
Fu H., Loellind J.H., Areadt C.S., Bochstrassor M., Vierstra R.D.;
"Molecular organization of the 20S proteasome gene family from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BEDONIS TO PEPTIDASE FAMILY THE ALSO KINWA AS THE PROTEASOME B-TYPE FAMILY.
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Proteasome: Hydrolase; Protease.
SEUJENTE - 223 AA; 24e44 MW; PROSOU79P353D4CO CRC64;
oj ett.zoon (Rel. 40. Last sequence update)
ol ett zoon (Rel. 40. Last annotation urbate
                                                                                                                                                                                                                                                                Brassicales: Brassicacéae, Arabidopsis.
N'BL_TaxID (702)
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MEDLINE 95078945; Pubmed 7987412;
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EMBL: AL162295; CAB32686.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            keneties 149:677-692(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thallana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN 'V. CHUMBIA;
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This SWISS-PROT entry is empyright if is produced through a collaboration between the SWISS Institute of Bioinformatics and the FWBL outstaining the European Bioinformatics Listitute. There are no restrictions on its use by non-profit institutions as long as its content, is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified and this statement is not removed. Usage by and for commercial children requires a license of removing (ver Virg.) *** [4] of the law and or send an email to licenserish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bult C.J., White O., Olsen G.L., Zhou L., Fleischmann K.D., Sutten G.S., Blake J.A., Fitzerald L.M., Chyton F.A., Godayne J.D., Seitten G.S., Blake J.A., Fitzerald L.M., Chyton F.A., Godayne J.D., Owerbeck F., Kirkness F.F., Weinstewek E., Marrier L.M., Glodek A., Scott J.L., Geoghagen N.S.M., Weidman J.E., Fuhrmann J.L., Nanyen D., Utterback T.B., Kelley J.M., Feterson J.D., Sadow F.W., Hanna M.C., Cotten M.D., Eckerts K.M., Hirst M.A., Kaine K.P., Heredovsky M., Klenk H. P., Presert C.M., Szith H. O., Warser C.R., Venter J.G.,
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Site
                                                                          1491 ESQEEMLQVFNVETHISKQLRHFKFLSVSFMSQLLSSNNFLKKVVESGGPE1LKGLEE 1548
                                                                                                  0.5%; Score 57; DB 1; Length 259; 29.3%; Pred. No. 93;
                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Metharococcales; Methanococcacae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archaea; Euryaichaeota, Methanococcales, Methanocommander
0.5%; score 57; DB 1; Length 223;
                                  30; Indels
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SEQUENCE 259 AA; 29192 MW; 50528A176B1C2D36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1825 AIKKTYKQIEKNWKNHMSPFWSILQFHIGXMKKEELISHQS 1865
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01-NOV-1997 (Rel. 35, Last secuence update)
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01-NOV-1997 (Ref. 35, Last annotation update)
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                                ii; Mismatches
                    Fred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=JAL-1 / DSM 2661 / AIRC 43067;
MEDLINE-96337999; PubMed-8688687;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
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              Best Local Similarity 29.3%;
Matches 17, Conservative 1
                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN MJ0500.
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                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                   Methanococcus jannaschii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methanococcus jannaschii.
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Best Local Similarity
Post 12, Octaberra
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-2190;
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Query Match
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METAL 114 114 2
SEQUENCE 315 AA; 34708 MW;
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    CLYCOPROTEASE FAMILY.
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hes 15; Conserv
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Q04866;
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                                                                                                       Bull CJJ, White O., Olsen GJJ, Zhou L., Fleischmann R.D., Suffor C G. Rlaber LA. Filt-predd LM. Clayton P.A., Goragne J.S., Selfon C G. Rlaber T.A. Filt-predd LM. Clayton P.A., Goragne J.S., Overboek R., Kirkness E.F., Weinstock K.G., Merrin J.M., Glodeh A., Scott J.L., Googhagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D., Bliterbark T.P., Kalan M. Hanna M.C., Gotton M.D., Roberts K.M., Hurst M.A., Kaline R.P., Brodewsky M., Klenk H.-P., Frasor C.M., Smith H.O., Woose C.R., Swith H.O., Woose C.R., Swith H.O., Woose C.R., Venter J.G., "Complete groome sequence of the methanogenic archaeon, Methanocenus
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33.3%; Pred. No. 1.1e+92;
Fre 8, Mismatches 16, Indels
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30-MAY-2000 (Rel. 39, Last annotation update)
PROBABLE O-STALOGIYCOPECTEIN ENEOPERTIDASE (RC 3.4.24.57)
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Matches 12, Conservative
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SEQUENCE 295 AA; 3
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  NCB1_Tax1D-2190;
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-i. Encorton: Confere A. Agona, Distribution OF CHAIN LENGTH ON THE CANTIGEN COMPONENT OF LIPOPOLYSACCHARIDE (LPS). GIVES RISE TO
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01-FEB 1994 (Rel. 28, Last Sequence update)
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CHAIN LENGTH DEFERMINANT PROTEIN (POLYSACCHARIDE ANTIGEN CHAIN
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28.8%; Pred. No. 1.2c+02;
Live 10; Mismatches 27;
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MEDLINE-93225815; PubMed-7682279;
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MEDLINE 92355404, Fubmed 1379582,
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PKINTS; PKUU/89; OSIALOPTASE.
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## Wishotor R., Harqrayo P.A., McDowell J.; "Alliantor rhologsin: sequence and biochemical properties."; Exp. Eye Post. 61:560-578(1995). MEDIJNE 96262274; Pubmed 865450); Smith W., Adamus 51, der Wel H., limmers A., Palczewski K., LINNER Retinat

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PRINTS; PRO0579; HODODSIN.
PROSTITE: PSG0257; G\_PROTEIN\_RECEP\_F1\_1: 1.
PROSTITE, PSG0262; G\_PROTEIN\_RECEP\_F1\_2: 1. (POTENTIAL). 3 (POTENTIAL) BY SIMILARITY (POTENTIAL) 4 (POTENTIAL) EMBL; U23802; AAC59737.1; -. GCRPb; GCR\_1250; -. InterPro; IPR000276; -. InterPro; IPR0U372; -. InterPro; IPR0U760; -. Prom; PF00001; 7tm\_1; 1. PRINTS; PR00237; GPCRRHODOPSN. 39347 MW; PROSITE; PS00238; OPSIN; 1. 309 61 73 58 110 352 AA; 322 323 37 253 DOMAIN TRANSMEM DOMAIN TRANSMEM DISULFID SEQUENCE TRANSMEM FRANSMEM TRANSMEM CARBOHYD CARBOHYD RANSMEM **LKANSMEM** BINDING DOMA I N DOMA I N DOMAIN DOMAIN MA WELL DOMA!N Lipin LIPID SOUTH THE TENT THE TE

Gabs .. = 0.5%; Score 57; DB 1; Length 352; 50.0%; Pred. No. 1.3e-02; Even 4; Mismatches 6; Indels Query Match 0.5%; Best Local Similarity 50.0%; Conservative 10, Matches

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RESULT 192 OPSD\_PETMA

01-N.VV-1997 (Rel. 35, Greated) 01-N.VV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 35 3 AA. PK1; STANDARD; OPSD\_PETMA RHODOPSIN. RHO. 

Petromyzob marinus (Sea lamprey). Eskaryota, Metazea, Chordata, Graniata: Vertebrata: Hyperoarlia, Simos: Petremyzentidae: Petromyzon. NCB1\_Tax1D=7757; Petromycont:

INE-97354287; PubMed-9210581; SEQUENCE FROM N.A.

"Molecular evolution of the rhodopsin gene of marine lamprey, Petromyzon marinus."; Gene 191:1-6(1997). Zhang H., Yokoyama S.

FUNCTION, VISUAL PIGMENTS ARE THE LIGHT ARSARING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, CONVELENTLY

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SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the function Bioinformatics institute. There are no restrictions on its mass by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities pequipes a present (See http://www.isb-sib.ch/announce/
                            PTM: SOME OR ALL OF THE CARBOXYL TERMINAL SER OR THE RESTOURS MAY
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N-LINKED GLOBAC. . .) (BY SIMILARITY).
N-LINKED (GLOBAC. . .) (BY SIMILARITY).
RETINAL CHROMOPHORE.
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Photorocoptor; Retinal protein; Transmembrane; Glycoprotein; Vision;
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                                                                SIMILARITY: BELONGS to FAMILY I of G-PROTEIN COURLED RECEPTORS.
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PALMITATE (BY SIMILARITY).
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                 SUBJETLIGIAR LOCATION: INTEGRAE MEMBRANE PROTEIN.
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5 (POTENTIAL).

    (POTENTIAL).

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PRINTS: PROS759; REMEMBININ.
PROSTITE: PSOD247: G_PRODEIN_RECEP_FL_D_1.
PROSTITE: PSSO262; G_PROTEIN_RECEP_FL_Z, 1.
                                                                                                                                                                                                              or send an email to license (isb-sib.ch).
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                                                 BE PHESPHORYLATED.
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P10.885; 01-MAR-1989 (Rel. 10, Created) MAR-1989 (Rel. 10, Last sequence update) 15-J0L-1999 (Rel. 38, Last annotation update)

PRT;

STANDARD;

GLIA\_WHEAI

E8555

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                                                                                                                                                                                                                                                                                                                                                                                                      VISCO-FLASTIC PROPERTY OF WHEAT DOUGH.
SUBUNIT: DISULFIDE-BRIDGE LINKED ASSERBISTES.
MISCELLANEOUS: GLUTENINS ARE CODED BY SEVERAL GENES ON EACH OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1145 OTVSSVPROTSVNARQVPTELEPPPRARPLOTVOORPPORMOORRSODLESVOEVOGSYW 1204
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Viruses, dsDRA viruses, DO ENA Stakk, Adenoviridary Mirrardenovirus.
NCHI_TaxID-28292;
                                                      Eskarycta; Viridiplantar; Embryophyta: Tracheophyta; Spermatophyta;
                                                                                                                                                                                                     Sprengel J., Schmitz R., Heuss Neitzel D., Zock C., Doeifler W.; "Nucleotide sequence of human ademovirus type 12 DNA: comparative
                                                                                                                                                                                                                                                                                                                                                                         PROTEIN OF WHIME ENDUSPERM, THOUGHT TO BE RESPONSIBLE FOR THE
                                                                                   Maqnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Friticeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.5%; score 57; DB 1; Length 356;
19.1%; Pred. No. 1.4e+02;
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Seed storage profeix, Repeat, Mulliatene family; Signal.
GLOTENIN, TOW MOLECULAR WEIGHT SUBUNIT PRECURSOR. Trillicum aestiyum (Wheat).
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01-NOV-1997 (Pol. 35, last annotation update)
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J. Virol. 68:379-389(1994).
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Rest Local Similarity
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InterPro: 1PR001926;

and the EMBL outstation

between the Swiss institute of Biointormatics

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TO PIN'TENE THE BELA SUBURE IS REGENERABLE FOR THE SYNTHESIS

OF LIPPETOPHAN FROM THOSE AND L'SERINE (BY SIMILARITY).

ALABATHE ATTIVITY IN SIRENCE (1000), 4-YI)GLYCEROL 3-PHOSPHAFE

LIPPETOPHAN GLYPERALDEHYDE (-FBGSPHALE + H(2)0).

PATHWAT: PYELOWAL PHOSPHAFE (BY SIMILARITY).

PATHWAT: LAST (-FFTH) SIEP IN BUSYNIHESIS OF INYFIDEMAN.

PATHWAT: LAST (-FFTH) SIEP IN BUSYNIHESIS OF INYFIDEMAN.
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Local Similarity (1.66) Prod. N. 1.46-92;
os 18; conservative 5; Mismatches 4; Indels
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85 MAY-2050 (Feel, 9) Last ammoration update)
TRYPO-PHAN SYNTHASE BELA FHAIN (E1 4.2.1.20).
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of NeV 1997 (Red., 35, Last seep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Characterization and primary structures of bovine and porcine hypoxine-binding alobulin."; submitted (NCV 1959) to the PMH, Chemistry Jatahases. in FONCTION, NAJOR THYNGIE HERMONE TRANSPORT PROJEIN IN SERUM (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER; FOUND IN PLASMA.
-i- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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Mammalia, Butheria, Cetartiodaetyla, Ruminantia, Pecora, Bovoidoa,
                     Pfam: PF00291: S_T_dehydratase: 1.
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PRESTE: PS00168: TRP.SYNHBASE_REIA: 1.
PFF4-pshan biosynthesis: Pyrfdoxal phosphate: Lyase.
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SEQUENCE: 393 AA: 42684 MW: 3370AIB4D5B89371 CRF94;
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HEYROXINE-BINDING GLOBULIN PRECURSER (14-BINDING SLOBULIN).
                                                                                                                                                                                                                                                                   0.5%; Score 57; DR 1; Length 493; 44.4%; Yed; No. 1.56+02;
Live 9: Mismatches 12; Indels
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Matches 14; Conservative 12; Mismatches
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-!- SUBTELLULAR LOCATION: EXTRACELLULAR.
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34 34 N-1

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411 AA; 45017 MW; 8
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PRINIS; PR00780; LEUSERPINII.
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Matches 11: Conservative
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InterPro; IPR000295;
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09TT 46;
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                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Biointormatics and the LMBL outstation
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Viruses; dsbNA viruses, no KNA stage; Adenoviridae; Mastadenovirus.
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                                                                                                                                                                                                          dsiona viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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 136 AQUAPUERFULDIVENTET EVESTDESINSAAQQETINSHVERQTKORTVOLIQ 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.5%, Score 57; DB 1; Length 415;
29.8%; Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 AA; 46995 MW; B82845AFB9E7C20A CRC64,
                                                                                                                                                                                                                                                                                            Koberts R.J., O'Neill K.E., Yen C.E.;
"DNA sequences from the adenovirus 2 genome.";
J. Biol. Chem. 259:13968-13975(1984).
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01-NoV-1997 (Ref. 35, Last annotation update)
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                                                                                                                         21-JIII-1986 (Rel. 91, Created)
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es 17; Conservative
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                                                                                          STANDARD:
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P04496;
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ENGINEER
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between the Swiss Institute of Bioinformatics and the EMBL outstaffor
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Histidin biosynthesis; Multifunctional enzyme; oxidoreductase; NAU.
SEQUENCE 434 Aa; 46533 MW. 76F07AC33439B1E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2006 DYQHELSKIJPAXALMMELYEYQLEHIFLOGEPPPYPYPPITLI DOTAQPSVAMADUSTM 2062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kanekor T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Bokandi T., Matsura A., Maraki A., Yakarusi N., Matsura S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yashada M., Pubata S., "Sequence analysis of the qenome of the unicellular eyanobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION, THIS PROFÉIN IS CONCIDENED AS A BIFCHCHICHGE ENEXME, POSSESSING TWO ACTIVE SITES, ONE AN ALCOHOL DEHYDROGENASE AND THE OTHER AN ALDEHYDE DEHYDROGENASE (BY SIMILAKITY).
-i- CATALYTIC ACTIVITY, L HISTIDINOL + 2 NAD(+) + L-HISTIDINE +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: TENTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Symechocystis sp. (strain PCC 6803).
Bacieria: Cyanobacteria: Chromococalos Symechocystis.
NCBI_TaxID-1148:
                                                                                                                                                                                                                                                                                                                                                                                                                   415 AA; 47059 MW, DA51834066BA0129 CRC64;
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36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISTIDING, DEHYDROGENASE (EC 1.1.1.23) (HDH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE 97061201; PubMed 8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pram; PF30815; Histidinol_db; 1.
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                                                                                                                                                                                                                                                                   EMBL; M73260; AAA96406.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sest Local Similarity
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0.5%; Score 57; DB 1; Length 444;

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Fred. No. 1.7e+02; 4; Mismatches 37; Indels

Host Local Similarity 23,9%; Pr Matches 15; Conservation 14;

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1705 EMOSASQANTRUISLEETLATITADEVITPATERTYRQTERNWENHWIDEMSTLOEHTOX 1854
                      Gaps
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"Isolation and characterization of a recombinant heat shock protein of Aspergillus fundadas.";
"Aspergillus fundadas.";
"I Albergy Clin. Immunol. 91:1024-1030(1993).
                                                                                                                                                                                                                                                                                                                       Asperaillus Tumiquius (Sartorya fumiquia).
Sakuryota i Pundi: Assemyesta: Pezizamyentina; Eurotiomyeetes;
Eurotiaiss: Triebosomaceae; mitosporie Triebocomaceae; Asperaillus,
NFBE, Exils 5045;
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HEAL SHOCK PECHETM HSPI (15 KDA LOE BINDING PROFILM) (FRACMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                         SECTION TO PROBE MILE.
Kurup V.P., Banerjee H.;
Submitted (MAR 1987, 1988, 1988, 1988 H.), 1987 H. abaess.
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Tebrime: 270 sec
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MEDLINE 93260199; Pubmed 8491935;
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Ptam: PF00183; HSP90; 1.
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